

Genome version 5.1.3
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OM protein - protein search, using SW model

Run on: September 30, 2003, 10:07:04, 1 Search time 41.0833 Seconds
(without alignments)
42.494 Million cell updates/sec

Title: US-09-787-443-1
Perfect score: 11
Sequence: 1 ASKKPKRNIKA 11

Scoring table: CLICG
Gapop 60.0, Gapext 60.0

Searched: 1107863 seqs, 154726574 residues

Word size: 3

Total number of hits satisfying chosen parameters: 27822

Minimum hit seq length: 8
Maximum hit seq length: 15

Post-processing: Listing first 500 summaries

Database: A_Geneseq_19Jun01.*

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- 2: /SIDSI/qcqdta/qeneseq/qeneseq-emb//AA1981.DAT.*
- 3: /SIDSI/qcqdta/qeneseq/qeneseq-emb//AA1982.DAT.*
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- 23: /SIDSI/qcqdta/qeneseq/qeneseq-emb//AA2002.DAT.*
- 24: /SIDSI/qcqdta/qeneseq/qeneseq-emb//AA2003.DAT.*

red. No. is the number of results produced by choice to have a score greater than or equal to the score of the best being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DE	ID	Description
1	11	100.0	11	21	AAV85527	NCAM Iq1 binding p
2	11	100.0	11	23	ABG69429	Human neural cell
3	6	54.5	11	21	AAV85534	NCAM Iq1 binding p
4	6	54.5	11	21	AAV85537	NCAM Iq1 binding p
5	5	45.5	11	21	AAV85534	NCAM Iq1 binding p
6	5	45.5	14	22	AAV855118	Human peptide 403
7	4	36.4	8	15	AAK65518	peptide 3441 seq
8	4	36.4	8	16	AAK65519	peptide 3441 seq
9	4	36.4	8	22	AAV855126	SV40 V12 epitope 5

10	4	36.4	9	16	AAV78787	Rapla (172-180) pe
11	4	36.4	9	21	AAV32302	HIA A24 binding TA
12	4	36.4	9	21	AAV32325	HIA B7 binding TAD
13	4	36.4	9	21	AAV32328	HIA B8 binding TAD
14	4	36.4	9	22	AAV68984	Human TALG-12 immu
15	4	36.4	9	22	AAV69007	Human TALG-12 immu
16	4	36.4	9	22	AAV69010	Human TALG-12 immu
17	4	36.4	9	23	ABV74680	Transcription fact
18	4	36.4	10	12	AAV10698	LHRH analogue 2
19	4	36.4	10	12	AAV12068	Gonadotropin relea
20	4	36.4	10	18	AAV32642	Human platelet gly
21	4	36.4	10	19	AAV73155	Human amphirequlin
22	4	36.4	10	19	AAV71771	Mimotope capable o
23	4	36.4	10	22	AAV43286	Mycoplasma genital
24	4	36.4	10	22	AAV94727	Human complementar
25	4	36.4	10	22	AAV95284	Human complementar
26	4	36.4	10	22	AAV96370	Human complementar
27	4	36.4	10	22	AAV96927	Human complementar
28	4	36.4	10	22	AAV96929	Human complementar
29	4	36.4	10	22	AAV96959	Human complementar
30	4	36.4	10	22	AAV85248	Saccharomyces cere
31	4	36.4	10	22	AAV85595	Saccharomyces cere
32	4	36.4	10	22	AAV17417	Target cyclic pept
33	4	36.4	10	23	AAV17417	Human respiratory
34	4	36.4	11	19	AAV53153	PTP activity deter
35	4	36.4	11	21	AAV88555	NCAM Iq1 binding p
36	4	36.4	11	21	AAV88556	NCAM Iq1 binding p
37	4	36.4	11	23	ABV74833	Nuclear protein nu
38	4	36.4	12	19	AAV20609	Human neurofilamen
39	4	36.4	12	21	AAV19494	Antigenic peptide
40	4	36.4	12	23	AAV99715	Human Ghrelin (C-t
41	4	36.4	12	23	AAV17334	Recombinant transp
42	4	36.4	12	23	AAV17424	Human respiratory
43	4	36.4	12	23	AAV74843	Nuclear protein nu
44	4	36.4	13	12	AAV11344	Anti-rhodopsin mon
45	4	36.4	13	15	AAV47395	PDGF-activity-disp
46	4	36.4	13	20	AAV95068	Putative HS bindin
47	4	36.4	13	21	AAV08046	Signal peptidase 1
48	4	36.4	13	21	AAV08047	Signal peptidase 1
49	4	36.4	13	21	AAV08048	Signal peptidase 1
50	4	36.4	13	23	AAV15448	Rat C/RAP-beta pep
51	4	36.4	13	23	AAV97272	Phosphorylated epi
52	4	36.4	13	23	AAV21387	S. cerevisiae 3-is
53	4	36.4	14	21	AAV35908	Peptide conveying
54	4	36.4	14	23	AAV12044	Human Sox-11 trans
55	4	36.4	15	18	AAV29482	Peptide #3 derived
56	4	36.4	15	18	AAV29483	Peptide #4 derived
57	4	36.4	15	18	AAV14672	p53 activating pep
58	4	36.4	15	20	AAV36272	KDR/Flk-1 targetin
59	4	36.4	15	20	AAV34045	Histone H1S 3 deri
60	4	36.4	15	20	AAV34046	Histone H1S-3 deri
61	4	36.4	15	21	AAV08340	Signal peptidase 1
62	4	36.4	15	21	AAV57143	Human histone H1 p
63	4	36.4	15	21	AAV57144	Human histone H1 p
64	4	36.4	15	22	AAV09222	Unique region #2 o
65	4	36.4	15	23	AAV01171	Human SHARP 1 tran
66	4	36.4	15	23	AAV04245	Caspase cleavage s
67	4	36.4	15	23	AAV47738	Human ubiquitin-bi
68	4	36.4	15	24	ABV73195	Muskelon 9-hydrox
69	4	36.4	15	24	ABV73195	Sequence of cyclic
70	4	36.4	15	24	ABV73195	Formula 1b for new
71	4	36.4	15	24	ABV73195	Synthetic substrat
72	4	36.4	15	24	ABV73195	PE-Lys246, 247, 24
73	4	36.4	15	24	ABV73195	ID2 plasmidium sur
74	4	36.4	15	24	ABV73195	Angiotensin-conver
75	4	36.4	15	24	ABV73195	Sequence of the NH
76	4	36.4	15	24	ABV73195	Hepatitis C virus
77	4	36.4	15	24	ABV73195	Sm B/B' epitope 47
78	4	36.4	15	24	ABV73195	Sm B/B' epitope 76
79	4	36.4	15	24	ABV73195	Sm B/B' epitope 77
80	4	36.4	15	24	ABV73195	Sm B/B' epitope 78
81	4	36.4	15	24	ABV73195	Sm B/B' epitope 79
82	4	36.4	15	24	ABV73195	Sm B/B' epitope 80

84	8	14	AA341245	cytochrome c	156	8	22	ARP21045	HIV All motif ref
85	8	15	AA342229	HIV All motif RHA to	157	8	22	ARP21045	HIV All motif tat
86	8	15	AA342199	Hepatitis C virus	158	8	22	ARP21045	HIV All motif vif
87	8	15	AA342200	Hepatitis C virus	159	8	22	ARP21045	HIV All motif vif
88	8	15	AA342202	Hepatitis C virus	160	8	22	ARP21045	HIV All motif vif
89	8	15	AA342203	Hepatitis C virus	161	8	22	ARP21045	Human papilloma #127
90	8	15	AA342204	Hepatitis C virus	162	8	22	ARP21045	p21 C-terminus del
91	8	15	AA342205	Hepatitis C virus	163	8	22	ARP21045	p21-activated prot
92	8	15	AA342206	Hepatitis C virus	164	8	22	ARP21045	HLA-B8 octamer #21
93	8	15	AA342207	Hepatitis C virus	165	8	22	ARP21045	HLA-B8 octamer #28
94	8	15	AA342208	Hepatitis C virus	166	8	22	ARP21045	HLA-B8 octamer #20
95	8	15	AA342209	Hepatitis C virus	167	8	22	ARP21045	HLA-B8 octamer #35
96	8	15	AA342210	Hepatitis C virus	168	8	22	ARP21045	Myristic acid link
97	8	15	AA342211	Hepatitis C virus	169	8	22	ARP21045	HBs-17 epitope pep
98	8	15	AA342212	Hepatitis C virus	170	8	22	ARP21045	Nuclear localisat1
99	8	15	AA342213	Hepatitis C virus	171	8	22	ARP21045	Retinoblastoma bin
100	8	15	AA342214	Hepatitis C virus	172	8	22	ARP21045	Retinoblastoma bin
101	8	15	AA342215	Hepatitis C virus	173	8	22	ARP21045	Replikin sequence
102	8	15	AA342216	Hepatitis C virus	174	8	22	ARP21045	Replikin sequence
103	8	15	AA342217	Hepatitis C virus	175	8	22	ARP21045	Myristoylation org
104	8	15	AA342218	Hepatitis C virus	176	8	22	ARP21045	Hepatitis B virus
105	8	15	AA342219	Hepatitis C virus	177	8	22	ARP21045	Hepatitis B virus
106	8	15	AA342220	Hepatitis C virus	178	8	22	ARP21045	Hepatitis B virus
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108	8	15	AA342222	Hepatitis C virus	180	8	22	ARP21045	Hepatitis B virus
109	8	15	AA342223	Hepatitis C virus	181	8	22	ARP21045	Hepatitis B virus
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155	8	15	AA342269	Hepatitis C virus	227	8	22	ARP21045	Hepatitis B virus
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376	3	27.3	9	22	AAH16443	HIV B27 Super motif	449	3	27.3	9	22	AAH08125	HLA-A1 nonamer #30
377	3	27.3	9	22	AAH16458	HIV B27 Super motif	450	3	27.3	9	22	AAH08139	HLA-B *0702 noname
378	3	27.3	9	22	AAH17271	HIV B27 Super motif	451	3	27.3	9	22	AAH08160	HLA-B *0702 noname
379	3	27.3	9	22	AAH17334	HIV B27 Super motif	452	3	27.3	9	22	AAH08198	HLA-B *2705 noname
380	3	27.3	9	22	AAH17341	HIV B27 Super motif	453	3	27.3	9	22	AAH08229	HLA-B *2705 noname
381	3	27.3	9	22	AAH17341	HIV B27 Super motif	454	3	27.3	9	22	AAH08298	HLA-A *0201 noname
382	3	27.3	9	22	AAH17899	HIV B27 Super motif	455	3	27.3	9	22	AAH08436	HLA-B *2705 noname
383	3	27.3	9	22	AAH18001	HIV B27 Super motif	456	3	27.3	9	22	AAH08437	HLA-B *2705 noname
384	3	27.3	9	22	AAH18296	HIV B27 Super motif	457	3	27.3	9	22	AAH08561	HLA-A1 nonamer #48
385	3	27.3	9	22	AAH18471	HIV B27 Super motif	458	3	27.3	9	22	AAH08624	HLA-B *0702 noname
386	3	27.3	9	22	AAH18474	HIV B27 Super motif	459	3	27.3	9	22	AAH08665	HLA-B *0702 noname
387	3	27.3	9	22	AAH19133	HIV B27 Super motif	460	3	27.3	9	22	AAH08954	HLA-A *0201 noname
388	3	27.3	9	22	AAH21927	HIV B27 Super motif	461	3	27.3	9	22	AAH08978	HLA-A26 nonamer #3
389	3	27.3	9	22	AAH19336	HIV B27 Super motif	462	3	27.3	9	22	AAH08858	HLA-A26 nonamer #7
390	3	27.3	9	22	AAH19522	HIV B27 Super motif	463	3	27.3	9	22	AAH10947	HLA-B8 nonamer #4
391	3	27.3	9	22	AAH21498	HIV A24 motif 1	464	3	27.3	9	22	AAH10948	HLA-B8 nonamer #5
392	3	27.3	9	22	AAH21498	HIV A24 motif 1	465	3	27.3	9	22	AAH10961	HLA-B8 nonamer #18
393	3	27.3	9	22	AAH21498	HIV A24 motif 1	466	3	27.3	9	22	AAH11025	HLA-A26 nonamer #9
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396	3	27.3	9	22	AAH21498	HIV A24 motif 1	469	3	27.3	9	22	AAH11698	HLA-A26 nonamer #2
397	3	27.3	9	22	AAH21498	HIV A24 motif 1	470	3	27.3	9	22	AAH11950	HLA-B *1510 noname
398	3	27.3	9	22	AAH21498	HIV A24 motif 1	471	3	27.3	9	22	AAH11951	HLA-B *1510 noname
399	3	27.3	9	22	AAH21498	HIV A24 motif 1	472	3	27.3	9	22	AAH11952	HLA-B *1510 noname
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404	3	27.3	9	22	AAH21498	HIV A24 motif 1	477	3	27.3	9	22	AAH12259	HLA-B8 nonamer #33
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406	3	27.3	9	22	AAH21498	HIV A24 motif 1	479	3	27.3	9	22	AAH12649	HLA-B *1510 noname
407	3	27.3	9	22	AAH21498	HIV A24 motif 1	480	3	27.3	9	22	AAH94453	Post-translational
408	3	27.3	9	22	AAH21498	HIV A24 motif 1	481	3	27.3	9	22	AAH04922	Nuclear Dbp2-relat
409	3	27.3	9	22	AAH21498	HIV A24 motif 1	482	3	27.3	9	22	AAH04923	Nuclear Dbp2-relat
410	3	27.3	9	22	AAH21498	HIV A24 motif 1	483	3	27.3	9	22	AAH05201	Human HLA-A1 bindi
411	3	27.3	9	22	AAH21498	HIV A24 motif 1	484	3	27.3	9	22	AAH00567	Human MUC1 polypep
412	3	27.3	9	22	AAH21498	HIV A24 motif 1	485	3	27.3	9	22	AAH03244	Fruit fly G protei
413	3	27.3	9	22	AAH21498	HIV A24 motif 1	486	3	27.3	9	22	AAH03273	Fruit fly G protei
414	3	27.3	9	22	AAH21498	HIV A24 motif 1	487	3	27.3	9	22	AAH98374	Buffalo rat liver
415	3	27.3	9	22	AAH21498	HIV A24 motif 1	488	3	27.3	9	22	AAH02467	Mammalian SCF (ste
416	3	27.3	9	22	AAH21498	HIV A24 motif 1	489	3	27.3	9	22	AAH02782	Mammalian SCF (ste
417	3	27.3	9	22	AAH21498	HIV A24 motif 1	490	3	27.3	9	22	AAH33583	Mammalian SCF (ste
418	3	27.3	9	22	AAH21498	HIV A24 motif 1	491	3	27.3	9	22	AAH31905	Amino acid sequenc
419	3	27.3	9	22	AAH21498	HIV A24 motif 1	492	3	27.3	9	22	AAH96959	Mammalian stem cel
420	3	27.3	9	22	AAH21498	HIV A24 motif 1	493	3	27.3	9	22	AAH81089	Human CASB6411 epi
421	3	27.3	9	22	AAH21498	HIV A24 motif 1	494	3	27.3	9	22	AAH83123	Human CASB6411 epi
422	3	27.3	9	22	AAH21498	HIV A24 motif 1	495	3	27.3	9	22	AAH90874	Growth hormone pep
423	3	27.3	9	22	AAH21498	HIV A24 motif 1	496	3	27.3	9	22	AAH00915	Hepatitis C virus
424	3	27.3	9	22	AAH21498	HIV A24 motif 1	497	3	27.3	9	22	AAH00500	Hepatitis C virus
425	3	27.3	9	22	AAH21498	HIV A24 motif 1	498	3	27.3	9	22	AAH00757	Hepatitis C virus
426	3	27.3	9	22	AAH21498	HIV A24 motif 1	499	3	27.3	9	22	AAH00774	Hepatitis C virus
427	3	27.3	9	22	AAH21498	HIV A24 motif 1	500	3	27.3	9	22	AAH96413	HIV-1 Vpr epitope
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430	3	27.3	9	22	AAH21498	HIV A24 motif 1							
431	3	27.3	9	22	AAH21498	HIV A24 motif 1							
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434	3	27.3	9	22	AAH21498	HIV A24 motif 1							
435	3	27.3	9	22	AAH21498	HIV A24 motif 1							
436	3	27.3	9	22	AAH21498	HIV A24 motif 1							
437	3	27.3	9	22	AAH21498	HIV A24 motif 1							
438	3	27.3	9	22	AAH21498	HIV A24 motif 1							
439	3	27.3	9	22	AAH21498	HIV A24 motif 1							
440	3	27.3	9	22	AAH21498	HIV A24 motif 1							
441	3	27.3	9	22	AAH21498	HIV A24 motif 1							
442	3	27.3	9	22	AAH21498	HIV A24 motif 1							
443	3	27.3	9	22	AAH21498	HIV A24 motif 1							
444	3	27.3	9	22	AAH21498	HIV A24 motif 1							
445	3	27.3	9	22	AAH21498	HIV A24 motif 1							
446	3	27.3	9	22	AAH21498	HIV A24 motif 1							
447	3	27.3	9	22	AAH21498	HIV A24 motif 1							

ALIGNMENTS

RESULT: 1

AAH98527

1: AAH98527 standard; peptide: 11 AA

XX

AAH98527

1: 07 AAH98527 (first entry)

XX

NFAM 101 binding peptide 04

XX

NFAM 101 adhesion molecule; lgl; immunoglobulin domain 1;

KW

neurotrophic factor; proliferation; nerve damage; sclerosis;

KW

impairment; degeneration; stroke; Parkinson's disease; memory; schizophrenia;

KW

Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW

treatment; prosthetic nerve guide; treatment; nervous system;


```

CC metastatic spreading.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 8 AA.
Query Match 36.4% Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ASKK 4
DB 3 ASKK 6
IIII
RESULT 9
AAR51526
IU AAM51526 standard; peptide: 8 AA.
AC AAM51526;
XX
UT 02 JAN 2002 (first entry)
DE SV40 VP1 protein nuclear localisation signal.
XX
XX SV40: simian virus 40; VP1 capsid; virus like particles;
XX nuclear localisation signal; VP1.
XX
OS Rhesus macaque polyoma virus.
XX
PN JP2001107777.A.
XX
DB 26 JUN 2001
XX
PF 09 JUL 1999; 99JP-0249140.
XX
PF 30 JUL 1999; 99JP-0249140.
XX
EA (HANEZ) HANOA H.
XX
DB WPI: 2001 599554/68.
XX
XX New virus like particles from VP1 capsid protein of adenovirus
XX connected to its N-terminal.
XX
PS Claim 6; Page 2; 3pp; Japanese.
CC
CC The present sequence is provided in a specifically claimed example of a
XX virus-like particle-forming protein and a peptide containing a
XX nuclear-shifting signal at its N-terminus that can form virus-like
XX particles by shifting to the nucleus of a mammalian cell in which it
XX is expressed. The method is used for removal of virus-like particles
XX from the VP1 capsid protein of adenovirus (ADV).
XX
SQ Sequence 8 AA.
Query Match 36.4% Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KKKK 6
DB 3 KKKK 6
IIII
RESULT 10
AAR78787
IU AAR78787 standard; peptide: 9 AA.
XX
AC AAR78787;
XX
XX 25-MAR-2004 (updated)
UT 25-NOV 1995 (first entry)

```

```

XX
DE Rapia (172-183) peptide sequence.
XX
XX superoxide inhibition; phagocyte; GTP-binding; G protein; Rap;
XX mastoparan; anti-inflammatory; inflammation; ICS4; GAP.
XX
XX Synthetic.
XX
PN W09503839-A1.
XX
PF 09 FEB 1995.
XX
DE 29-JUL 1994; 94WO 0509431.
XX
XX 02 APR-1993; 94US-019244.
XX
PF 15-NOV-1993; 93US-015652.
XX
XX (SRI) SCRIPPS RES INST.
XX
XX Bokoch GM, Carnutte JJ;
XX
XX WPI: 1995 082027/11.
XX
XX New peptide(s) inhibiting superoxide produ. in phagocyte(s)
XX derived e.g. from GTP binding proteins or mastoparan, useful for
XX inhibiting inflammation, e.g. in cases of auto-immune disease,
XX gout, asthma, etc.
XX
XX Claim 5, Page 9; 10pp; English.
XX
XX An optionally substituted, non-toxic peptide of not more than 40
XX amino acids in length is claimed, the peptide being capable of
XX inhibiting superoxide produ. in phagocytic cells and therefore being
XX useful in inhibiting inflammation and treating inflammatory disorders
XX such as autoimmune diseases, gout, ARDS, asthma, myocardial
XX infarction and various dermatological disorders. Preferably the
XX protein is a low mol. wt. GTP binding protein (LWBG), a mastoparan,
XX or an ICS4 peptide.
XX
XX The present sequence is a specifically claimed example of a
XX preferred peptide.
XX
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 9 AA.
Query Match 66.4% Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KKKK 6
DB 3 KKKK 6
IIII
RESULT 11
AAR32302
IU AAR32302 standard; Peptide: 9 AA.
XX
AC AAR32302;
XX
UT 11-JAN 2001 (first entry)
XX
DE HLA A24 binding TACG-12 peptide SEQ ID 86.
XX
XX Transmembrane serine protease; TACG-12; chromosome 17; vaccination;
XX tumour associated differentially-expressed gene 12; cystostatic; human;
XX malignant hyperplasia; cancer; ovary; breast; lung; colon; prostate.
XX
XX Homo sapiens.
XX
XX W0200052044-A1.
XX
PF 09-SEP-2000.
XX

```

02 MAR 2000; 2000W0-US05612.
 03 MAR 1999; 99US-0261416.
 (UYAR-) UNIV ARKANSAS.
 (Britten LJ, Underwood LJ)
 WPI: 2000 53261/48.
 DNA fragment encoding tumor associated differentially-expressed gene 12
 protein used for diagnosing and treating malignant hyperplasia and
 cancers including ovarian cancer
 Example 14; Page 49; 118pps English.
 This invention relates to a novel transmembrane serine protease called
 tumor associated differentially-expressed gene 12 (TAG-12). TAG-12 is
 located on chromosome 17. Sequences AAA93842-A93845 and AAB32245-B32249
 represent human TAG-12 cDNA and their corresponding protein sequences.
 A splice variant of TAG-12 (TAG-12V) leads to a truncated protein
 product. TAG-12 is overexpressed in ovarian carcinomas. TAG-12
 exhibits cytoskeletal activity, and can be used in vaccines and in gene
 therapy. TAG-12 nucleotide and protein sequences are used in the
 diagnosis of malignant hyperplasia and cancers of the ovary, breast,
 lung, colon, prostate and other cancers where TAG-12 is overexpressed.
 TAG-12 is particularly used as tumor marker for early disease
 diagnosis. TAG-12 proteins or fragments can be used to vaccinate an
 individual with cancer, suspected of having a cancer or at risk of
 getting cancer. Sequences AAA93842-A93845 represent PCR primers used for
 amplifying the TAG-12 cDNA sequence, and in the quantitative analysis of
 TAG-12 mRNA. AAB32250 represents a peptide fragment of TAG-12, used to
 create anti-TAG-12 antibodies. Sequences AAB32251-B32369 represent
 TAG-12 peptides which target hLA, and may be used in a vaccine or for
 immune stimulation.
 Sequence: 9 AA;
 Query Match: 46.4%; Score 4; DB 21; Length 9;
 Best Local Similarity: 100.0%; Pred. No. 9; se-05;
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 05 4 KPRK 7
 06 1 KPRK 4
 RESULT 14
 AAB3212
 ID AAB32128 standard; Peptide: 9 AA.
 AC AAB32125;
 07 JAN 2001 (first entry)
 08 HLA B7 binding TAG-12 peptide SEQ ID 112.
 KW Transmembrane serine protease; TAG-12; chromosome 17; vac-malish;
 KW tumor associated differentially-expressed gene 12; cytoskeletal; human;
 KW malignant hyperplasia; cancer; ovary; breast; lung; colon; prostate.
 OS Homo sapiens.
 09 W0200052844-A1.
 10 06-SEP-2000.
 11 02-MAR-2000; 2000W0-US05612.
 12 04-MAR-1999; 99US-0261416.
 (UYAR-) UNIV ARKANSAS.
 (Britten LJ, Underwood LJ)
 WPI: 2000 53261/48
 DNA fragment encoding tumor associated differentially-expressed gene 12
 protein used for diagnosing and treating malignant hyperplasia and

02 MAR 2000; 2000W0-US05612.
 03 MAR 1999; 99US-0261416.
 (UYAR-) UNIV ARKANSAS.
 (Britten LJ, Underwood LJ)
 WPI: 2000 53261/48.
 DNA fragment encoding tumor associated differentially-expressed gene 12
 protein used for diagnosing and treating malignant hyperplasia and
 cancers including ovarian cancer
 Example 14; Page 49; 118pps English.
 This invention relates to a novel transmembrane serine protease called
 tumor associated differentially-expressed gene 12 (TAG-12). TAG-12 is
 located on chromosome 17. Sequences AAA93842-A93845 and AAB32245-B32249
 represent human TAG-12 cDNA and their corresponding protein sequences.
 A splice variant of TAG-12 (TAG-12V) leads to a truncated protein
 product. TAG-12 is overexpressed in ovarian carcinomas. TAG-12
 exhibits cytoskeletal activity, and can be used in vaccines and in gene
 therapy. TAG-12 nucleotide and protein sequences are used in the
 diagnosis of malignant hyperplasia and cancers of the ovary, breast,
 lung, colon, prostate and other cancers where TAG-12 is overexpressed.
 TAG-12 is particularly used as tumor marker for early disease
 diagnosis. TAG-12 proteins or fragments can be used to vaccinate an
 individual with cancer, suspected of having a cancer or at risk of
 getting cancer. Sequences AAA93842-A93845 represent PCR primers used for
 amplifying the TAG-12 cDNA sequence, and in the quantitative analysis of
 TAG-12 mRNA. AAB32250 represents a peptide fragment of TAG-12, used to
 create anti-TAG-12 antibodies. Sequences AAB32251-B32369 represent
 TAG-12 peptides which target hLA, and may be used in a vaccine or for
 immune stimulation.
 Sequence: 9 AA;
 Query Match: 46.4%; Score 4; DB 21; Length 9;
 Best Local Similarity: 100.0%; Pred. No. 9; se-05;
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 05 4 KPRK 7
 06 1 KPRK 4
 RESULT 14
 AAB3212
 ID AAB32128 standard; Peptide: 9 AA.
 AC AAB32125;
 07 JAN 2001 (first entry)
 08 HLA B7 binding TAG-12 peptide SEQ ID 112.
 KW Transmembrane serine protease; TAG-12; chromosome 17; vaccination;
 KW tumor associated differentially-expressed gene 12; cytoskeletal; human;
 KW malignant hyperplasia; cancer; ovary; breast; lung; colon; prostate.
 OS Homo sapiens.
 09 W0200052844-A1.
 10 06-SEP-2000.
 11 02-MAR-2000; 2000W0-US05612.
 12 04-MAR-1999; 99US-0261416.
 (UYAR-) UNIV ARKANSAS.
 (Britten LJ, Underwood LJ)
 WPI: 2000 53261/48
 DNA fragment encoding tumor associated differentially-expressed gene 12
 protein used for diagnosing and treating malignant hyperplasia and

PI cancers including ovarian cancer.

PS Example 14: Page 50; 118pp; English.

XX This invention relates to a novel transmembrane serine protease called

CC tumor associated differentially expressed gene-12 (TAGD-12). TAGD-12 is

CC located on chromosome 17. Sequences AAB9042, AAB9043, and AAB92246-632249

CC represent human TAGD-12 cDNA and their corresponding protein sequences.

CC A splice variant of TAGD-12 (TAGD-12V) leads to a secreted protein

CC product. TAGD-12 is overexpressed in ovarian carcinomas. TAGD-12

CC exhibits cytoskeletal activity, and can be used in vaccines and in gene

CC therapy. TAGD-12 nucleotide and protein sequences are used in the

CC diagnosis of malignant hyperplasia and cancers of the ovary, breast,

CC lung, colon, prostate and other cancers where TAGD-12 is overexpressed.

CC TAGD-12 is particularly used as tumor marker for early disease

CC diagnosis. TAGD-12 proteins or fragments can be used to vaccinate at-

CC t-risk individuals with cancer, suspected of having a cancer or at risk of

CC getting cancer. Sequences AAB93846, AAB93847 represent PCR primers used for

CC amplifying the TAGD-12 cDNA sequence, and in the quantitative analysis of

CC TAGD-12 mRNA. AAB92250 represents a peptide fragment of TAGD-12, used to

CC create anti-TAGD-12 antibodies. Sequences AAB92251-932253 represent

CC TAGD-12 peptides which target HLA, and may be used in a vaccine or for

CC immune stimulation.

XX Sequence: 9 AA.

SQ

Query Match: 36.4%; Score 4; DB 21; Length 9;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 KPRR 7

DE IIII

DE 5 KPRR 6

DE

RESULT 14

AA028984

DE AAB90984 standard; Peptide: 9 AA.

XX

XX AA028984:

XX 29-JAN-2002 (first entry)

XX Human TAGD-12 immunogenic peptide. Seq ID 109.

XX

XX Human tumor associated differentially expressed gene-12 (TAGD-12)

XX expressed in ovarian cancer; transmembrane serine protease;

XX CDLK-A domain; SRCR domain; protease domain; vaccine; immunogenic peptide.

XX Homo sapiens.

XX US6294563-B1.

XX 25-SEP-2001.

XX 02-MAR-2000; 2600US-0518046.

XX 03-MAR-1999; 99US-0261416.

XX (YAK) UNIV ARKANSAS.

XX referred to underwood et.

XX WPI: 2001-647267/74.

XX

XX Tumor associated differentially expressed gene-12 and its encoded

XX protein, useful for detecting early and treating cancer, particularly

XX ovarian and other malignancies

XX Example 14: Column 23; 63pp; English.

XX The invention relates to DNA encoding Tumor Associated Differentially

XX Expressed Gene-12 (TAGD-12) protein, the TAGD-12 protein, a vector

XX expressing the TAGD-12 protein, a host cell containing the vector and

XX antisense molecules directed against the nucleic acid. The TAGD-12

XX protein and DNA are useful for detecting early and treating cancer,

XX particularly ovarian and other malignancies (e.g. by gene therapy). The

XX TAGD-12 protein (and peptides derived from it) is useful as a vaccine

XX for treating cancer. TAGD-12 is a transmembrane serine protease which

XX contains an ILK-A (not defined) domain, an SRCR (not defined) domain and

XX a protease domain. The present sequence represents an immunogenic

XX peptide derived from the TAGD-12 protein.

XX Sequence: 9 AA.

SQ

Query Match: 36.4%; Score 4; DB 22; Length 9;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

CC expressing the TAGD-12 protein, a host cell containing the vector and

CC antisense molecules directed against the nucleic acid. The TAGD-12

CC protein and DNA are useful for detecting early and treating cancer,

CC particularly ovarian and other malignancies (e.g. by gene therapy). The

CC TAGD-12 protein (and peptides derived from it) is useful as a vaccine

CC for treating cancer. TAGD-12 is a transmembrane serine protease which

CC contains an ILK-A (not defined) domain, an SRCR (not defined) domain and

CC a protease domain. The present sequence represents an immunogenic

CC peptide derived from the TAGD-12 protein.

XX Sequence: 9 AA.

SQ

Query Match: 36.4%; Score 4; DB 22; Length 9;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 KPRR 7

DE IIII

DE 3 KPRR 6

DE

RESULT 15

AA069607

DE AAB69007 standard; Peptide: 9 AA.

XX

XX AAB69007:

XX 29-JAN-2002 (first entry)

XX Human TAGD-12 immunogenic peptide. Seq ID 109.

XX

XX Human tumor associated differentially expressed gene-12; TAGD-12;

XX CDLK-A domain; ovarian cancer; transmembrane serine protease;

XX CDLK-A domain; SRCR domain; protease domain; vaccine; immunogenic peptide.

XX Homo sapiens.

XX US6294563-B1.

XX 25-SEP-2001.

XX 02-MAR-2000; 2600US-0518046.

XX 03-MAR-1999; 99US-0261416.

XX (YAK) UNIV ARKANSAS.

XX referred to underwood et.

XX WPI: 2001-647267/74.

XX

XX Tumor associated differentially expressed gene-12 and its encoded

XX protein, useful for detecting early and treating cancer, particularly

XX ovarian and other malignancies

XX Example 14: Column 23; 63pp; English.

XX The invention relates to DNA encoding Tumor Associated Differentially

XX Expressed Gene-12 (TAGD-12) protein, the TAGD-12 protein, a vector

XX expressing the TAGD-12 protein, a host cell containing the vector and

XX antisense molecules directed against the nucleic acid. The TAGD-12

XX protein and DNA are useful for detecting early and treating cancer,

XX particularly ovarian and other malignancies (e.g. by gene therapy). The

XX TAGD-12 protein (and peptides derived from it) is useful as a vaccine

XX for treating cancer. TAGD-12 is a transmembrane serine protease which

XX contains an ILK-A (not defined) domain, an SRCR (not defined) domain and

XX a protease domain. The present sequence represents an immunogenic

XX peptide derived from the TAGD-12 protein.

XX Sequence: 9 AA.

SQ

Query Match: 36.4%; Score 4; DB 22; Length 9;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

CC To monoclonal antibody C-14. The invention also provides an associated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesized molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion
 CC aggregation or agglutination of platelets, where the method comprises
 CC screening platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein IIb/III receptor, which mediates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.

XX
 XX
 SQ Sequence 10 AA:

Query Match: 96.4%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 SKKP 5
 I I I
 D 2 SKKP 5

RESULT 24
 AAG94727
 IL AAG94727 standard; Peptide: 10 AA.
 XX
 XX AAG94727;
 AC
 XX 18-SEP-2001 (first entry)
 DI
 XX Human complementary peptide; SEQ ID NO: 921.
 DE
 KW Human complementary peptide; ligand; drug discovery; drug design.
 XX
 XX Homo sapiens.
 GS
 XX W0200142277-A2.
 PN
 XX 14 JUN 2001.
 ED
 XX EX-085 2000; 2903W0-GR94776.
 IF
 XX 13-DEC-1999; 9903 0029464.
 PR
 XX (PRT) PROTEOM LTD.
 PA
 XX Roberts GW, Heal JK.
 FI
 XX WPI: 2001-614249/56.
 DS
 XX Example 2; Page 132; 16pp; English.

CC The present sequence is one of a large number of complementary peptide
 CC ligands generated from Mycoplasma genitalium genome sequences. These
 CC specific complementary peptides interact with their relevant target
 CC proteins encoded by the microbial genome. They are capable of
 CC antagonising or agonising specific interaction of a protein with
 CC another protein or receptor and are thus useful as reagents and drugs.
 CC and as lead ligands to facilitate drug design and development. They
 CC are useful as tools for functional genomic studies, reagents for the
 CC confirmation of high-throughput screens, as a starting point for
 CC medicinal chemistry manipulation, for peptide synthesis and as
 CC therapeutic agents. The analysis and deposition of peptide sequences
 CC facilitates understanding of protein-protein interactions. The method

CC allows for analysis of an entire database at a time, thus overcoming
 CC sampling problems. The set of complementary peptides includes both
 CC intermolecular (between proteins) and intermolecular (within a
 CC protein) sequences.

XX
 XX
 SQ Sequence 10 AA:

Query Match: 96.4%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKKP 5
 I I I
 D 2 SKKP 5

RESULT 24
 AAG94727
 IL AAG94727 standard; Peptide: 10 AA.
 XX
 XX AAG94727;
 AC
 XX 18-SEP-2001 (first entry)
 DI
 XX Human complementary peptide; SEQ ID NO: 921.
 DE
 KW Human complementary peptide; ligand; drug discovery; drug design.
 XX
 XX Homo sapiens.
 GS
 XX W0200142277-A2.
 PN
 XX 14 JUN 2001.
 ED
 XX EX-085 2000; 2903W0-GR94776.
 IF
 XX 13-DEC-1999; 9903 0029464.
 PR
 XX (PRT) PROTEOM LTD.
 PA
 XX Roberts GW, Heal JK.
 FI
 XX WPI: 2001-614249/56.
 DS
 XX Example 2; Page 132; 16pp; English.

CC The invention relates to a set of complementary peptide ligands
 CC generated from the human genome. The complementary peptides
 CC interact with their relevant target proteins encoded in the human
 CC genome. They can be used as reagents in drug discovery and as lead
 CC ligands to facilitate drug design and development. The present
 CC sequence is a complementary peptide provided in the specification.

XX
 XX
 SQ Sequence 10 AA:

Query Match: 96.4%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASKK 4
 I I I
 D 7 ASKK 10

RESULT 25
 AAG95284
 IL AAG95284 standard; Peptide: 10 AA.
 XX


```

Query Match: 36.4%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 5 PRRN 8
DB 4 PRRN 7

RESULT 28
AAG96929
ID AAC96929 standard; Peptide: 10 AA.
XX AC AAG96929;
XX XX
XX XX
XX 18-SEP-2001 (first entry)
XX XX
XX Human complementary peptide, SEQ ID NO: 3123.
XX XX
XX Human; complementary peptide; ligand; drug discovery; drug design.
XX XX
XX Homo sapiens.
XX OS
XX WO200142277-A2.
XX PN
XX 14-JUN-2001.
XX PE
XX 13-DEC-2000; 2000WO-GB04776.
XX PF
XX 13-DEC-1999; 99GB-0029464.
XX PP
XX (PROT-) PROTEOM LTD.
XX XX
XX Roberts GW, Heal JR;
XX WPI: 2001-408419/43.
XX XX
XX A set of peptide ligands consisting of specific complementary peptides
XX to proteins encoded by genes of the human genome, useful in an assay
XX for screening and identifying of one or more novel peptides which are
XX drug candidates or pro-drugs.
XX XX
XX Example 4; Page 492; 646pp; English.
XX PS
XX The invention relates to a set of complementary peptide ligands
XX generated from the human genome. The complementary peptides
XX interact with their relevant target proteins encoded in the human
XX genome. They can be used as reagents in drug discovery and as lead
XX ligands to facilitate drug design and development. The present
XX sequence is a complementary peptide provided in the specification.
XX SQ
XX Sequence 10 AA:

Query Match: 36.4%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 5 PRRN 8
DB 4 PRRN 4

RESULT 40
AAG85248
ID AAC85248 standard; Peptide: 10 AA.
XX AC AAC85248;
XX XX
XX 11-SEP-2001 (first entry)
XX PE
XX Saccharomyces cerevisiae peptide, SEQ ID NO: 197.
XX DE
XX Saccharomyces cerevisiae; complementary peptide; peptide identification;
XX KW drug discovery; drug design.
XX KW Saccharomyces cerevisiae.
XX OS
XX WO200142277-A2.
XX PN
XX 14-JUN-2001.
XX PE
XX 13-DEC-2000; 2000WO-GB04776.
XX PF
XX 13-DEC-1999; 99GB-0029471.
XX PP
XX (PROT-) PROTEOM LTD.
XX XX
XX Roberts GW, Heal JR;
XX WPI: 2001-362664/48.
XX XX
XX Homology to complementary peptides by analysis of protein and
XX nucleotide sequence databases, useful in drug design.
XX PT
```

```

XX Example 4; Page 57; 488pp; English.
XX
XX The invention relates to the identification of complementary peptides
XX by analysis of protein and nucleotide sequence databases from higher
XX eukaryotic genomes, excluding human and primate, the specific
XX complementary peptides interact with their relevant target proteins
XX encoded in the eukaryote genome. The peptides may be used as reagents
XX and drugs for drug discovery and as lead targets for drug design and
XX development. The present sequence is a complementary peptide from
XX Saccharomyces cerevisiae.
XX
XX Sequence 10 AA:
XX
XX Query Match 36.4%; Score 4; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 RNK 10
XX III
XX 7 RNK 10
XX
XX DB
XX
XX RESULT 3;
XX AAC86555;
XX ID AAC86555 standard; peptide: 10 AA.
XX AC AAC86555;
XX DE Target cyclic peptide, SEQ ID NO: 55.
XX XX
XX XX Peptide mimetic, beta-hairpin loop mimetic; binding motif identification;
XX KW drug design; protein target identification; cyclic.
XX US Synthetic.
XX ER Key Location/Qualifiers
XX FT Modified site 1..10 "the amino group of the residue at position 1
XX FT is condensed on to the carboxy group of the residue
XX FT at position 10 to form a cyclic peptide"
XX FT Base-difference 5
XX FT /note "D-form residue"
XX XX
XX XX W200142276 A1.
XX XX 08-MAR-2001.
XX XX 30-AUG-1999; 99WO-EP06369.
XX XX 30-AUG-1999; 99WO-BI06369.
XX XX (POLY-) POLYPHOS AG.
XX XX Robinson JA, Obrecht D.
XX XX WPI; 2001-273342/28.
XX XX
XX XX Method for manufacturing template-fixed beta-hairpin loop mimetics,
XX XX useful for designing small peptidomimetic drug candidates, involves
XX XX process based on mixed solid and solution phase synthetic strategy.
XX XX Example 6; Page 55; 8pp; English.
XX XX
XX XX The present peptide was synthesised in an example illustrating an
XX XX invention relating to a method for manufacturing template-fixed,
XX XX beta-hairpin loop peptidomimetics. The method comprises employing a
XX XX process that is based on a mixed solid and solution phase synthetic
XX XX strategy. The method is useful for determining key amino acids and
XX XX motifs important for binding large surface and flat protein interfaces
XX XX in their sequential and/or spatial arrangement. This information can
XX XX ultimately be used for the design of small peptidomimetic drug
XX XX candidates. The peptidomimetics may be used to probe large surface
XX XX protein-protein interactions and to find protein targets.
XX
XX SQ Sequence 10 AA;
XX
XX Query Match 36.4%; Score 4; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ASKK 4
XX III
XX 7 ASKK 10
XX
XX DB
XX
XX RESULT 33
XX AAEL1747
XX ID AAEL1747 standard; peptide: 10 AA.
XX
XX QY 4 RNK 9

```

```

XX Example 4; Page 57; 488pp; English.
XX
XX The invention relates to the identification of complementary peptides
XX by analysis of protein and nucleotide sequence databases from higher
XX eukaryotic genomes, excluding human and primate, the specific
XX complementary peptides interact with their relevant target proteins
XX encoded in the eukaryote genome. The peptides may be used as reagents
XX and drugs for drug discovery and as lead targets for drug design and
XX development. The present sequence is a complementary peptide from
XX Saccharomyces cerevisiae.
XX
XX Sequence 10 AA:
XX
XX Query Match 36.4%; Score 4; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 RNK 10
XX III
XX 7 RNK 10
XX
XX DB
XX
XX RESULT 3;
XX AAC86555;
XX ID AAC86555 standard; peptide: 10 AA.
XX AC AAC86555;
XX DE Target cyclic peptide, SEQ ID NO: 54;
XX XX
XX XX Saccharomyces cerevisiae peptide, SEQ ID NO: 54;
XX KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
XX KW drug discovery; drug design.
XX XX
XX XX Saccharomyces cerevisiae.
XX XX W200142276 A1.
XX XX 14-MAR-2001.
XX XX 13-AUG-2000; 2000WO-GR04774.
XX XX 13-AUG-1999; 99GB-0029471.
XX XX (PROT-) PROTEIN LTD.
XX XX Roberts GW, Heal JR.
XX XX WPI; 2001-367863/38.
XX XX
XX XX Identifying complementary peptides by analysis of protein and
XX XX nucleotide sequence databases, useful in drug design.
XX
XX Example 3; Page 105; 488pp; English.
XX
XX The invention relates to the identification of complementary peptides
XX by analysis of protein and nucleotide sequence databases from higher
XX eukaryotic genomes, excluding human and primate, the specific
XX complementary peptides interact with their relevant target proteins
XX encoded in the eukaryote genome. The peptides may be used as reagents
XX and drugs for drug discovery and as lead targets for drug design and
XX development. The present sequence is a complementary peptide from
XX Saccharomyces cerevisiae.
XX
XX Sequence 10 AA:
XX
XX Query Match 36.4%; Score 4; DB 22; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 RNK 9

```


AAFL7417;
 18 APR-2002 (first entry)
 Human respiratory syncytial virus (HRSV-G) Type A peptide, M1836;
 Mevlin; cosmetic; membrane translocation; antithrombotic; anti-thrombotic;
 pestivirus infection; pharmacological; drug delivery system; virotoxin;
 vaccine; human respiratory syncytial virus, HRSV;
 Human respiratory syncytial virus;
 Key: Location/Qualifiers
 Modified site 1 /note= "Biotinylated lys"
 WO200200882-A2;
 04-JAN-2002;
 28-JUN-2001: 2001WO-NI00484;
 28-JUN-2000: 2000EP-0202255;
 (HRSV) ID-FLYSTAD INST DIERKHOFFERIJ EN DIERGEE;
 Landerijk JMW;
 WPI: 2002 149922/18;
 Novel isolated, synthetic or recombinant transport peptide molecule
 called movin; useful for preparation of pharmaceutical/cosmetic
 composition capable of membrane transport or capable of eliciting
 antibiotic activity;
 Disclosure: Page 58; 78pp; English;
 The invention relates to an isolated, synthetic or recombinant transport
 peptide molecule called movin. The peptide or its functional equivalent
 comprises a sequence that is identical to an amino acid sequence of a
 peptide capable of binding heparin. The peptide molecule is useful for
 the preparation of a pharmaceutical or cosmetic composition capable of
 membrane translocation or capable of eliciting antibiotic activity. The
 peptide molecule is useful type specific diagnosis of infection such as
 pestivirus infection, for transport of substances into a cell, as
 antibacterial, for detecting the presence or absence of an antibody
 directed against pestivirus in a sample, to elicit antibodies which are
 specific for pestivirus types and/or salivases, for differentiating an
 animal from another animal, for preparation of a vaccine system capable of
 inducing antibodies (a vaccine), as drug delivery system, to provide for
 synergy in antibacterial activity, transport of a translocation, and
 in vaccines to prevent infection with pestivirus. A pharmaceutical
 composition is useful for the prophylaxis of pestivirus infections.
 The present sequence is human respiratory syncytial virus (HRSV-G)
 Type A peptide which is a heparin binding peptide.
 Sequence 10 AA;
 Query Match 36.4%; Score 4; DB 25; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5, 5e-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;
 QY 4 KKPK 6
 1 1 1
 6 KKPK 9
 RESULT 34
 AAWS3153
 ID AAWS3153 standard; peptide; 11 AA;
 AC AAWS3153;
 XX
 XX
 DT 14-JUL-1998 (first entry)
 XX PTP activity determining peptide substrate 8;
 DE Protein tyrosine phosphatase; PTP; peptide substrate; phosphorylation;
 KW Synthetic;
 XX US5739278-A;
 XX 14-APR-1998;
 XX 30-MAR-1995; 95US-0416035;
 XX 10-MAY-1993; 94US-0059949;
 XX 30-MAR-1995; 95US-0416035;
 XX (UNIV) UNIV WASHINGTON;
 XX COOL DE, Daum G, Fischer EH;
 XX WPI: 1998-250491/22;
 XX New nona peptide, phosphorylated derivative and related compositions
 - useful for measuring activity of protein tyrosine phosphatases
 Disclosure: Columns 13-14; 5pp; English;
 This peptide substrate can be used for the determination of activity of
 protein tyrosine phosphatases (PTP). The peptides with a tyrosine residue
 phosphorylated and related compositions containing the peptides are
 useful for determining the amount or presence of PTP. Determination of
 PTP activity by prior art methods could be affected by a number of
 factors, including the type of enzyme being assayed, the conditions under
 which the assay was performed and the presence of external effectors. The
 peptide of the current invention, when used as a substrate for
 determination purposes is not subject to the limitations of prior art
 methods. The new determination method is highly sensitive, with the assay
 permitting the detection and characterization of a wide variety of PTP's.
 Due to the increased sensitivity of the methods, PTP's can be detected in
 situations where only limiting amounts of samples, e.g tissue extracts or
 immunoprecipitates, are available.
 Sequence 11 AA;
 Query Match 46.4%; Score 4; DB 19; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5, 9e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASKK 4
 1 1
 7 ASKK 10
 RESULT 35
 AAY88555
 ID AAY88555 standard; peptide; 11 AA;
 XX AAY88555;
 XX 07-AUG-2000 (first entry)
 XX NCAM Igl binding peptide 118 used as a control peptide;
 DE NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;
 KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
 KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
 KW treatment; prosthetic nerve guide; treatment; nervous system.
 XX Synthetic;
 XX OS
 XX WO200018401-A2;
 PN

```

XX 06-APR-2000.
XX 23-SEP-1999; 99WO-DK00500.
XX 29-SEP-1998; 98DK-0001232.
XX 29-APR-1999; 98DK-0000592.
XX (RONN/) RONN L C B.
XX (BOCK/) BOCK E.
XX (HOLM/) HOLM A.
XX (OLSE/) OLSEN M.
XX (OLSE/) OLSEN M.
XX (JENSE/) JENSEN P H.
XX (POUL/) POULSEN F M.
XX (SORO/) SOROKA V.
XX (RALE/) RALETS I.
XX (BEKE/) BEREZIN V.
XX Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
XX Poulsen FM, Soroka V, Ralets I, Berezin V;
XX WPI: 2000-293111/25.
XX Compositions that bind neural cell adhesion molecules useful for
XX treating disorders of the nervous system and muscles e.g. Alzheimer's
XX and Parkinson's diseases -
XX Example 5; Fig 7; 119pp; English.
XX Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
XX NCAM is found in three forms, two of which are transmembrane forms, while
XX the third is attached via a lipid anchor to the cell membrane. All three
XX NCAM forms have an extracellular structure consisting five immunoglobulin
XX domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX N-terminal. The invention relates to a compound containing a peptide
XX which binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2
XX from NCAM presenting cells, and is also capable of promoting the
XX proliferation of NCAM presenting cells. The present sequence represents a
XX control peptide used in the identification of those binding peptides
XX which can be used in the compound. The compound may be used in the
XX treatment of normal, degenerated or damaged NCAM presenting cells. The
XX compound may in particular be used to treat diseases of the central and
XX peripheral nervous systems such as post operative nerve damage, traumatic
XX nerve damage, impaired myelination of nerve fibres, conditions resulting
XX from a stroke, Parkinson's disease, Alzheimer's disease, dementias,
XX sclerosis, nerve degeneration associated with diabetes mellitus,
XX disorders affecting the circadian clock or neuro-muscular transmission
XX and schizophrenia. Conditions affecting the muscles may also be treated
XX with the compound, such as conditions associated with impaired function
XX of neuromuscular connections (e.g. genetic or traumatic shock or
XX traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX liver and bowel may also be treated using the compound. The compound is
XX used in a prosthetic nerve guide, and also to stimulate the ability to
XX learn, and to stimulate the memory of a subject.
XX Sequence 11 AA:
XX
XX Query Match 36.4% Score 4: 18 21 Length 11;
XX Best Local Similarity 100.0% Prod. No. 5,36-02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 8 NIKA 11
XX 11.1
XX 8 NIKA 11
XX
XX RESULT 36
XX AAY8556
XX ID AAY8556 standard; peptide: 11 AA.
XX

```

```

AC AAY8556;
XX 07-AUG-2000 (first entry)
XX NCAM Ig1 binding peptide 119 used as a control peptide.
XX
XX NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;
XX neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
XX impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
XX Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
XX treatment; prosthetic nerve guide; treatment; nervous system.
XX Synthetic.
XX WO2000/18801-A2.
XX 06-APR-2000.
XX 23-SEP-1999; 99WO-DK00500.
XX 29-SEP-1998; 98DK-0001232.
XX 29-APR-1999; 98DK-0000592.
XX (RONN/) RONN L C B.
XX (BOCK/) BOCK E.
XX (HOLM/) HOLM A.
XX (OLSE/) OLSEN M.
XX (OLSE/) OLSEN M.
XX (JENSE/) JENSEN P H.
XX (POUL/) POULSEN F M.
XX (SORO/) SOROKA V.
XX (RALE/) RALETS I.
XX (BEKE/) BEREZIN V.
XX Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
XX Poulsen FM, Soroka V, Ralets I, Berezin V;
XX WPI: 2000-293111/25.
XX Compositions that bind neural cell adhesion molecules useful for
XX treating disorders of the nervous system and muscles e.g. Alzheimer's
XX and Parkinson's diseases -
XX Example 5; Fig 7; 119pp; English.
XX Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
XX NCAM is found in three forms, two of which are transmembrane forms, while
XX the third is attached via a lipid anchor to the cell membrane. All three
XX NCAM forms have an extracellular structure consisting five immunoglobulin
XX domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX N-terminal. The invention relates to a compound containing a peptide
XX which binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2
XX from NCAM presenting cells, and is also capable of promoting neurite outgrowth
XX domains, and is capable of stimulating or promoting neurite outgrowth
XX from NCAM presenting cells, and is also capable of promoting the
XX proliferation of NCAM presenting cells. The present sequence represents a
XX control peptide used in the identification of those binding peptides
XX which can be used in the compound. The compound may be used in the
XX treatment of normal, degenerated or damaged NCAM presenting cells. The
XX compound may in particular be used to treat diseases of the central and
XX peripheral nervous systems such as post operative nerve damage, traumatic
XX nerve damage, impaired myelination of nerve fibres, conditions resulting
XX from a stroke, Parkinson's disease, Alzheimer's disease, dementias,
XX sclerosis, nerve degeneration associated with diabetes mellitus,
XX disorders affecting the circadian clock or neuro-muscular transmission
XX and schizophrenia. Conditions affecting the muscles may also be treated
XX with the compound, such as conditions associated with impaired function
XX of neuromuscular connections (e.g. genetic or traumatic shock or
XX traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX liver and bowel may also be treated using the compound. The compound is
XX used in a prosthetic nerve guide, and also to stimulate the ability to
XX learn, and to stimulate the memory of a subject.
XX

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Seq Sequence 11 AA; Query Match 36.4%; Score 4; Pos 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.9e+27;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY R NIKK 11
 IIII
 DB R NIKK 11

RESULT 47
 ABB74833
 ID ABB74833 standard; Peptide: 11 AA.
 AC ABB74833;
 XX
 XX 18 APR 2002 (first entry)
 DE Nuclear protein nuclear localisation signal; peptide SEQ ID NO:517.
 XX
 KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
 KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
 KW peptide lipid polynucleotide complex; neoplastic disease; gene therapy;
 KW breast carcinoma; prostate carcinoma.
 XX
 OS Paracanthus anandinus.
 XX W6200194836-A2.
 PN 13-DEC-2001.
 XX
 XX 08-JUN-2001: 2001WO-US18657.
 XX
 XX 09-JUN-2002: 2000US-210925P.
 XX (B40L/) BOBILIKAS T.
 XX
 XX Boulikas T;
 PI WPI: 2002 164295/21.
 DR
 XX Encapsulation of plasmid DNA (lipogenes) and therapeutic agents with
 PT nuclear localization signal/tusogenic peptide conjugates into targeted
 PT liposome complexes -
 XX
 PS Claim 14: Page 85; 107pp; English.
 CC The present invention describes a method for producing micelles with
 CC entrapped therapeutic agents. The method comprises: (1) combining
 CC negatively charged agent with a cationic lipid in a ratio where 30-99 %
 CC of the negatively charged atoms are neutralised by positive charges on
 CC lipid molecules to form an electrostatic micelle complex in 20-80 %
 CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
 CC karyophilic peptide conjugates in a 0.0-0.5 ratio, therefore producing
 CC micelles with entrapped therapeutic agents. Also described is a method
 CC for delivering a therapeutic agent in vivo, comprising the administration
 CC of the micelle. ABB74255 to ABB74854 represent specifically claimed
 CC nuclear localisation signal (NLS) peptides for use in the method as the
 CC tusogenic-karyophilic peptides. The micelles produced can have cytostatic
 CC and antitumour activities. The peptide-lipid-polynucleotide complexes
 CC produced are useful for inhibiting the progression of neoplastic
 CC diseases. The invention relates to the field of gene therapy and is
 CC directed toward methods for producing peptide-lipid-polynucleotide
 CC complexes suitable for delivery of polynucleotides. The encapsulated
 CC molecules display therapeutic efficacy in eradicating solid tumours
 CC including but not limited to breast carcinoma or prostate carcinoma.
 CC ABB74235 to ABB74255 are used in the exemplification of the present
 CC invention.

XX Sequence 11 AA;
 Query Match 36.4%; Score 4; Pos 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRPK 6
 IIII
 DB 5 KRPK 8

RESULT 38
 AAY20609
 ID AAY20609 standard; Protein: 12 AA.
 XX AAY20609;
 AC AAY20609;
 XX
 DE 22-JUL-1999 (first entry)
 DE Human neurofilament-L mutant protein fragment 116.
 XX
 KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin 1; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GRAP; p53; semaphorin III; HUPF-1;
 KW bel-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN W09845322-A2.
 XX
 PD 15-OCT-1998.
 XX
 PD 02-APR-1998: 98WO-IB00705.
 XX
 PD 10-APR-1997: 97US-0043163.
 XX
 XX (UYUT-) RIJKSUNIV UTRECHT.
 XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 XX (UYRO-) UNIV ROTTERDAM ERASMUS.
 XX
 XX Burbach JPH, Grosveld FG, Van Leeuwen FW;
 DR WPI: 1998-609901/51.
 DR N PSDB: AAX75758.
 XX
 XX Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific ribozymes or wild-type
 RNA
 PS
 XX Disclosure: Figure 7: 258pp; English.
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma

CC 2 (bel 2) proto-oncogene, seraphorin III, BDNF -- high mobility group
 CC protein-C (HMG-C) and neuroendocrine specific protein A.

XX Sequence 12 AA;

Query Match: 36.48; Score 4; Lb 19; Length 12;
 Best Local Similarity 100.0%; Prod. No. 6.40-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKKP 6

DB 1 11

DB 8 KKKP 11

RESULT 39

AAB19494

ID AAB19494 standard; peptide; 12 AA;

A2 AAB19494;

XX 06-MAR-2001 (first entry)

XX Antigenic peptide derived from gamma hydroxy butyrate dehydrogenase.

XX Gamma-aminobutyric acid; GABA; GABA transaminase; GABA-T;

XX gamma hydroxy butyrate dehydrogenase; GHBH; succinic semialdehyde;

XX gamma hydroxybutyrate;

XX Synthetic;

XX Arabidopsis thaliana.

XX W0200061763 A2.

XX 19-OCT-2000.

XX 06-APR-2000; 2000WO-CA00378.

XX 09-APR-1999; 99US-012851R.

XX (UNIV-) UNIV GUELPH.

XX Sheilp H.J. Reitzkreuz KE, Van Gaasbeek et al.

XX WPI: 2000-679492/66.

XX Novel proteins related to gamma-aminobutyrate dehydrogenase (GABA-T) and gamma-hydroxybutyrate dehydrogenase (GHBH) are useful for screening and isolation of homologous genes from other organisms.

XX Example 3; Page 26; 48pp; English.

XX The present sequence represents a peptide derived from a plant.

XX gamma-hydroxy butyrate dehydrogenase (GHBH), which was used to raise antibodies. The specification also describes a plant gamma-aminobutyrate dehydrogenase (GABA-T) and gamma-hydroxybutyrate dehydrogenase (GHBH) and their use in the treatment of GABA-T deficiency. The proteins are involved in the metabolism of GABA in plants. GABA-T is used to transaminate GABA to form succinic semialdehyde, which may be converted to gamma-hydroxybutyrate by GHBH. The polynucleotides are used to produce GABA-T and GHBH recombinantly. The proteins are useful for screening and isolation of homologous genes from other organisms.

XX Sequence 12 AA;

Query Match: 36.48; Score 4; Lb 21; Length 12;

Best Local Similarity 100.0%; Prod. No. 6.40-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKKP 5

DB 1 11

DB 8 SKKP 11

RESULT 40

AAU99715
 ID AAU99715 standard; Peptide; 12 AA.

XX AAU99715;

XX 24-SEP-2002 (first entry)

XX Human Ghrelin (C-terminus) peptide sequence.

XX Human; angiotensin converting enzyme-2; ACE-2; body weight disorder;
 KW muscle mass; body fat; obesity; diabetes; atherosclerosis; weight loss;
 KW lipid metabolism; weight gain; anorexia; cachexia; bulimia; sepsis;
 KW familial partial lipodystrophy; hypercholesterolaemia; hyperlipidaemia;
 KW aberrant metabolic rate; heart failure; left ventricular hypertrophy;
 KW neurodegenerative disorder; peptide hormone; cytokine processing;
 KW myocardial infarction; cardiomyopathy; inflammatory bowel disease;
 KW systemic inflammation response syndrome; polytrauma; pain; stroke;
 KW bone destruction; rheumatoid arthritis; osteoarthritis; asthma;
 KW periodontal disease; dysmenorrhea; premature labour; brain oedema;
 KW focal injury; diffuse axonal injury; reperfusion injury; scar formation;
 KW cerebral vasospasm; subarachnoid haemorrhage; allergic disorder;
 KW adult respiratory distress syndrome; wound healing; appetite;
 KW body mass index; Ghrelin.

XX Homo sapiens.

XX W020023997-A2.

XX 23-MAY-2002.

XX 31-OCT-2001; 2001WO-US45703.

XX 01-NOV-2000; 2000US-0704216.

XX 29-MAY-2001; 2001US-0870382.

XX 19-OCT-2001; 2001US-371741P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Acton SL, Ocain ID, Gould AE, Dales NA, Guan B, Brown JA;

XX Patane M, Kadambi VJ, Solomon M, Stricker-Krongrad A;

XX WPI: 2002-547572/58.

XX Treating body weight disorder and increasing muscle mass comprises administering angiotensin converting enzyme-2 modulating compound.

XX Example 1b; Page 22; 395pp; English.

XX The present invention describes a new method of treating a body weight disorder, increasing muscle mass and decreasing body fat by administration of angiotensin converting enzyme (ACE)-2 modulating compound. The invention can be used for treating body weight disorders, particularly obesity of at least grade 1, diabetes, atherosclerosis and a state associated with lipid metabolism. The method is used for treating rapid weight loss, rapid weight gain, anorexia, cachexia, bulimia, generalised partial lipodystrophy, familial partial lipodystrophy, hypercholesterolaemia, hyperlipidaemia, an aberrant metabolic rate, congestive heart failure, chronic heart failure, left ventricular hypertrophy, acute heart failure, neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease and Huntington's disease), diseases associated with peptide hormones or cytokine processing, myocardial infarction, cardiomyopathy, systemic inflammation response syndrome, sepsis, polytrauma, inflammatory bowel disease, acute and chronic pain, bone destruction in rheumatoid arthritis and osteoarthritis and periodontal disease, dysmenorrhea, premature labour, brain oedema following focal injury, diffuse axonal injury, stroke, reperfusion injury, cerebral vasospasm after subarachnoid haemorrhage, allergic disorders including asthma, adult respiratory distress syndrome, wound healing and scar formation. The invention decreases the appetite, increases muscle mass and decreases body fat of subject having body mass index of greater than 25 (preferably 24.9 kg/m²). The present amino acid sequence represents the human Ghrelin (C-terminus) peptide that was used in the invention for hydrolysis of biologically active peptides

Query Match 36.4% Score 4; DB 23; Length 12;

Best Local Similarity 100.0%; Prod. No. 6.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Sequence 12 AA:
 QY 4 SKKP 5
 DB 2 SKKP 5

Query Match 36.4% Score 4; DB 23; Length 12;

Best Local Similarity 100.0%; Prod. No. 6.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SKKP 5

DB 2 SKKP 5

RESULT 41

AAE17344
 ID: AAE17344 standard; peptide: 12 AA.

XX

AC AAE17344;

XX

DT 18-APR-2002 (first entry)

XX

DE Recombinant; transport peptide module #11.

XX

KW Moving; cosmetic; membrane translocation; antibacterial; antibiotic;

XX

KW pestivirus infection; pharmaceutical; drug-delivery system; virucide;

XX

KW vaccine;

XX

OS Unidentified.

XX

PN W0200200862-A2.

XX

PD 03 JAN-2002.

XX

PE 28-JUN-2001; 2001WO-NL00484.

XX

PR 28-JUN-2000; 2000EP-0202255.

XX

PA (ID:E-) ID-LELYSTAD INST DIERHOUTDERIJ EN DIERGEZ.

XX

PI Langedijk JPM;

XX

DR WPI: 2002-139922/18.

XX

PT Novel isolated, synthetic or recombinant transport peptide module

XX

PT called moving, useful for preparation of pharmaceutical/cosmetic

XX

PT composition capable of membrane transport or capable of eliciting

XX

PT antibiotic activity

XX

PS (Claim 5): Page 64; 78pp; English.

XX

CC The invention relates to an isolated, synthetic or recombinant transport

XX

CC peptide module called movin. The peptide or its functional equivalent

XX

CC comprises a sequence that is identical to an amino acid sequence of a

XX

CC peptide capable of binding heparin. The invention also relates to

XX

CC transport peptides, for example derived from the first protein of

XX

CC pestiviruses for type-specific diagnosis of infection. The peptide module

XX

CC is useful for the preparation of a pharmaceutical or cosmetic composition

XX

CC capable of membrane translocation or capable of eliciting antibiotic

XX

CC activity. The peptide module is useful for type-specific diagnosis of

Query Match 36.4% Score 4; DB 23; Length 12;

Best Local Similarity 100.0%; Prod. No. 6.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6

DB 9 KKPK 12

RESULT 42

AAE17424

XX AAE17424 standard; peptide: 12 AA.

XX

AC AAE17424;

XX

DT 18-APR-2002 (first entry)

XX

DE Human respiratory syncytial virus (HRSV) type B region 2 peptide.

XX

KW Moving; cosmetic; membrane translocation; antibacterial; antibiotic;

XX

KW pestivirus infection; pharmaceutical; drug-delivery system; virucide;

XX

KW vaccine; human respiratory syncytial virus; HRSV.

XX

OS Human respiratory syncytial virus.

XX

PH Key location/Qualifiers

XX

FT Modified-site 1 /note- "Biotinylated Lys"

XX

PN W0200200862-A2.

XX

PD 03-JAN-2002.

XX

PE 28-JUN-2001; 2001WO-NL00484.

XX

PR 28-JUN-2000; 2000EP-0202255.

XX

PA (ID:E-) ID-LELYSTAD INST DIERHOUTDERIJ EN DIERGEZ.

XX

PI Langedijk JPM;

XX

DR WPI: 2002-139922/18.

XX

PT Novel isolated, synthetic or recombinant transport peptide module

XX

PT called moving, useful for preparation of pharmaceutical/cosmetic

XX

PT composition capable of membrane transport or capable of eliciting

XX

PT antibiotic activity

XX

PS Disclosure: Page 54; 78pp; English.

XX

CC The invention relates to an isolated, synthetic or recombinant transport

XX

CC peptide module called movin. The peptide or its functional equivalent

XX

CC comprises a sequence that is identical to an amino acid sequence of a

XX

CC peptide capable of binding heparin. The peptide module is useful for

XX

CC the preparation of a pharmaceutical or cosmetic composition capable of

XX

CC membrane translocation or capable of eliciting antibiotic activity. The

XX

CC peptide module is useful for type-specific diagnosis of infection such as

XX

CC pestivirus infection, for transport of substances into a cell, as

XX

CC antibacterial, for detecting the presence or absence of an antibody

CC directed against pestivirus in a sample, to obtain antibodies which are

CC specific for pestivirus types and/or subtypes, for differentiating an

CC animal from another animal, for preparation of a composition capable of

CC inducing antibodies (a vaccine), as drug-delivery system, to provide for

CC synergy in antibacterial activity, translocation or translocation, and

CC in vaccines to prevent infection with pestivirus. A pharmaceutical

CC composition is useful for the prophylaxis of pestivirus infections.

CC The present sequence is human respiratory syncytial virus (HRSV-G)

CC type A peptide which is a heparin binding peptide.

XX

Sequence 12 AA:

Query Match 36.4% Score 4; DB 23; Length 12;

Best Local Similarity 100.0%; Prod. No. 6.3e+02;

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKPK 6
 III
 BB 9 KKPK 12

RESULT 43
 ID ABB74843 standard; Peptide: 12 AA.
 XX AC ABB74843;
 XX DE 18-APR-2002 (first entry)
 XX DE Nuclear protein nuclear localisation signal peptide SEQ ID NO:40?
 XX DE Fusogenic; nuclear localisation signal; NLS; encapsulation; liposome;
 KW liposome; micelle; karyophilic; cytostatic; anti-tumor; solid tumor;
 KW Peptide-lipid:polynucleotide complex; neoplastic disease; gene therapy;
 KW breast carcinoma; prostate carcinoma;
 XX AC Acetabula;
 XX PN W026019486 A2;
 XX DE 13 DEC 2001;
 XX PF 08 JUN 2001; 2001WG-US18657;
 XX PR 09 JUN 2001; 2006DS-210925P;
 XX VA (publ.) BOULIKAS T;
 XX PI Boulikas T;
 XX WP1: 2012 164295/21;
 XX Encapsulation of plasmid DNA (liposomes) and therapeutic agents with
 TT nucleic acid localization signal/liposome peptide complexes into targeted
 ET liposome complexes;
 XX Claim 14; Page 85; 107pp; English;
 CC The present invention describes a method for producing micelles with
 CC entrapped therapeutic agents. The method comprises (a) combining
 CC negatively charged agent with a cationic lipid to form a complex where the cationic
 CC lipid molecules to form an entrapped polynucleotide complex in 20 mM NaCl
 CC ethanol; and (b) combining the mixture of (a) and (b) with fusogenic
 CC karyophilic peptide conjugates to a final mixture to form micelles
 CC micelles with entrapped therapeutic agents. A gene agent is a method
 CC for delivering a therapeutic agent in vivo. A gene agent is the administration
 CC of the micelle. ABB74256 to ABB74494 represent specifically claimed
 CC nuclear localisation signal (NLS) peptides for use in the method as the
 CC fusogenic karyophilic peptides. The micelles produced can have cytostatic
 CC and anti-tumor activities. The peptide lipid conjugated complexes
 CC produced are useful for inhibiting the proliferation of neoplastic
 CC diseases. The invention relates to the field of gene therapy and is
 CC directed toward methods for producing peptide-lipid polynucleotide
 CC complexes suitable for delivery of polynucleotides. The encapsulated
 CC molecules display therapeutic efficacy in treatment of solid tumors
 CC including but not limited to breast carcinoma or prostate carcinoma.
 CC ABB74245 to ABB74255 are used in the exemplification of the present
 CC invention.

XX Sequence 12 AA;
 Query Match 36.4%; Score 4; DB 21; Length 12;
 Best Local Similarity 100.0%; Prod. No. 6; Re402;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 3 KKPK 6
 III
 BB 9 KKPK 12

DB 2 KKPK 5
 III

RESULT 44
 ID AAB11344 standard; peptide: 13 AA.
 XX AC AAB11344;
 XX XX 25-MAR-2003 (updated)
 XX DT 05-JUN-1991 (first entry)
 XX DE Anti-rhodopsin monoclonal antibody epitope.
 XX KW Monoclonal antibody; rhodopsin; metarhodopsin.
 XX GS Paroctopus defilem.
 XX PN EP420151-A.
 XX XX 03-APR-1991;
 XX XX 25 SEP-1990; 90EP 0118499;
 XX XX 30-MAY-1990; 90JP 0148269;
 XX PR 27-SEP-1989; 89JP 0249148;
 XX PR 28-FEB-1990; 90JP 0045410;
 XX XX (H11A) HITACHI LTD.
 XX XX Ishibashi T, Kozuka H, Yoshino S, Shimizu N, Tsuda M;
 XX PI Imazeki S;
 XX WP1: 1991-095637/14;
 XX Claim 9; Page 15; 21pp; English;
 CC Monoclonal antibodies specific to rhodopsin - useful for
 CC immobilising rhodopsin or monitoring its photochemical reactions
 XX Anti rhodopsin antibodies having a greater affinity for metarhodopsin
 CC than for rhodopsin; recognising this sequence, were produced by
 CC conventional hybridoma techniques.
 CC The peptide is the hydrophilic region connecting the third helix
 CC to the fourth helix of the N-terminus of the octopus rhodopsin.
 CC Both antibodies Ig2 and Ig1 were reactive with this peptide.
 CC (Updated on 25 MAR 2003 to correct PA field.)
 XX Sequence 13 AA;
 Query Match 36.4%; Score 4; DB 12; Length 13;
 Best Local Similarity 100.0%; Prod. No. 6; Re402;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 3 ASKK 4
 III
 DB 8 ASKK 11

RESULT 45
 AAR47395
 ID AAR47395 standard; peptide: 13 AA.
 XX AC AAR47395;
 XX XX 25 MAR-2003 (updated)
 XX DT 29-JUN-1994 (first entry)
 XX DE PGE-activity-displaying peptide.
 XX KW Platelet derived growth factor; A-chain; therapy; assay agent;
 KW mitogen; chemotactic agent; wound healing; vascular disease effects;

KW injury: calcium uptake modulation.
 GS Synthetic.
 XX W0932576-A2.
 PN
 XX 24-DEC-1993.
 PD
 XX 03-JUN-1993; 93WO-US05325.
 PF
 XX 06-JUN-1992; 92US-0894497.
 PK
 XX (SMK) SK: INI.
 PA
 XX Judd AK;
 PI
 XX WPI: 1994-007454/01.
 DR
 XX Peptide(s) having platelet derived growth factor activity - derived
 PT from platelet-derived growth factor A and B chain sequences, useful
 PI in therapy and as assay agents
 XX
 XX Claim 1; Page 50; 58pp; English.
 PS
 XX The sequence is that of a peptide corresponding to platelet derived
 CC growth factor (PDGF) A-chain amino acids 55-78. It shows PDGF
 CC activity and can be used in assays for PDGF. It may also be used as
 CC a mitogen and a chemotactic agent for use in wound healing, in the
 CC alleviation of the effects of vascular disease or injury and in the
 CC modulation of calcium uptake into the cells. The peptide is also
 CC easier to produce than native PDGF.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 XX Sequence 13 AA:
 SQ
 Query Match 36.4%; Score 4; DB 10; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KKPK 6
 DB 9 KKPK 12
 RESULT 46
 AAW5068
 ID AAW5068 standard; Protein: 13 AA.
 XX
 XX AAW5068;
 A*
 XX 20-MAY 1999 (first entry)
 GT
 XX Putative HS binding domain of HSV gp glycoprotein.
 DE
 XX Herpes simplex virus; HSV; viral envelope protein non native ligand;
 KW gene therapy: ectopic infection; gp glycoprotein HS binding domain.
 KW
 XX Herpes simplex virus.
 GS
 XX W39526583-A1.
 PN
 XX 11 FEB-1999.
 PD
 XX 31-JUL-1998; 98WO-US16051.
 PF
 XX 31-JUL-1997; 97US-0054329.
 PK
 XX (JYP) UNIV PITTSBURGH.
 PA
 XX Glorioso JC, Laquerre S;
 PI
 XX WPI: 1995-153808/13.
 DR
 XX N-PSDB: AAX22297.
 XX
 XX New herpes simplex virus including non-native ligand for use in gene
 PT therapy - has specific affinity for particular cells and reduced
 PT affinity for native host cells, resulting in reduced ectopic
 PT expression
 XX
 XX Example 1; Fig 1; 40pp; English.
 PS
 XX The invention relates to targeting Herpes simplex virus (HSV) vectors,
 CC chiefly by modifying viral proteins. The invention provides a HSV having
 CC an envelope that includes a non-native ligand. The HSV vector binds to
 CC the surface of selected cells and can be internalised, i.e. it is a gene
 CC therapy targeting vector for specific cell types. It may also be used to
 CC study attachment to, and infection of, cells by HSV, while the non-native
 CC ligand-envelope protein chimeras are reagents for receptor-ligand assays
 CC and as adhesion promoters in vitro or in vivo. The new HSV vectors can
 CC deliver genes with minimal ectopic infection, particularly when the
 CC natural broad cell range of HSV is altered by deletion of native ligands.
 CC These vectors are safe and can be produced efficiently. The present
 CC sequence represents a putative binding domain of the HS ligand of the HSV
 CC gB glycoprotein. A region from this sequence can be deleted to create a
 CC modified HSV lacking its native ligand.
 XX
 XX Sequence 13 AA:
 SQ
 Query Match 36.4%; Score 4; DB 20; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KKPK 6
 DB 9 KKPK 12
 RESULT 47
 AAB08046
 ID AAB08046 standard; Peptide: 13 AA.
 XX
 XX AAB08046;
 AC
 XX 04-DEC-2000 (first entry)
 DT
 XX Signal peptidase inhibitor peptide compound E18.
 DE
 XX Enzyme substrate: bacterial signal peptidase; Staphylococcus aureus SpsB;
 KW Escherichia coli leader peptidase; signal peptidase inhibitor;
 KW bacterial infection;
 XX Synthetic.
 QS
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "decanoyl attached to residue"
 FT Modified-site 13 /note= "hydroxyl attached to residue"
 FT
 XX W0200046250-A1.
 PN
 XX 10-AUG-2000.
 PD
 XX 01-FEB-2000; 2000WO-EP00751.
 PF
 XX 03-FEB-1999; 99GB-0002399.
 PR
 XX (SMK) SMITHKLINE BEECHAM PLC.
 PA
 XX Ashman S, Black MT, Bruton G, Humphries AJ, Moore KJM;
 PI
 XX WPI: 2000-514950/46.
 DR
 XX New peptide compound used as enzyme substrates for bacterial signal
 PT peptidases in assays to detect inhibitors of the peptidases.
 PT
 XX

PS Example 18: Page 17: 36pp; English.

XX The specification describes peptide compounds, which are used as enzyme
 CC substrates for bacterial signal peptidases, in particular Staphylococcus
 CC aureus SpsB and Escherichia coli leader peptidases. They are useful in
 CC assay systems for testing for signal peptidase inhibitors. The assay is
 CC used to test for inhibition of cleavage at specified time points or the
 CC rate of cleavage. Compounds identified by the assay as inhibitors of
 CC cleavage by the peptidases may be used to treat bacterial infections.
 CC The present sequence represents a peptide compound of the invention,
 CC which is used as a signal peptidase inhibitor in the course of the
 CC invention.

XX Sequence 13 AA;

Query Match: 36.4%; Score 4; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASKK 4

DB 8 ASKK 11

RESULT 49

AAB08047

ID AAB08047 standard; Peptide: 13 AA

AC AAB08047;

XX 04-DEC-2000 (first entry)

DE Signal peptidase inhibitor peptide compound.

XX Enzyme substrate: bacterial signal peptidase; Staphylococcus aureus SpsB;
 KW Escherichia coli leader peptidase; signal peptidase inhibitor;
 KW bacterial infection.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note- "decanoyl attached to residue"

FT Modified-site 4 Lys(fluorescein 5/6 carbonyl) or Lys(TAMRA);

FT Modified-site 11 /note- "biotin-X, TAMRA or fluorescein 5/6 carbonyl

FT Modified-site 13 attached"

FT Modified-site 13 /note- "hydroxyl attached to residue"

XX W0200046250-A1.

XX 10 AUG 2000.

XX 01-FEB-2000: 2000MO-EP00751.

XX 03-FEB-1999: 99GB-0002399.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Ashman S, Black M, Bruton G, Humphries AJ, Moore KJM.

XX WPI: 2000-514950/46.

XX New peptide compound used as enzyme substrates for bacterial signal

XX peptidases in assays to detect inhibitors of the peptidases .

XX Example 19: Page 18: 36pp; English.

XX The specification describes peptide compounds, which are used as enzyme
 CC substrates for bacterial signal peptidases, in particular Staphylococcus
 CC aureus SpsB and Escherichia coli leader peptidases. They are useful in
 CC assay systems for testing for signal peptidase inhibitors. The assay is

CC used to test for inhibition of cleavage at specified time points or the
 CC rate of cleavage. Compounds identified by the assay as inhibitors of
 CC cleavage by the peptidases may be used to treat bacterial infections.
 CC The present sequence represents a peptide compound of the invention,
 CC which is used as a signal peptidase inhibitor in the course of the
 CC invention.

XX Sequence 13 AA;

Query Match: 36.4%; Score 4; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASKK 4

DB 8 ASKK 11

RESULT 49

AAB08048

ID AAB08048 standard; Peptide: 13 AA.

XX AAB08048;

XX 04-DEC-2000 (first entry)

XX Signal peptidase inhibitor peptide compound.

XX Enzyme substrate: bacterial signal peptidase; Staphylococcus aureus SpsB;
 KW Escherichia coli leader peptidase; signal peptidase inhibitor;
 KW bacterial infection.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note- "decanoyl attached to residue"

FT Modified-site 4 /note- "biotin-X or fluorescein-5/6-carbonyl attached"

FT Modified-site 11 /note- "fluorescein-5/6-carbonyl, TAMRA or biotin-X is

FT Modified-site 13 attached"

FT Modified-site 13 /note- "hydroxyl attached to residue"

XX W0200046250-A1.

XX 10 AUG 2000.

XX 01-FEB 2000: 2000MO-EP00751.

XX 03-FEB-1999: 99GB-0002399.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Ashman S, Black M, Bruton G, Humphries AJ, Moore KJM.

XX WPI: 2000-514950/46.

XX New peptide compound used as enzyme substrates for bacterial signal

XX peptidases in assays to detect inhibitors of the peptidases -

XX Example 20: Page 20: 36pp; English.

XX The specification describes peptide compounds, which are used as enzyme
 CC substrates for bacterial signal peptidases, in particular Staphylococcus
 CC aureus SpsB and Escherichia coli leader peptidases. They are useful in
 CC assay systems for testing for signal peptidase inhibitors. The assay is
 CC used to test for inhibition of cleavage at specified time points or the
 CC rate of cleavage. Compounds identified by the assay as inhibitors of
 CC cleavage by the peptidases may be used to treat bacterial infections.
 CC The present sequence represents a peptide compound of the invention,
 CC which is used as a signal peptidase inhibitor in the course of the

Search completed: September 30, 2003, 10:24:32
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CC Invention.
XX
SQ Sequence 13 AA;
Query Match 36.4%; Score 4; 18 21, Length 18;
Best Local Similarity 100.0%; Pred. No. 6, 8+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ASKK 4
IIII
LB 8 ASKK 11

RESULT 50
AA015448
ID AA015448 standard, Peptide: 13 AA.
XX
AC AA015448;
XX
DT 27-SEP-2002 (first entry)
XX
DE Rat C/EBP-beta peptide epitope.
XX
KW Rat: CCAAT/Enhancer binding protein; apoptosis; C/EBP-beta protein;
KW fibrosis-related disease; brain damage; myocardial infarction;
KW arteriosclerosis; ocular fibrosis; fibrotic skin condition; epitope;
KW fibrotic pulmonary disease; wound healing.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Modified-site 7 /note= "Amino acid is phosphorylated"
XX
XX W020025493b-A2.
XX 18-JUL-2002.
XX
XX 26-NOV-2001; 2002MO-US02393.
XX
XX 27-OCT-2000; 2000US-244018P.
XX
XX (REGN) UNIV CALIFORNIA.
XX
XX ChaJkier M. Buck M;
XX WPI: 2002-566706/60.
XX
XX New modified CCAAT/Enhancer binding protein for inducing apoptosis and
XX treating a fibrosis-related disease, and a hepatic disease, brain
XX damage, myocardial infarction, or arteriosclerosis
XX
XX Example 5; Page 52; 79pp; English.

XX The invention comprises modified CCAAT/Enhancer binding proteins that are
XX capable of inducing apoptosis. The invent ion specifically comprises
XX modified mouse, rat and human C/EBP-beta proteins. The C/EBP-beta
XX proteins of the invention are useful for inducing apoptosis in a cell of
XX tissue. The C/EBP-beta proteins are also useful for treating a fibrosis-
XX related disease, such as: brain damage; myocardial infarction;
XX arteriosclerosis; ocular fibrosis; fibrotic skin conditions; fibrotic
XX pulmonary disease; and to improve wound healing. The present amino acid
XX sequence represents an epitope of the rat C/EBP-beta protein.

XX SQ Sequence 13 AA;
Query Match 36.4%; Score 4; 18 21, Length 18;
Best Local Similarity 100.0%; Pred. No. 6, 8+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKKP 5
IIII
LB 4 SKKP 6

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(without alignments)
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Gapop 60.0 , Gapext 60.0

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Procs. No. is the number of results (entries) for which to take a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	11	100.0	11	15	US-10-147-954-28			Sequence 28, Appl
2	4	36.4	9	9	US-09-796-294-45			Sequence 35, Appl
3	4	36.4	9	9	US-09-796-294-54			Sequence 54, Appl
4	4	36.4	9	11	US-09-876-904A-444			Sequence 444, Appl
5	4	36.4	9	12	US-10-291-250-14			Sequence 14, Appl
6	4	36.4	9	12	US-10-348-504-91			Sequence 86, Appl
7	4	36.4	9	12	US-10-348-504-92			Sequence 109, Appl
8	4	36.4	9	12	US-10-348-504-93			Sequence 112, Appl
9	4	36.4	10	11	US-09-572-434B-124			Sequence 921, Appl
10	4	36.4	10	11	US-09-572-434B-124			Sequence 1474, Appl
11	4	36.4	10	11	US-09-572-434B-124			Sequence 2564, Appl
12	4	36.4	10	11	US-09-572-434B-124			Sequence 3121, Appl
13	4	36.4	10	11	US-09-572-434B-124			Sequence 3123, Appl
14	4	36.4	10	11	US-09-572-434B-124			Sequence 3151, Appl
15	4	36.4	11	13	US-09-876-904A-576			Sequence 576, Appl

16	4	36.4	12	11	US-09-876-904A-607			Sequence 607, Appl
17	4	36.4	12	15	US-10-185-815-2			Sequence 2, Appl
18	4	36.4	13	10	US-09-897-107-60			Sequence 60, Appl
19	4	36.4	13	12	US-10-291-250-30			Sequence 30, Appl
20	4	36.4	14	11	US-09-992-665-49			Sequence 49, Appl
21	4	36.4	15	9	US-09-884-260A-2			Sequence 2, Appl
22	4	36.4	15	11	US-09-992-665-16			Sequence 16, Appl
23	4	36.4	15	15	US-10-229-567-17			Sequence 17, Appl
24	4	36.4	15	15	US-10-229-567-18			Sequence 18, Appl
25	3	27.3	8	8	US-08-817-832B-9			Sequence 9, Appl
26	3	27.3	8	8	US-08-817-832B-14			Sequence 14, Appl
27	3	27.3	8	8	US-09-879-936-19			Sequence 19, Appl
28	3	27.3	8	10	US-09-854-799-48			Sequence 48, Appl
29	3	27.3	8	10	US-09-984-056-34			Sequence 34, Appl
30	3	27.3	8	10	US-09-984-056-79			Sequence 79, Appl
31	3	27.3	8	10	US-09-984-057-34			Sequence 34, Appl
32	3	27.3	8	10	US-09-984-057-79			Sequence 79, Appl
33	3	27.3	8	10	US-09-938-497-6			Sequence 6, Appl
34	3	27.3	8	11	US-09-726-470A-69			Sequence 69, Appl
35	3	27.3	8	11	US-09-876-904A-57			Sequence 57, Appl
36	3	27.3	8	11	US-09-876-904A-84			Sequence 84, Appl
37	3	27.3	8	11	US-09-876-904A-203			Sequence 203, Appl
38	3	27.3	8	11	US-09-876-904A-258			Sequence 258, Appl
39	3	27.3	8	11	US-09-876-904A-266			Sequence 266, Appl
40	3	27.3	8	11	US-09-876-904A-267			Sequence 267, Appl
41	3	27.3	8	11	US-09-876-904A-405			Sequence 405, Appl
42	3	27.3	8	11	US-09-876-904A-438			Sequence 438, Appl
43	3	27.3	8	11	US-09-876-904A-536			Sequence 536, Appl
44	3	27.3	8	11	US-09-876-904A-537			Sequence 537, Appl
45	3	27.3	8	11	US-09-876-904A-576			Sequence 576, Appl
46	3	27.3	8	11	US-09-876-904A-584			Sequence 584, Appl
47	3	27.3	8	11	US-09-876-904A-599			Sequence 599, Appl
48	3	27.3	8	11	US-09-876-904A-613			Sequence 613, Appl
49	3	27.3	8	11	US-09-827-542-12			Sequence 12, Appl
50	3	27.3	8	12	US-09-791-524-149			Sequence 149, Appl
51	3	27.3	8	12	US-09-974-992-18			Sequence 18, Appl
52	3	27.3	8	12	US-10-079-167-4			Sequence 4, Appl
53	3	27.3	8	12	US-10-348-504-72			Sequence 72, Appl
54	3	27.3	8	12	US-10-348-504-90			Sequence 90, Appl
55	3	27.3	8	12	US-10-348-504-91			Sequence 91, Appl
56	3	27.3	8	12	US-10-348-504-92			Sequence 92, Appl
57	3	27.3	8	12	US-10-348-504-93			Sequence 93, Appl
58	3	27.3	8	12	US-10-348-504-113			Sequence 113, Appl
59	3	27.3	8	12	US-10-350-258-2			Sequence 2, Appl
60	3	27.3	8	12	US-10-209-187A-4			Sequence 4, Appl
61	3	27.3	8	12	US-10-209-187A-6			Sequence 6, Appl
62	3	27.3	8	12	US-10-224-999A-1325			Sequence 1325, Appl
63	3	27.3	8	14	US-10-061-395-67			Sequence 67, Appl
64	3	27.3	8	15	US-10-216-810A-7			Sequence 7, Appl
65	3	27.3	8	15	US-10-128-711-17			Sequence 17, Appl
66	3	27.3	8	15	US-10-052-942-73			Sequence 73, Appl
67	3	27.3	8	15	US-10-215-435-13			Sequence 13, Appl
68	3	27.3	9	7	US-10-156-570A-11			Sequence 11, Appl
69	3	27.3	9	7	US-08-344-824-110			Sequence 110, Appl
70	3	27.3	9	7	US-08-344-824-160			Sequence 160, Appl
71	3	27.3	9	8	US-08-452-843A-19			Sequence 19, Appl
72	3	27.3	9	8	US-08-821-739A-58			Sequence 58, Appl
73	3	27.3	9	9	US-09-113-924-6			Sequence 6, Appl
74	3	27.3	9	9	US-09-005-243-69			Sequence 69, Appl
75	3	27.3	9	9	US-09-224-683-69			Sequence 69, Appl
76	3	27.3	9	9	US-09-834-765-218			Sequence 218, Appl
77	3	27.3	9	9	US-09-834-765-330			Sequence 330, Appl
78	3	27.3	9	9	US-09-845-867-20			Sequence 20, Appl
79	3	27.3	9	9	US-09-192-854-44			Sequence 44, Appl
80	3	27.3	9	9	US-09-832-723-99			Sequence 99, Appl
81	3	27.3	9	10	US-09-780-053-38			Sequence 38, Appl
82	3	27.3	9	10	US-09-780-053-49			Sequence 49, Appl
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86	3	27.3	9	10	US-09-780-053-260			Sequence 260, Appl
87	3	27.3	9	10	US-09-780-053-321			Sequence 321, Appl
88	3	27.3	9	10	US-09-780-053-321			Sequence 321, Appl

89	3	27.3	9	10	US-09-786-053-134	Sequence 433, App	162	3	27.3	9	12	US-10-062-109A-147	Sequence 147, App
90	3	27.3	9	10	US-09-786-053-134	Sequence 434, App	163	3	27.3	9	12	US-10-062-109A-266	Sequence 266, App
91	3	27.3	9	10	US-09-786-053-134	Sequence 435, App	164	3	27.3	9	12	US-10-062-109A-294	Sequence 294, App
92	3	27.3	9	10	US-09-786-053-134	Sequence 518, App	165	3	27.3	9	12	US-10-062-109A-297	Sequence 297, App
93	3	27.3	9	10	US-09-786-053-134	Sequence 522, App	166	3	27.3	9	12	US-10-062-109A-381	Sequence 381, App
94	3	27.3	9	10	US-09-786-053-134	Sequence 224, App	167	3	27.3	9	12	US-10-062-109A-485	Sequence 485, App
95	3	27.3	9	10	US-09-786-053-134	Sequence 5, App11	168	3	27.3	9	12	US-10-062-109A-489	Sequence 489, App
96	3	27.3	9	10	US-09-786-053-134	Sequence 9, App11	169	3	27.3	9	12	US-10-062-109A-581	Sequence 581, App
97	3	27.3	9	10	US-09-786-053-134	Sequence 97, App1	170	3	27.3	9	12	US-10-062-109A-667	Sequence 667, App
98	3	27.3	9	10	US-09-786-053-134	Sequence 99, App1	171	3	27.3	9	12	US-10-062-109A-842-10	Sequence 10, App1
99	3	27.3	9	10	US-09-786-053-134	Sequence 106, App	172	3	27.3	9	12	US-10-224-999A-1330	Sequence 1330, App
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101	3	27.3	9	10	US-09-786-053-134	Sequence 129, App	174	3	27.3	9	12	US-10-224-999A-1332	Sequence 1332, App
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103	3	27.3	9	10	US-09-786-053-134	Sequence 30, App2	176	3	27.3	9	12	US-10-315-520-16	Sequence 16, App1
104	3	27.3	9	10	US-09-786-053-134	Sequence 97, App1	177	3	27.3	9	14	US-10-042-202-15	Sequence 12, App1
105	3	27.3	9	10	US-09-786-053-134	Sequence 99, App1	178	3	27.3	9	14	US-10-042-202-15	Sequence 15, App1
106	3	27.3	9	10	US-09-786-053-134	Sequence 106, App	179	3	27.3	9	14	US-10-042-202-16	Sequence 16, App1
107	3	27.3	9	10	US-09-786-053-134	Sequence 107, App	180	3	27.3	9	14	US-10-042-202-37	Sequence 37, App1
108	3	27.3	9	10	US-09-786-053-134	Sequence 129, App	181	3	27.3	9	14	US-10-081-281-75	Sequence 75, App1
109	3	27.3	9	10	US-09-786-053-134	Sequence 136, App	182	3	27.3	9	15	US-10-010-184A-8	Sequence 8, App11
110	3	27.3	9	10	US-09-786-053-134	Sequence 18, App1	183	3	27.3	9	15	US-10-102-283-134	Sequence 134, App
111	3	27.3	9	10	US-09-786-053-134	Sequence 18, App1	184	3	27.3	9	15	US-10-108-795-8	Sequence 8, App11
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114	3	27.3	9	10	US-09-786-053-134	Sequence 112, App	187	3	27.3	9	15	US-10-094-699-46	Sequence 46, App1
115	3	27.3	9	10	US-09-786-053-134	Sequence 21, App1	188	3	27.3	9	15	US-10-062-710-139	Sequence 139, App
116	3	27.3	9	10	US-09-786-053-134	Sequence 8, App11	189	3	27.3	9	15	US-10-193-934-1	Sequence 1, App11
117	3	27.3	9	10	US-09-786-053-134	Sequence 566, App	190	3	27.3	9	15	US-10-158-596A-35	Sequence 35, App1
118	3	27.3	9	10	US-09-786-053-134	Sequence 630, App	191	3	27.3	9	15	US-10-158-596A-38	Sequence 38, App1
119	3	27.3	9	10	US-09-786-053-134	Sequence 10, App1	192	3	27.3	9	15	US-10-157-775B-35	Sequence 35, App1
120	3	27.3	9	10	US-09-786-053-134	Sequence 83, App1	193	3	27.3	9	15	US-10-157-775B-38	Sequence 38, App1
121	3	27.3	9	10	US-09-786-053-134	Sequence 84, App1	194	3	27.3	9	15	US-10-115-365-8	Sequence 8, App11
122	3	27.3	9	10	US-09-786-053-134	Sequence 47, App	195	3	27.3	9	15	US-10-115-365-9	Sequence 9, App11
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125	3	27.3	9	10	US-09-786-053-134	Sequence 45, App1	198	3	27.3	9	15	US-10-105-901-25	Sequence 25, App1
126	3	27.3	9	10	US-09-786-053-134	Sequence 74, App1	199	3	27.3	9	15	US-10-338-462-18	Sequence 18, App1
127	3	27.3	9	10	US-09-786-053-134	Sequence 272, App	200	3	27.3	9	15	US-10-015-328-3	Sequence 3, App11
128	3	27.3	9	10	US-09-786-053-134	Sequence 336, App	201	3	27.3	9	15	US-10-211-088-271	Sequence 271, App
129	3	27.3	9	10	US-09-786-053-134	Sequence 370, App	202	3	27.3	9	15	US-10-196-174-40	Sequence 0, App11
130	3	27.3	9	10	US-09-786-053-134	Sequence 489, App	203	3	27.3	9	15	US-10-254-446A-35	Sequence 35, App1
131	3	27.3	9	10	US-09-786-053-134	Sequence 562, App	204	3	27.3	9	15	US-10-254-446A-38	Sequence 38, App1
132	3	27.3	9	10	US-09-786-053-134	Sequence 589, App	205	3	27.3	9	15	US-10-095-818A-18	Sequence 18, App1
133	3	27.3	9	10	US-09-786-053-134	Sequence 34, App1	206	3	27.3	10	7	US-08-344-824-210	Sequence 210, App
134	3	27.3	9	12	US-09-786-053-134	Sequence 165, App	207	3	27.3	10	9	US-09-151-450-15	Sequence 15, App1
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137	3	27.3	9	12	US-09-786-053-134	Sequence 438, App	210	3	27.3	10	9	US-09-870-162A-41	Sequence 41, App1
138	3	27.3	9	12	US-09-786-053-134	Sequence 440, App	211	3	27.3	10	9	US-09-870-162A-42	Sequence 42, App1
139	3	27.3	9	12	US-09-786-053-134	Sequence 440, App	212	3	27.3	10	9	US-09-976-787-1	Sequence 1, App11
140	3	27.3	9	12	US-09-786-053-134	Sequence 440, App	213	3	27.3	10	9	US-09-845-667-19	Sequence 19, App1
141	3	27.3	9	12	US-09-786-053-134	Sequence 875, App	214	3	27.3	10	9	US-09-845-667-23	Sequence 23, App1
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143	3	27.3	9	12	US-09-786-053-134	Sequence 37, App1	216	3	27.3	10	9	US-09-780-662A-1	Sequence 1, App11
144	3	27.3	9	12	US-10-135-853-35	Sequence 66, App1	217	3	27.3	10	10	US-09-780-053-72	Sequence 72, App1
145	3	27.3	9	12	US-10-135-853-35	Sequence 45, App1	218	3	27.3	10	10	US-09-780-053-103	Sequence 103, App
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152	3	27.3	9	12	US-10-308-073-41	Sequence 21, App1	225	3	27.3	10	10	US-09-865-198-1	Sequence 1, App11
153	3	27.3	9	12	US-09-785-454-11	Sequence 11, App1	226	3	27.3	10	10	US-09-984-056-85	Sequence 85, App1
154	3	27.3	9	12	US-09-945-454-424	Sequence 324, App	227	3	27.3	10	10	US-09-520-698-8	Sequence 8, App11
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156	3	27.3	9	12	US-09-945-454-563	Sequence 533, App	229	3	27.3	10	10	US-09-071-838-33	Sequence 33, App1
157	3	27.3	9	12	US-09-945-454-663	Sequence 637, App	230	3	27.3	10	10	US-09-902-432-5	Sequence 5, App11
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160	3	27.3	9	12	US-10-062-109A-24	Sequence 24, App1	233	3	27.3	10	11	US-09-882-291-66	Sequence 66, App1
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243	3	27.3	10	11	US-09-876-904A-598	Sequence 598, App	316	3	27.3	10	12	US-09-572-270A-847	Sequence 761, App
244	3	27.3	10	11	US-09-876-904A-611	Sequence 611, App	317	3	27.3	10	12	US-09-572-270A-847	Sequence 847, App
245	3	27.3	10	11	US-09-572-404B-348	Sequence 348, App	318	3	27.3	10	12	US-09-572-270A-889	Sequence 889, App
246	3	27.3	10	11	US-09-572-404B-350	Sequence 350, App	319	3	27.3	10	12	US-09-572-270A-899	Sequence 899, App
247	3	27.3	10	11	US-09-572-404B-370	Sequence 370, App	320	3	27.3	10	12	US-10-153-185-13	Sequence 957, App
248	3	27.3	10	11	US-09-572-404B-425	Sequence 425, App	321	3	27.3	10	12	US-10-190-082-385	Sequence 13, Appl
249	3	27.3	10	11	US-09-572-404B-458	Sequence 458, App	322	3	27.3	10	12	US-10-376-383-10	Sequence 385, App
250	3	27.3	10	11	US-09-572-404B-467	Sequence 467, App	323	3	27.3	10	12	US-10-116-212-1	Sequence 10, Appl
251	3	27.3	10	11	US-09-572-404B-525	Sequence 525, App	324	3	27.3	10	12	US-10-116-212-4	Sequence 1, Appl1
252	3	27.3	10	11	US-09-572-404B-541	Sequence 541, App	325	3	27.3	10	12	US-10-116-212-5	Sequence 4, Appl1
253	3	27.3	10	11	US-09-572-404B-698	Sequence 698, App	326	3	27.3	10	12	US-10-116-212-6	Sequence 5, Appl1
254	3	27.3	10	11	US-09-572-404B-913	Sequence 913, App	327	3	27.3	10	12	US-10-116-212-10	Sequence 10, Appl
255	3	27.3	10	11	US-09-572-404B-939	Sequence 939, App	328	3	27.3	10	12	US-10-116-212-12	Sequence 12, Appl
256	3	27.3	10	11	US-09-572-404B-954	Sequence 954, App	329	3	27.3	10	12	US-10-116-212-19	Sequence 19, Appl
257	3	27.3	10	11	US-09-572-404B-965	Sequence 965, App	330	3	27.3	10	12	US-09-935-384-53	Sequence 53, Appl
258	3	27.3	10	11	US-09-572-404B-973	Sequence 973, App	331	3	27.3	10	12	US-09-935-384-88	Sequence 88, Appl
259	3	27.3	10	11	US-09-572-404B-1480	Sequence 1480, App	332	3	27.3	10	12	US-09-935-384-280	Sequence 280, App
260	3	27.3	10	11	US-09-572-404B-1488	Sequence 1488, App	333	3	27.3	10	12	US-09-935-384-359	Sequence 359, App
261	3	27.3	10	11	US-09-572-404B-1774	Sequence 1774, App	334	3	27.3	10	12	US-09-935-384-388	Sequence 388, App
262	3	27.3	10	11	US-09-572-404B-1891	Sequence 1891, App	335	3	27.3	10	12	US-09-935-384-454	Sequence 454, App
263	3	27.3	10	11	US-09-572-404B-2180	Sequence 2180, App	336	3	27.3	10	12	US-09-935-384-656	Sequence 656, App
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265	3	27.3	10	11	US-09-572-404B-2191	Sequence 2191, App	338	3	27.3	10	12	US-10-062-109A-57	Sequence 57, Appl
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270	3	27.3	10	11	US-09-572-404B-3188	Sequence 3188, App	343	3	27.3	10	12	US-10-062-109A-521	Sequence 521, App
271	3	27.3	10	11	US-09-572-404B-3324	Sequence 3324, App	344	3	27.3	10	12	US-10-062-109A-615	Sequence 615, App
272	3	27.3	10	11	US-09-572-404B-3565	Sequence 3565, App	345	3	27.3	10	12	US-10-062-109A-628	Sequence 628, App
273	3	27.3	10	11	US-09-572-404B-3567	Sequence 3567, App	346	3	27.3	10	12	US-10-182-303-1	Sequence 1, Appl1
274	3	27.3	10	11	US-09-572-404B-3912	Sequence 3912, App	347	3	27.3	10	12	US-10-189-976-1	Sequence 1, Appl1
275	3	27.3	10	11	US-09-572-404B-3913	Sequence 3913, App	348	3	27.3	10	12	US-10-219-561-13	Sequence 13, Appl
276	3	27.3	10	11	US-09-572-404B-4018	Sequence 4018, App	349	3	27.3	10	12	US-10-325-021-6	Sequence 6, Appl1
277	3	27.3	10	11	US-09-572-404B-4020	Sequence 4020, App	350	3	27.3	10	12	US-10-224-999A-1336	Sequence 1336, App
278	3	27.3	10	11	US-09-572-404B-4160	Sequence 4160, App	351	3	27.3	10	12	US-10-224-999A-1337	Sequence 1337, App
279	3	27.3	10	11	US-09-572-404B-4161	Sequence 4161, App	352	3	27.3	10	12	US-10-224-999A-1338	Sequence 1338, App
280	3	27.3	10	11	US-09-572-404B-4162	Sequence 4162, App	353	3	27.3	10	12	US-10-224-999A-1339	Sequence 1339, App
281	3	27.3	10	11	US-09-572-404B-4164	Sequence 4163, App	354	3	27.3	10	12	US-09-833-039-101	Sequence 101, App
282	3	27.3	10	11	US-09-572-404B-4164	Sequence 4163, App	355	3	27.3	10	12	US-10-239-313A-691	Sequence 691, App
283	3	27.3	10	11	US-09-572-404B-4164	Sequence 4163, App	356	3	27.3	10	14	US-10-042-202-30	Sequence 30, Appl
284	3	27.3	10	11	US-09-832-084-7	Sequence 1, Appl1	357	3	27.3	10	14	US-10-081-281-74	Sequence 74, Appl
285	3	27.3	10	12	US-09-932-165-176	Sequence 176, App	358	3	27.3	10	14	US-10-081-281-78	Sequence 78, Appl
286	3	27.3	10	12	US-09-932-165-558	Sequence 558, App	359	3	27.3	10	14	US-10-024-918-5	Sequence 5, Appl1
287	3	27.3	10	12	US-09-932-165-576	Sequence 576, App	360	3	27.3	10	15	US-10-108-795-1	Sequence 1, Appl1
288	3	27.3	10	12	US-09-932-165-751	Sequence 751, App	361	3	27.3	10	15	US-10-108-795-4	Sequence 4, Appl1
289	3	27.3	10	12	US-09-932-165-754	Sequence 754, App	362	3	27.3	10	15	US-10-108-795-5	Sequence 5, Appl1
290	3	27.3	10	12	US-09-932-165-761	Sequence 761, App	363	3	27.3	10	15	US-10-108-795-6	Sequence 6, Appl1
291	3	27.3	10	12	US-09-932-165-1369	Sequence 1369, App	364	3	27.3	10	15	US-10-108-795-10	Sequence 10, Appl
292	3	27.3	10	12	US-09-932-165-1472	Sequence 1372, App	365	3	27.3	10	15	US-10-108-795-12	Sequence 12, Appl
293	3	27.3	10	12	US-09-974-992-1	Sequence 1, Appl1	366	3	27.3	10	15	US-10-108-795-19	Sequence 19, Appl
294	3	27.3	10	12	US-09-974-992-26	Sequence 26, Appl	367	3	27.3	10	15	US-10-094-699-45	Sequence 45, Appl
295	3	27.3	10	12	US-09-974-992-27	Sequence 27, Appl	368	3	27.3	10	15	US-10-094-699-47	Sequence 47, Appl
296	3	27.3	10	12	US-09-974-992-29	Sequence 29, Appl	369	3	27.3	10	15	US-10-062-710-79	Sequence 79, Appl
297	3	27.3	10	12	US-09-974-992-30	Sequence 30, Appl	370	3	27.3	10	15	US-10-115-365-1	Sequence 1, Appl1
298	3	27.3	10	12	US-09-974-992-31	Sequence 31, Appl	371	3	27.3	10	15	US-10-115-365-4	Sequence 4, Appl1
299	3	27.3	10	12	US-09-974-992-32	Sequence 32, Appl	372	3	27.3	10	15	US-10-115-365-5	Sequence 5, Appl1
300	3	27.3	10	12	US-09-974-992-33	Sequence 33, Appl	373	3	27.3	10	15	US-10-115-365-6	Sequence 6, Appl1
301	3	27.3	10	12	US-09-974-992-35	Sequence 35, Appl	374	3	27.3	10	15	US-10-115-365-10	Sequence 10, Appl
302	3	27.3	10	12	US-09-974-992-37	Sequence 37, Appl	375	3	27.3	10	15	US-10-115-365-12	Sequence 12, Appl
303	3	27.3	10	12	US-10-172-785-7	Sequence 7, Appl1	376	3	27.3	10	15	US-10-115-365-19	Sequence 19, Appl
304	3	27.3	10	12	US-10-193-764-22	Sequence 22, Appl	377	3	27.3	10	15	US-10-267-849-41	Sequence 41, Appl
305	3	27.3	10	12	US-09-572-270A-87	Sequence 87, Appl	378	3	27.3	10	15	US-10-062-848-53	Sequence 53, Appl
306	3	27.3	10	12	US-09-572-270A-94	Sequence 94, Appl	379	3	27.3	10	15	US-10-219-329-13	Sequence 13, Appl
307	3	27.3	10	12	US-09-572-270A-112	Sequence 112, App	380	3	27.3	10	15	US-10-133-210-19	Sequence 19, Appl

381	3	27.3	10	15	US-10-131-210-147	Sequence 147, App	454	3	27.3	11	15	US-10-160-290-4	Sequence 4, Appl
382	3	27.3	10	15	US-10-201-187-14	Sequence 14, Appl	455	3	27.3	11	15	US-10-095-818A-19	Sequence 19, Appl
383	3	27.3	10	15	US-10-211-088-192	Sequence 192, App	456	3	27.3	11	16	US-10-234-579-12	Sequence 12, Appl
384	3	27.3	10	15	US-10-211-312-3	Sequence 3, App	457	3	27.3	12	9	US-09-113-924-2	Sequence 2, Appl
385	3	27.3	10	15	US-10-106-804H 5	Sequence 3, Appl	458	3	27.3	12	9	US-09-030-619-74	Sequence 74, Appl
386	3	27.3	10	15	US-10-165-742A-7	Sequence 7, Appl	459	3	27.3	12	10	US-09-810-385-26	Sequence 26, Appl
387	3	27.3	11	7	US-09-444-824-44	Sequence 44, Appl	460	3	27.3	12	10	US-09-766-353A-1	Sequence 1, Appl
388	3	27.3	11	9	US-09-129-112-77	Sequence 17, Appl	461	3	27.3	12	10	US-09-848-664-5	Sequence 5, Appl
389	3	27.3	11	9	US-09-939-662-12	Sequence 12, Appl	462	3	27.3	12	10	US-09-848-967-7	Sequence 7, Appl
390	3	27.3	11	9	US-09-839-884-53	Sequence 53, Appl	463	3	27.3	12	11	US-09-899-046-127	Sequence 127, App
391	3	27.3	11	10	US-09-869-734-2	Sequence 2, Appl	464	3	27.3	12	11	US-09-962-955C-30	Sequence 30, Appl
392	3	27.3	11	10	US-09-941-611-5	Sequence 3, Appl	465	3	27.3	12	11	US-09-747-802-29	Sequence 29, Appl
393	3	27.3	11	10	US-09-982-254-4	Sequence 4, Appl	466	3	27.3	12	11	US-09-878-281-127	Sequence 127, App
394	3	27.3	11	10	US-09-813-53-10	Sequence 15, Appl	467	3	27.3	12	11	US-09-726-470A-9	Sequence 9, Appl
395	3	27.3	11	10	US-09-966-871-5	Sequence 5, Appl	468	3	27.3	12	11	US-09-865-294-21	Sequence 21, Appl
396	3	27.3	11	10	US-09-946-522-2	Sequence 2, Appl	469	3	27.3	12	11	US-09-876-904A-297	Sequence 297, App
397	3	27.3	11	10	US-09-872-832-37	Sequence 37, Appl	470	3	27.3	12	11	US-09-954-385-106	Sequence 106, App
398	3	27.3	11	10	US-09-791-378-202	Sequence 202, App	471	3	27.3	12	11	US-09-954-385-115	Sequence 115, App
399	3	27.3	11	10	US-09-953-587-31	Sequence 31, Appl	472	3	27.3	12	11	US-09-954-385-133	Sequence 133, App
400	3	27.3	11	10	US-09-839-743-15	Sequence 15, Appl	473	3	27.3	12	11	US-09-954-385-181	Sequence 181, App
401	3	27.3	11	10	US-09-849-741-17	Sequence 17, Appl	474	3	27.3	12	11	US-09-954-385-385	Sequence 385, App
402	3	27.3	11	10	US-09-849-743-19	Sequence 18, Appl	475	3	27.3	12	11	US-10-190-082-560	Sequence 560, App
403	3	27.3	11	10	US-09-839-743-24	Sequence 24, App	476	3	27.3	12	12	US-10-229-368-83	Sequence 83, Appl
404	3	27.3	11	10	US-09-671-638-39	Sequence 39, Appl	477	3	27.3	12	12	US-10-221-984-2	Sequence 2, Appl
405	3	27.3	11	10	US-09-982-254-4	Sequence 4, Appl	478	3	27.3	12	12	US-10-224-999A-1351	Sequence 1351, Ap
406	3	27.3	11	11	US-09-931-375A-77	Sequence 77, App	479	3	27.3	12	12	US-10-224-999A-1352	Sequence 1352, Ap
407	3	27.3	11	11	US-09-936-494A-9	Sequence 9, Appl	480	3	27.3	12	12	US-10-224-999A-1353	Sequence 1353, Ap
408	3	27.3	11	11	US-09-982-264-4	Sequence 4, Appl	481	3	27.3	12	12	US-10-224-999A-1354	Sequence 1354, Ap
409	3	27.3	11	11	US-09-982-287-4	Sequence 4, Appl	482	3	27.3	12	12	US-10-224-999A-1355	Sequence 1355, Ap
410	3	27.3	11	11	US-09-862-291-54	Sequence 64, Appl	483	3	27.3	12	12	US-10-225-087-73	Sequence 73, Appl
411	3	27.3	11	11	US-09-803-391-598	Sequence 68, App	484	3	27.3	12	12	US-10-168-445-59	Sequence 59, Appl
412	3	27.3	11	11	US-09-224-402-31	Sequence 31, Appl	485	3	27.3	12	12	US-10-239-313A-608	Sequence 608, App
413	3	27.3	11	11	US-09-876-904A-13	Sequence 13, Appl	486	3	27.3	12	12	US-10-239-313A-671	Sequence 671, App
414	3	27.3	11	11	US-09-876-904A-202	Sequence 202, App	487	3	27.3	12	12	US-10-081-281-58	Sequence 58, Appl
415	3	27.3	11	11	US-09-876-904A-581	Sequence 581, App	488	3	27.3	12	14	US-10-081-281-67	Sequence 67, Appl
416	3	27.3	11	11	US-09-876-904A-591	Sequence 591, App	489	3	27.3	12	14	US-10-081-281-72	Sequence 72, Appl
417	3	27.3	11	11	US-09-876-904A-610	Sequence 610, App	490	3	27.3	12	14	US-10-081-281-76	Sequence 76, Appl
418	3	27.3	11	11	US-09-876-904A-622	Sequence 622, App	491	3	27.3	12	14	US-10-062-710-138	Sequence 138, App
419	3	27.3	11	11	US-09-849-884-63	Sequence 53, Appl	492	3	27.3	12	15	US-10-174-105A-167	Sequence 167, App
420	3	27.3	11	11	US-09-992-645-32	Sequence 12, Appl	493	3	27.3	12	15	US-10-244-715-24	Sequence 24, Appl
421	3	27.3	11	11	US-09-852-910-131	Sequence 131, App	494	3	27.3	12	15	US-10-023-282-845	Sequence 845, App
422	3	27.3	11	11	US-09-852-913-248	Sequence 248, App	495	3	27.3	12	15	US-10-100-957A-102	Sequence 102, App
423	3	27.3	11	11	US-09-865-548A-35	Sequence 35, Appl	496	3	27.3	12	15	US-10-075-869-15	Sequence 15, Appl
424	3	27.3	11	12	US-09-791-524-15	Sequence 15, Appl	497	3	27.3	12	15	US-10-226-007-385	Sequence 385, App
425	3	27.3	12	12	US-09-974-942-39	Sequence 39, Appl	498	3	27.3	12	15	US-10-226-007-394	Sequence 394, App
426	3	27.3	11	12	US-09-974-942-39	Sequence 40, Appl	499	3	27.3	12	15	US-10-148-936-1	Sequence 1, Appl
427	3	27.3	11	12	US-10-073-167-4	Sequence 6, Appl	500	3	27.3	12	15		
428	3	27.3	11	12	US-09-824-922-4	Sequence 4, Appl							
429	3	27.3	11	12	US-10-224-999A-1351	Sequence 1343, Ap							
430	3	27.3	11	12	US-10-224-999A-1351	Sequence 1344, Ap							
431	3	27.3	11	12	US-10-224-999A-1351	Sequence 1345, Ap							
432	3	27.3	11	12	US-10-224-999A-1346	Sequence 1346, Ap							
433	3	27.3	11	12	US-10-224-999A-1347	Sequence 1347, Ap							
434	3	27.3	11	12	US-09-854-248-21	Sequence 21, App							
435	3	27.3	11	12	US-09-882-177-638	Sequence 68, App							
436	3	27.3	11	12	US-10-001-245-215	Sequence 216, App							
437	3	27.3	11	12	US-10-020-259-7	Sequence 7, Appl							
438	3	27.3	11	12	US-10-239-313A-264	Sequence 263, App							
439	3	27.3	11	12	US-10-387-645-3	Sequence 14, Appl							
440	3	27.3	11	14	US-10-049-645-5	Sequence 5, Appl							
441	3	27.3	11	14	US-10-081-281-59	Sequence 59, Appl							
442	3	27.3	11	14	US-10-081-281-74	Sequence 71, Appl							
443	3	27.3	11	14	US-10-081-281-77	Sequence 77, Appl							
444	3	27.3	11	14	US-10-044-703-13	Sequence 10, Appl							
445	3	27.3	11	15	US-10-044-995-3	Sequence 3, Appl							
446	3	27.3	11	15	US-10-059-261-45	Sequence 45, Appl							
447	3	27.3	11	15	US-10-059-261-143	Sequence 143, App							
448	3	27.3	11	15	US-10-139-084-5	Sequence 5, Appl							
449	3	27.3	11	15	US-10-149-336-12	Sequence 12, Appl							
450	3	27.3	11	15	US-10-206-659-238	Sequence 238, App							
451	3	27.3	11	15	US-10-211-048-204	Sequence 202, App							
452	3	27.3	11	15	US-10-226-017-484	Sequence 384, App							
453	3	27.3	11	15	US-10-213-512-49	Sequence 39, App							

ALIGNMENTS

RESULT 1

US-10-157-954-28

; Sequence 28, Application US/10197954

; Publication No. US20030119021A1

; GENERAL INFORMATION:

; APPLICANT: K*ster, Hubert

; APPLICANT: Siddiqui, Subal

; APPLICANT: Little, Daniel

; TITLE OF INVENTION: Capture Compounds, Collections Thereof

; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex

; TITLE OF INVENTION: Compositions

; FILE REFERENCE: 24743-2305

; CURRENT FILING DATE: 2002-07-16

; PRIOR FILING DATE: 2002-07-16

; PRIOR FILING DATE: 2001-07-16

; PRIOR FILING DATE: 2001-07-16

; PRIOR FILING DATE: 2001-08-21

; PRIOR FILING DATE: 2002-03-11

; NUMBER OF SEQ ID NOS: 149

SOFTWARE: FastSeq for Windows Version 4.0
 ? SEQ ID NO 28
 ? LENGTH: 11
 ? TYPE: PRT
 ? ORGANISM: Homo Sapien
 US-10-197-954-28

Query Match 100.0%; Score 11; DB 15; Length 11;
 Best Local Similarity 100.0%; Pred. No. 28-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 ASKKPKRNKA 11
 |||||
 LB : ASKKPKRNKA 11

RESULT 2

US-09-796-294-35
 ? Sequence 35; Application US/09796294
 ? Patent No. US20020037581A1

GENERAL INFORMATION:
 ? APPLICANT: O'Brien, Timothy J.
 ? TITLE OF INVENTION: Extracellular Serrine Protease
 ? FILE REFERENCE: D6020CIP3
 ? CURRENT APPLICATION NUMBER: US/09/796,294
 ? CURRENT FILING DATE: 2001-02-28
 ? PRIOR APPLICATION NUMBER: US 09/618,259
 ? PRIOR FILING DATE: 2000-07-18
 ? NUMBER OF SEQ ID NOS: 72

SEQ ID NO 35

LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:

OTHER INFORMATION: Residues 71-79 of the LALC 14 protein
 US-09-796-294-35

Query Match 36.4%; Score 4; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 KKPK 6
 ||||
 LB 5 KKPK 8

RESULT 3

US-09-796-294-54
 ? Sequence 54; Application US/09796294
 ? Patent No. US20020037581A1

GENERAL INFORMATION:
 ? APPLICANT: O'Brien, Timothy J.
 ? TITLE OF INVENTION: Extracellular Serrine Protease
 ? FILE REFERENCE: D6020CIP3
 ? CURRENT APPLICATION NUMBER: US/09/796,294
 ? CURRENT FILING DATE: 2001-02-28
 ? PRIOR APPLICATION NUMBER: US 09/618,259
 ? PRIOR FILING DATE: 2000-07-18
 ? NUMBER OF SEQ ID NOS: 72

SEQ ID NO 54

LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:

OTHER INFORMATION: Residues 73-81 of the LALC 14 protein
 US-09-796-294-54

Query Match 36.4%; Score 4; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 KKPK 6
 ||||
 LB 3 KKPK 6

RESULT 4

US-09-876-904A-444
 ? Sequence 44; Application US/09876904A
 ? Publication No. US20030072794A1

GENERAL INFORMATION:
 ? APPLICANT: BOUTIKAS, TEN;
 ? TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
 ? TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
 ? FILE REFERENCE: TB-2002-00

CURRENT APPLICATION NUMBER: US/09/876,904A
 CURRENT FILING DATE: 2001-06-08
 PRIOR APPLICATION NUMBER: US 60/210,925
 PRIOR FILING DATE: 2000-06-09
 NUMBER OF SEQ ID NOS: 629
 SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 444

LENGTH: 9
 TYPE: PRT
 ORGANISM: Saccharomyces cerevisiae
 FEATURE:

OTHER INFORMATION: Yeast NP51 transcription protein factor (1359 aa)
 OTHER INFORMATION: Involved in cell growth control at G2 phase.

US-09-876-904A-444

Query Match 36.4%; Score 4; DB 11; Length 9;

Best Local Similarity 100.0%; Pred. No. 5e-05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 KKPK 5
 ||||
 LB 5 KKPK 6

RESULT 5

US-10-291-250-14

Sequence 14; Application US/10291250
 Publication No. US20030133912A1

GENERAL INFORMATION:
 ? APPLICANT: University of Iowa Research Foundation
 ? APPLICANT: Davidson, Beverly L.

APPLICANT: Xia, Haibin
 APPLICANT: Law, Lane K.
 TITLE OF INVENTION: RECEPTION-TARGETED ADENO VIRAL VECTORS

FILE REFERENCE: 675,051,051
 CURRENT APPLICATION NUMBER: US/10/291,250
 CURRENT FILING DATE: 2002-11-07
 PRIOR APPLICATION NUMBER: US 60/349,282
 PRIOR FILING DATE: 2001-12-11

NUMBER OF SEQ ID NOS: 40

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14

LENGTH: 9
 TYPE: PRT
 ORGANISM: Adenovirus

US-10-291-250-14

Query Match 36.4%; Score 4; DB 12; Length 9;

Best Local Similarity 100.0%; Pred. No. 5e-05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 KKPK 6
 ||||
 LB 5 KKPK 7

RESULT 6

US-10-357-176-57

Sequence 86, Application US/09/557175
 Publication No. US20030170707A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Transmembrane Serine Protease, secreted
 FILE REFERENCE: D6192CIP/D/CIP
 CURRENT APPLICATION NUMBER: US/09/557175
 PRIOR APPLICATION NUMBER: 2003-02-03
 PRIOR FILING DATE: 2003-02-03
 PRIOR FILING DATE: 2003-02-03
 NUMBER OF SEQ ID NOS: 158
 SEQ ID NO 86
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 LOCATION: 294..304
 OTHER INFORMATION: TAGS 12 peptide
 US-10-357-175-86

Query Match 36.4% Score 4; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPKR 7

DB 3 KPKR 6

RESULT 7

US-10-357-175-109
 Sequence 109, Application US/10/57175
 Publication No. US20030170707A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Transmembrane Serine Protease, secreted
 FILE REFERENCE: D6192CIP/D/CIP
 CURRENT APPLICATION NUMBER: US/10/57175
 CURRENT FILING DATE: 2003-02-03
 PRIOR APPLICATION NUMBER: 2003-02-03
 PRIOR FILING DATE: 2003-02-03
 NUMBER OF SEQ ID NOS: 158
 SEQ ID NO 109
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 LOCATION: 298..306
 OTHER INFORMATION: TAGS 12 peptide
 US-10-357-175-109

Query Match 36.4% Score 4; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPKR 7

DB 1 KPKR 4

RESULT 8

US-10-357-175-112
 Sequence 112, Application US/10/57175
 Publication No. US20030170707A1
 GENERAL INFORMATION:
 APPLICANT: O'Brien, Timothy J.
 TITLE OF INVENTION: Transmembrane Serine Protease, secreted
 FILE REFERENCE: D6192CIP/D/CIP
 CURRENT APPLICATION NUMBER: US/10/57175
 CURRENT FILING DATE: 2003-02-03

PRIOR APPLICATION NUMBER: US/09/550371
 PRIOR FILING DATE: 2003-08-28
 NUMBER OF SEQ ID NOS: 158
 SEQ ID NO 112
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 LOCATION: 294..302
 OTHER INFORMATION: TAGS 12 peptide
 US-10-357-175-112

Query Match 36.4% Score 4; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPKR 7

DB 5 KPKR 8

RESULT 9

US-09-572-404B-921
 Sequence 921, Application US/09572404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: ProPatent version 1.0
 SEQ ID NO 921
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURE:
 OTHER INFORMATION: Sequence located in ADRBK1 OR GRK2 OR BARK1 OR BARK at 22-31
 OTHER INFORMATION: Interact with Sequence 922 in this patent.
 US-09-572-404B-921

Query Match 36.4% Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 ASKK 4

DB 7 ASKK 10

RESULT 10

US-09-572-404B-1478
 Sequence 1478, Application US/09572404B
 Publication No. US20030078374A1
 GENERAL INFORMATION:
 APPLICANT: Proteom Ltd
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000-05-17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: ProPatent version 1.0
 SEQ ID NO 1478
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURE:
 OTHER INFORMATION: Sequence located in RGS13 at 50-59 and may interact with Sequ

Query Match 36.4% Score 4; DB 11; Length 10;

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Best Local Similarity 100.0%; Pred. No. 4 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKPK 6
   1 1 1
Db 7 KKPK 10

RESULT 11
US-09-572-404B-2564
: Sequence 2564, Application US/09572404B
: Publication No. US20030078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide ligands from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572.404B
: CURRENT FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 2564
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: sequence located in EMBL at 35 64 and may interact with Sequence
: US-09-572-404B-2564

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKPK 7
   1 1 1
Db 5 KKPK 8

RESULT 12
US-09-572-404B-3121
: Sequence 3121, Application US/09572404B
: Publication No. US20030078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide ligands from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572.404B
: CURRENT FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 3121
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: sequence located in GUCY2F OR GUC2F OR RETGC2 at 939 945 and may
: US-09-572-404B-3121

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKRN 8
   1 1 1
Db 4 PKRN 7

RESULT 13
US-09-572-404B-3123
: Sequence 3123, Application US/09572404B
: Publication No. US20030078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide ligands from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572.404B
: CURRENT FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 3123
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: sequence located in GUCY2F OR GUC2F OR RETGC2 at 938-947 and
: US-09-572-404B-3123

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKRN 8
   1 1 1
Db 1 PKRN 4

RESULT 14
US-09-572-404B-3153
: Sequence 3153, Application US/09572404B
: Publication No. US20030078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide ligands from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572.404B
: CURRENT FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 3153
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: sequence located in GUCY2F OR GUC2F OR RETGC2 at 942-951 and
: US-09-572-404B-3153

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKRN 8
   1 1 1
Db 1 PKRN 4

RESULT 15
US-09-876-904A-597
: Sequence 597, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMI DNA (LIPOGENES TM) AND THERAPEUTIC
: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876.904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 597
: LENGTH: 11
```



```

: TYPE: PRT
: ORGANISM: Parachinus angulosus
: FEATURE:
: OTHER INFORMATION: Sea urchin Parachinus angulosus sperm H1 (248 aa).
US-09-876-904A-597

Query Match          36.4%: Score 4; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.2e-02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
   III
Db 5 KKPK 8

RESULT 16
US-09-876-904A-607
: Sequence 607, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND PHARMACEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 607
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Unknown Organism
: FEATURE:
: OTHER INFORMATION: Description of Unknown Organism: Annealed sperm H1a (119 aa).
US-09-876-904A-607

Query Match          36.4%: Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.2e-02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
   III
Db 2 KKPK 5

RESULT 17
US 10 185-815-2
: Sequence 2; Application US/10185815
: Publication No. US20030096354A1
: GENERAL INFORMATION:
: APPLICANT: Elan Corporation, plc
: APPLICANT: O'Mahony, Daniel
: APPLICANT: Lambkin, Imelda
: APPLICANT: Higgins, Lisa
: TITLE OF INVENTION: Peyer's Patch And/or M-Cell Targeting Ligands
: FILE REFERENCE: E1067-20093
: CURRENT APPLICATION NUMBER: US/10/185,815
: CURRENT FILING DATE: 2002-10-09
: PRIOR APPLICATION NUMBER: 60/302,591
: PRIOR FILING DATE: 2001-07-02
: NUMBER OF SEQ ID NOS: 99
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: polypeptide ligand
US-10-185-815-2
```

```

Query Match          36.4%: Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.2e-02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KRNI 9
   III
Db 6 KRNI 9

RESULT 18
US-09-897-107-60
: Sequence 60, Application US/09897107
: Patent No. US20020137094A1
: GENERAL INFORMATION:
: APPLICANT: YAMAGISHI, Akihiko
: TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HA
: TITLE OF INVENTION: THERMOSTABILITY IMPROVED BY THE METHOD AND NUCLEIC ACIDS ENC
: FILE REFERENCE: 2103830S0
: CURRENT APPLICATION NUMBER: US/09/897,107
: CURRENT FILING DATE: 2001-07-03
: PRIOR APPLICATION NUMBER: JP2000-201920
: PRIOR FILING DATE: 2000-07-04
: PRIOR APPLICATION NUMBER: JP2001-164332
: PRIOR FILING DATE: 2001-05-31
: NUMBER OF SEQ ID NOS: 104
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 60
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
: OTHER INFORMATION:
US-09-897-107-60

Query Match          36.4%: Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.5e-02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASKK 4
   III
Db 10 ASKK 13

RESULT 19
US-10-291-250-30
: Sequence 30, Application US/10291250
: Publication No. US20030133912A1
: GENERAL INFORMATION:
: APPLICANT: University of Iowa Research Foundation
: APPLICANT: Davidson, Beverly L.
: APPLICANT: Xia, Haibin
: APPLICANT: Law, Lane K.
: TITLE OF INVENTION: RECEPTOR TARGETED ADENO VIRAL VECTORS
: FILE REFERENCE: 875 0510S1
: CURRENT APPLICATION NUMBER: US/10/291,250
: CURRENT FILING DATE: 2002-11-07
: PRIOR APPLICATION NUMBER: US 60/339,282
: PRIOR FILING DATE: 2001-12-11
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 30
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: A protein motif.
US-10-291-250-30

Query Match          36.4%: Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.5e-02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
   III
Db 7 KKPK 10
```

```

RESULT 20
US-09-992-665-49
? Sequence 49, Application US/09992665
? Publication No. US20030092009A1
? GENERAL INFORMATION:
? APPLICANT: Kaia Palm
? TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
? FILE REFERENCE: CEMINES 002A
? CURRENT APPLICATION NUMBER: US/09/992-665
? PRIOR FILING DATE: 2001-11-13
? PRIOR FILING DATE: 2000-11-16
? NUMBER OF SEQ ID NOS: 380
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 49
? LENGTH: 14
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Probe
US-09-992-665-49

```

```

Query Match 36.4%; Score 4; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 11 KKPK 14

```

```

RESULT 21
US-09-884-260A-2
? Sequence 2, Application US/09884260A
? Patent No. US20020098570A1
? GENERAL INFORMATION:
? APPLICANT: Alan Brash
? APPLICANT: Nathalie Tillet
? TITLE OF INVENTION: MUSKELON (CUCUMIS MEL) HYDROPEROXIDE
? FILE REFERENCE: 06027.000202
? CURRENT APPLICATION NUMBER: US/09/884-260A
? PRIOR FILING DATE: 2001-06-19
? PRIOR FILING DATE: 2000-03-29
? NUMBER OF SEQ ID NOS: 56
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 2
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Cucumis melo
US-09-884-260A-2

```

```

Query Match 36.4%; Score 4; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KRNI 9
DB 10 KRNI 13

```

```

RESULT 22
US-09-992-665-16
? Sequence 16, Application US/09992665
? Publication No. US20030092009A1
? GENERAL INFORMATION:
? APPLICANT: Kaia Palm
? TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
? FILE REFERENCE: CEMINES 002A
? CURRENT APPLICATION NUMBER: US/09/992-665
? PRIOR FILING DATE: 2001-11-13
? PRIOR FILING DATE: 2000-11-16
? NUMBER OF SEQ ID NOS: 380
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 16
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Probe
US-09-992-665-16

```

```

? FILE REFERENCE: CEMINES 002A
? CURRENT APPLICATION NUMBER: US/09/992-665
? CURRENT FILING DATE: 2001-11-13
? PRIOR FILING DATE: 2000-11-16
? PRIOR FILING DATE: 2000-11-16
? NUMBER OF SEQ ID NOS: 380
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 16
? LENGTH: 15
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Probe
US-09-992-665-16

```

```

Query Match 36.4%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 4 KPKR 7
DB 2 KPKR 5

```

```

RESULT 23
US-10-229-567-17
? Sequence 17, Application US/10229567
? Publication No. US20030092080A1
? GENERAL INFORMATION:
? APPLICANT: Braum, Jonathan
? APPLICANT: Cohavy, Offer
? TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
? ulcerative Colitis, and Clinical Subtypes Thereof, Usin
? Microbial UC PANCA antigens
? NUMBER OF SEQUENCES: 41
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Campbell & Flores LLP
? STREET: 4370 La Jolla Village Drive, Suite 700
? CITY: San Diego
? STATE: California
? COUNTRY: USA
? ZIP: 92122
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/229,567
? FILING DATE: 27-Aug-2002
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/09/417,264
? FILING DATE: <Unknown>
? APPLICATION NUMBER: US 09/041,889
? FILING DATE: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Campbell, Cathryn A.
? REGISTRATION NUMBER: 31,815
? REFERENCE/DOCKET NUMBER: P-PM 3006
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (619) 535-9001
? TELEFAX: (619) 535-8949
? INFORMATION FOR SEQ ID NO: 17:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 15 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-229-567-17

```

```

Query Match 36.4%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5e+02;

```

```

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 3 KKKK 6
   11 1
DB 12 KKKK 15

RESULT 24
US-10-229-567-18
Sequence 18, Application US/102495/2
Publication No. US20030092080A1
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan;
Cohavy, Ofer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
Ulcerative Colitis, and Related Subtypes Thereof, Using
Microbial or PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10-229-567
FILING DATE: 27 Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE: <Unknown>
APPLICATION NUMBER: US/04/1,499
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,810
REFERENCE/DOCKET NUMBER: P 10 409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 545-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-229-567-18

Query Match 36.4%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. Gaps 0;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 3 KKKK 6
   11 1
DB 12 KKKK 15

RESULT 25
US-08-817-832B-9
Sequence 9, Application US/08817832B
Publication No. US20030104516A1
GENERAL INFORMATION:
APPLICANT: MANDELKOW, Eckhard, et al.
TITLE OF INVENTION: NO. US20030104516A1 Protein Kinase (NPK-110)
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 S. Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: US
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,832B
FILING DATE: 28-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/04258
FILING DATE: 30-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94 11 7122-5
FILING DATE: 26-OCT-1994
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

```

```

STREET: 233 S. Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: US
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,832B
FILING DATE: 28-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/04258
FILING DATE: 30-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94 11 7122-5
FILING DATE: 28-OCT-1994
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STEREOPHONESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: Peptide
LOCATION:
OTHER INFORMATION: /note- "Ser at position 3 is
OTHER INFORMATION: phosphorylated."
US-08-817-832B-9

Query Match 27.4%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. Se+05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 8 NIK 15
   11
DB 6 NIK 8

RESULT 26
US-08-817-832B-14
Sequence 14, Application US/08817832B
Publication No. US20030104516A1
GENERAL INFORMATION:
APPLICANT: MANDELKOW, Eckhard, et al.
TITLE OF INVENTION: NO. US20030104516A1 Protein Kinase (NPK-110)
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 S. Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: US
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,832B
FILING DATE: 28-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/04258
FILING DATE: 30-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94 11 7122-5
FILING DATE: 26-OCT-1994
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

```

LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 3
OTHER INFORMATION: /note "See at position 1 is phosphorylated"
US-08-817-832B-14

Query Match 27.3% Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NIK 10
DB 6 NIK 8

RESULT 27
US-09-879-936 19
Sequence 19, Application US/09879936
Patent No. US2002045564A1
GENERAL INFORMATION:
APPLICANT: Van Eyk, Jennifer E.
APPLICANT: Mak, Alan S.
FILE OF INVENTION: Methods of Modulating Muscle Contraction
FILE REFERENCE: 1997-021-0305
CURRENT APPLICATION NUMBER: US/09/879,936
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/050,474
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 60/089,505
PRIOR FILING DATE: 1998-06-16
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 8
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)-(8)
OTHER INFORMATION: Site C (catalytic site) and phosphorylation site
US-09-879-936-19

Query Match 27.3% Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 4 PKR 6

RESULT 28
US-09-854-799-48
Sequence 48, Application US/09854799
Patent No. US2002015064A1
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Corporation
TITLE OF INVENTION: Recombinant Feline Coronavirus S Proteins
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA

COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,799
FILING DATE: 14-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,459
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/613,066
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: King, William T.
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: SBC 14532B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5015
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-854-799-48

Query Match 27.3% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RNI 9
DB 2 RNI 4

RESULT 29
US-09-984-056-34
Sequence 34, Application US/09984056
Patent No. US20020120106A1
GENERAL INFORMATION:
APPLICANT: BOGACH, SAMUEL
TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICONS AND METHODS OF USE
FILE REFERENCE: 09425-459C3
CURRENT APPLICATION NUMBER: US/09/984,056
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 60/303,396
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/278,761
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 09/146,755
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 09/87,144
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 08/198,139
PRIOR FILING DATE: 1994-02-17
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn 2.1
SEQ ID NO 34
LENGTH: 8
TYPE: PRT
ORGANISM: Caldophora prolifera
US-09-984-056-34

Query Match 27.3% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 ASK 3
      111
DB      2 ASK 4
      111

Query Match: 27.3%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 30
US-09-984-056-79
: Sequence 79, Application US/09984056
: Patent No. US20020120166A1
: GENERAL INFORMATION:
: APPLICANT: BOGUCH, SAMUEL
: APPLICANT: BOGUCH, ELENORE S.
: TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICINS AND METHODS OF USE
: FILE REFERENCE: 09425-46903
: CURRENT APPLICATION NUMBER: US/09/984,056
: PRIOR FILING DATE: 2001-10-26
: PRIOR APPLICATION NUMBER: 60/303,396
: PRIOR FILING DATE: 2001-07-09
: PRIOR APPLICATION NUMBER: 60/278,761
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 09/146,755
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: 09/817,144
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 08/198,139
: PRIOR FILING DATE: 1994-02-17
: NUMBER OF SEQ ID NOS: 103
: SOFTWARE: PatentIn 2.1
: SEQ ID NO 79
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-984-056-79

Query Match: 27.3%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 KKP 5
      111
DB      2 KKP 4
      111

Query Match: 27.3%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 31
US-09-984-057-79
: Sequence 34, Application US/09984057
: Patent No. US20020151677A1
: GENERAL INFORMATION:
: APPLICANT: BOGUCH, SAMUEL
: APPLICANT: BOGUCH, ELENORE S.
: TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING
: TITLE OF INVENTION: REPLICIN-CONTAINING SEQUENCES
: FILE REFERENCE: 09425-46902
: CURRENT APPLICATION NUMBER: US/09/984,057
: CURRENT FILING DATE: 2001-10-26
: PRIOR APPLICATION NUMBER: 60/303,396
: PRIOR FILING DATE: 2001-07-09
: PRIOR APPLICATION NUMBER: 60/278,761
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 09/146,755
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: 09/817,144
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 08/198,139
: PRIOR FILING DATE: 1994-02-17
: NUMBER OF SEQ ID NOS: 90
: SOFTWARE: PatentIn 2.1
: SEQ ID NO 34
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Calophora prolifera
US-09-984-057-79

Query Match: 27.3%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 KKP 5
      111
DB      2 KKP 4
      111

Query Match: 27.3%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 32
US-09-984-057-79
: Sequence 79, Application US/09984057
: Patent No. US20020151677A1
: GENERAL INFORMATION:
: APPLICANT: BOGUCH, SAMUEL
: APPLICANT: BOGUCH, ELENORE S.
: TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING
: TITLE OF INVENTION: REPLICIN-CONTAINING SEQUENCES
: FILE REFERENCE: 09425-46902
: CURRENT APPLICATION NUMBER: US/09/984,057
: CURRENT FILING DATE: 2001-10-26
: PRIOR APPLICATION NUMBER: 60/303,396
: PRIOR FILING DATE: 2001-07-09
: PRIOR APPLICATION NUMBER: 60/278,761
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 09/146,755
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: 09/817,144
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 08/198,139
: PRIOR FILING DATE: 1994-02-17
: NUMBER OF SEQ ID NOS: 90
: SOFTWARE: PatentIn 2.1
: SEQ ID NO 79
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-984-057-79

Query Match: 27.3%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 KKP 5
      111
DB      2 KKP 4
      111

Query Match: 27.3%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 33
US-09-938-497-6
: Sequence 6, Application US/09938497
: Patent No. US20020173462A1
: GENERAL INFORMATION:
: APPLICANT: WASTFALL, Maria K. Boden
: APPLICANT: FLOCK, Jan-Ingmar
: TITLE OF INVENTION: FIBRINOGEN BINDING PROTEIN
: NUMBER OF SEQUENCES: 15
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/938,497
: FILING DATE: 27-Aug-2001
```

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/276,141
FILING DATE: <Unknown>
APPLICATION NUMBER: SE 9302955-1
FILING DATE: 13-SEP-1993
APPLICATION NUMBER: WO PCT/SE93/00759
FILING DATE: 20-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,400
REFERENCE/DOCKET NUMBER: 012889-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-948-497-6

Query Match 27.3% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
DB 5 KKP 7

RESULT 34

US-09-726-470A-69
Sequence 69, Application US/09726470A
Publication No. US20030036628A1
GENERAL INFORMATION:
APPLICANT: Zheleva, Dantella I
APPLICANT: Fischer, Peter M
APPLICANT: McInnes, Campbell
APPLICANT: Andrews, Martin JI
APPLICANT: Chan, Weng C
APPLICANT: Atkinson, Gail E
TITLE OF INVENTION: p21 Peptides
FILE REFERENCE: CCI-014
CURRENT APPLICATION NUMBER: US/09/726,470A
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 275
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 69
LENGTH: 8
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: p21 derived
OTHER INFORMATION: Synthesised with free amino terminus and as the C-terminal carboxamide
US-09-726-470A-69

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KRN 8
DB 3 KRN 5

RESULT 35
US-09-876-904A-57
Sequence 57, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002-00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 8
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Chicken Ets1
OTHER INFORMATION: core NLS peptide
US-09-876-904A-57

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
DB 6 KPK 8

RESULT 36

US-09-876-904A-84
Sequence 84, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002-00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 84
LENGTH: 8
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Putative core
OTHER INFORMATION: NLS of yeast TRM1
US-09-876-904A-84

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4
DB 3 SKK 5

RESULT 37

US-09-876-904A-203
Sequence 203, Application US/09876904A
Publication No. US20030072794A1

```
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 203
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Karyophilic peptide
US-09-876-904A-203

Query Match          27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
   III
Db 2 PKR 4

RESULT 38
US-09-876-904A-258
; Sequence 258, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 258
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Bos sp.
; FEATURE:
; OTHER INFORMATION: Calf thymus HMG 1
US-09-876-904A-258

Query Match          27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
   III
Db 2 KKP 4

RESULT 39
US-09-876-904A-266
; Sequence 266, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
```

```
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 266
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Redox factor 1 from HeLa cel
US-09-876-904A-266

Query Match          27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
   III
Db 2 PKR 4

RESULT 40
US-09-876-904A-267
; Sequence 267, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 267
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Apurinic/apyrimidinic
US-09-876-904A-267

Query Match          27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
   III
Db 2 PKR 4

RESULT 41
US-09-876-904A-405
; Sequence 405, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 405
```

```
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TFIIIE beta (general transcription initiation
; OTHER INFORMATION: protein factor; forms tetramer; alpha 2 beta 2 with
; OTHER INFORMATION: TFIIIE-alpha)
US-09-876-904A-405

Query Match          27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4
   |||
DB 1 SKK 3

RESULT 42
US-09-876-904A-438
; Sequence 438, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 438
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; OTHER INFORMATION: C. elegans sex determining Hra-1 protein.
US-09-876-904A-438

Query Match          27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
   |||
DB 2 KKP 4

RESULT 43
US-09-876-904A-536
; Sequence 536, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 536
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Xenopus laevis
; FEATURE:
; OTHER INFORMATION: Xenopus laevis L1 ribosomal protein (homologous to
```

```
; OTHER INFORMATION: yeast L2).
US-09-876-904A-536

Query Match          27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
   |||
DB 6 KKP 8

RESULT 44
US-09-876-904A-537
; Sequence 537, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 537
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Xenopus laevis
; FEATURE:
; OTHER INFORMATION: Xenopus laevis L1 ribosomal protein (homologous to
; OTHER INFORMATION: yeast L2).
US-09-876-904A-537

Query Match          27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
   |||
DB 6 KKP 8

RESULT 45
US-09-876-904A-576
; Sequence 576, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 576
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human H2B variant differentially expressed during
; OTHER INFORMATION: the cell cycle.
US-09-876-904A-576

Query Match          27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
```


Matches 1: Conservative 2: Mismatches 3: Indels 4: Gaps 5:

QY 2 SKK 4
111
DB 5 SKK 7

RESULT 46
US-09-876-904A-584
Sequence 584, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 584
LENGTH: 8
TYPE: PRT
ORGANISM: Bos sp.
FEATURE:
OTHER INFORMATION: Calf thymus h2H (125 aa).
US-09-876-904A-584

Query Match: 27.3%, Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 SKK 4
111
DB 5 SKK 7

RESULT 47
US-09-876-904A-599
Sequence 599, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 599
LENGTH: 8
TYPE: PRT
ORGANISM: Parechinus angulosus
FEATURE:
OTHER INFORMATION: Sea urchin Parechinus angulosus sperm H1 (248 aa).
US-09-876-904A-599

Query Match: 27.3%, Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKP 5
111
DB 4 KKP 8

RESULT 48
US-09-876-904A-613
Sequence 613, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 613
LENGTH: 8
TYPE: PRT
ORGANISM: Bos sp.
FEATURE:
OTHER INFORMATION: Calf thymus HMG 1 (259 aa).
US-09-876-904A-613

Query Match: 27.3%, Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKP 5
111
DB 2 KKP 4

RESULT 49
US-09-827-542-12
Sequence 12, Application US/09827542
Publication No. US20030088057A1
GENERAL INFORMATION:
APPLICANT: Traugh, Colinda A.
TITLE OF INVENTION: Peptide Substrates Phosphorylated By P21-Activated
TITLE OF INVENTION: Protein Kinase
FILE REFERENCE: JC Case No. US20030088057A1 1999-035-2/Traugh et al.
CURRENT APPLICATION NUMBER: US/09/827,542
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 09/290,964
PRIOR FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 12
LENGTH: 8
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-827-542-12

Query Match: 27.3%, Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 PKR 7
111
DB 2 PKR 4

RESULT 50
US-09-791-524-149
Sequence 149, Application US/09791524
Publication No. US2003014209A1
GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Inc.

! TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery of Heterologous Genes

! FILE REFERENCE: A3319A
! CURRENT APPLICATION NUMBER: US/99/791,524
! CURRENT FILING DATE: 2001-02-22
! PRIOR APPLICATION NUMBER: 60/09825
! PRIOR FILING DATE: 1998-08-27
! NUMBER OF SEQ ID NOS: 150
! SOFTWARE: PatentIn version 3.0
! SEQ ID NO 149
! LENGTH: 8
! TYPE: PRT
! ORGANISM: Adenovirus
US-09-791-524 149

Query Match 27.3% Score 47.05 bits Ident 87
Best Local Similarity 100.0% Ident No. 56-051
Matches 3: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

QY 5 PKR 7
db 1 PKR 3

Search completed: September 30, 2003, 16:42:47
Job time : 27.5 secs

GenCore version 5.1.6
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OM protein protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 11.333 Seconds
(without alignments)
93.140 Million cell updates/sec

Title: US-09-787-443-1

Perfect score: 11

Sequence: ASKKPRNIKA 11

Scoring table: OLLGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96166682 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2064

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	27.3	8	S4365	probable Na ⁺ trans
2	3	27.3	9	J56402	xenopsin-related p
3	3	27.3	9	A63326	xenopsin-related p
4	3	27.3	10	S76722	65.4K GTP-binding
5	3	27.3	10	F41a35	ribosomal protein
6	3	27.3	10	PA0116	ferredoxin-NADP re
7	3	27.3	10	PS0220	ferredoxin-NADP re
8	3	27.3	11	S42449	anti protein - pha
9	3	27.3	11	B41835	translational c.enga
10	3	27.3	11	S19775	wound-induced prot
11	3	27.3	13	T08533	hypothetical prote
12	3	27.3	13	S22955	hypothetical prote
13	3	27.3	13	JQ1350	hypothetical prote
14	3	27.3	13	E50396	antiquet 7H8/2 - ma
15	3	27.3	13	S52456	hypothetical prote
16	3	27.3	14	H64008	hypothetical prote
17	3	27.3	14	PA0013	photosystem II oxy
18	3	27.3	14	S33803	chaperone, Tcp1-re
19	3	27.3	14	H83778	hypothetical prote
20	3	27.3	14	A54370	inorganic diphosph
21	3	27.3	15	S36889	ribosomal protein
22	3	27.3	15	T09463	ribosomal protein
23	3	27.3	15	PA0046	protein QA10044 -
24	3	27.3	15	PT0082	protein QA60023 -
25	3	27.3	15	S71300	ICL3 protein - Par
26	3	27.3	15	S77987	cytochrome-c oxida
27	3	27.3	15	S03955	acidic fibroblast
28	3	27.3	15	PX0031	mixed lymphocyte r
29	2	18.2	8	LF5AME	probable msrA lead

30	2	18.2	8	A31570	angiotensin-conver
31	2	18.2	8	S70727	ipgf protein - Shi
32	2	18.2	8	A39308	glycine reductase
33	2	18.2	8	T10952	hypothetical prote
34	2	18.2	8	S21288	lectin - potato (f
35	2	18.2	8	A39892	P element, P cytot
36	2	18.2	8	A14683	aspartate transami
37	2	18.2	8	A28719	thymic humoral fac
38	2	18.2	8	A54823	olfactory receptor
39	2	18.2	8	PT0595	T-cell receptor be
40	2	18.2	8	PT0627	T-cell receptor be
41	2	18.2	8	PT0530	T-cell receptor be
42	2	18.2	8	PT0527	T-cell receptor be
43	2	18.2	8	PT0522	T-cell receptor be
44	2	18.2	8	PT0509	T-cell receptor be
45	2	18.2	8	PT0639	T-cell receptor be
46	2	18.2	8	PT0631	T-cell receptor be
47	2	18.2	8	PT0613	T-cell receptor be
48	2	18.2	8	PT0653	T-cell receptor be
49	2	18.2	8	PT0547	T-cell receptor be
50	2	18.2	8	PT0557	T-cell receptor be
51	2	18.2	8	PT0559	T-cell receptor be
52	2	18.2	8	PT0554	T-cell receptor be
53	2	18.2	8	PT0716	T-cell receptor be
54	2	18.2	8	PT0724	T-cell receptor be
55	2	18.2	8	PT0725	T-cell receptor be
56	2	18.2	8	PT0588	T-cell receptor be
57	2	18.2	8	PT0691	T-cell receptor be
58	2	18.2	8	A38887	T-cell receptor ga
59	2	18.2	8	148935	apolipoprotein A1
60	2	18.2	8	B54823	olfactory receptor
61	2	18.2	8	A42889	major postsynaptic
62	2	18.2	8	PH0934	T-cell receptor be
63	2	18.2	8	I57532	gene Tn150w prote
64	2	18.2	8	S66296	Na ⁺ -transporting A
65	2	18.2	8	I54017	granulocyte-colony
66	2	18.2	8	B28495	conopressin S - co
67	2	18.2	9	A28495	conopressin G - co
68	2	18.2	9	S35538	ribosomal protein
69	2	18.2	9	S30494	cat gene leader pe
70	2	18.2	9	B24362	chloramphenicol O-
71	2	18.2	9	JQ1202	leader peptide - p
72	2	18.2	9	QDRB	delta sleep-induci
73	2	18.2	9	C36730	hutu protein - Kle
74	2	18.2	9	S19523	orf AB protein - S
75	2	18.2	9	JP0073	ribosomal protein
76	2	18.2	9	C41170	photosystem II pro
77	2	18.2	9	PC2021	oxytocin-related p
78	2	18.2	9	D41978	calliFERFamide 4 -
79	2	18.2	9	F41978	calliFERFamide 6 -
80	2	18.2	9	S10920	venom protein HR-3
81	2	18.2	9	A45199	L-lysophorin - Ja
82	2	18.2	9	A60356	118K stomach cance
83	2	18.2	9	I54379	gene NF2 protein -
84	2	18.2	9	PC2197	zymogen granule me
85	2	18.2	9	S66636	alpha-2-macroglobu
86	2	18.2	9	B46250	alpha-adaptin - bo
87	2	18.2	9	PC7076	spectrin alpha cha
88	2	18.2	9	PT0670	T-cell receptor be
89	2	18.2	9	PT0634	T-cell receptor be
90	2	18.2	9	PT0562	T-cell receptor be
91	2	18.2	9	PC7078	unidentified 48.7K
92	2	18.2	9	149406	bone gla protein -
93	2	18.2	9	PH0943	T-cell receptor be
94	2	18.2	9	PH0935	T-cell receptor be
95	2	18.2	9	PH0937	T-cell receptor be
96	2	18.2	9	PH0902	T-cell receptor be
97	2	18.2	9	PH0917	T-cell receptor be
98	2	18.2	9	PH0918	T-cell receptor be
99	2	18.2	9	PH0921	T-cell receptor be
100	2	18.2	9	S78426	52.5K protein - sp
101	2	18.2	9	S56004	glucan 1,3-beta-gl
102	2	18.2	9	S39040	lysine-conopressin

103	2	18.2	9	2	PC7074	ab:guano-rytochro	176	11	2	S23308	substance p - rain
104	2	18.2	10	1	XASNP3	andiotensis-conver	177	11	2	S23306	ranatachykinin A -
105	2	18.2	10	1	RHIM5S	gonadoliberin - se	178	11	2	A61033	ranatachykinin D -
106	2	18.2	10	2	A45491	C3 homolag HX - in	179	11	2	D61033	hypothetical prote
107	2	18.2	10	2	S10526	inhibin beta A cha	180	11	2	QJ0395	beta-glucosidase (
108	2	18.2	10	2	A60410	beta-neoenderphin	181	11	2	PQ0231	quinoline 2-oxidor
109	2	18.2	10	2	S16834	apolipoprotein A2	182	11	2	S66606	celf protein - Esc
110	2	18.2	10	2	A37110	ornithine decarbox	183	11	2	S42587	acetoactate synth
111	2	18.2	10	2	S39030	lysi-Bradykinin -	184	11	2	S33782	58K heat shock pro
112	2	18.2	10	2	C61033	ranatachykinin C -	185	11	2	PC2172	probable secreted
113	2	18.2	10	2	B33143	preumadin - huma	186	11	2	S33519	protein QA300023 -
114	2	18.2	10	2	A33143	preumadin - rat	187	11	2	PT0081	seed protein ws-23
115	2	18.2	10	2	A21617	ecdysteroid UDPglu	188	11	2	G61497	ribosomal protein
116	2	18.2	10	2	S51912	hemagglutinin - in	189	11	2	PC4267	unidentified 5.7/3
117	2	18.2	10	2	G56501	48K Elle/gallblad	190	11	2	PQ0731	DNA-binding protei
118	2	18.2	10	2	A24407	amicydin - Paraco	191	11	2	A34135	probable substance
119	2	18.2	10	2	S66458	ferredoxin - Rhizo	192	11	2	S33300	talin - chicken (f
120	2	18.2	10	2	S59625	beta-galactosidase	193	11	2	D42965	Rhesus blood group
121	2	18.2	10	2	PC4442	cytochrome c553 -	194	11	2	I54193	T cell receptor V-
122	2	18.2	10	2	S70251	nitrogenase (EC 1	195	11	2	S57575	acetylcholinestera
123	2	18.2	10	2	S42282	parasporal crystal	196	11	2	S68637	ribosomal protein
124	2	18.2	10	2	F46644	neurotoxin-associ	197	11	2	S78765	tubulin beta chain
125	2	18.2	10	2	Jfe072	ribosomal protein	198	11	2	S54347	protein kinase C 1
126	2	18.2	10	2	C39745	sphingomyelinase -	199	11	2	PN0044	T-cell receptor be
127	2	18.2	10	2	PC2044	beta Kirilowin - M	200	11	2	PT0217	T-cell receptor ga
128	2	18.2	10	2	PA0050	protegin CA10052 -	201	11	2	C38887	T-cell receptor ga
129	2	18.2	10	2	A59272	peptide-M4 (N-acet	202	11	2	I41946	translatlon elonga
130	2	18.2	10	2	H28027	protein p11 - curl	203	11	2	PD0441	cytochrome-c oxida
131	2	18.2	10	2	A20489	transcription fact	204	11	2	S65377	ribosomal protein
132	2	18.2	10	2	A49187	gonadotropin-relea	205	11	2	S78422	T-cell receptor be
133	2	18.2	10	2	S77980	cytochrome-c oxida	206	11	2	PH0939	T-cell receptor be
134	2	18.2	10	2	B37196	bradykinin-potenti	207	11	2	PH0940	T-cell receptor be
135	2	18.2	10	2	B37482	platelet activatin	208	11	2	PH0941	T-cell receptor be
136	2	18.2	10	2	S23371	T-cell receptor al	209	11	2	PH0929	T-cell receptor be
137	2	18.2	10	2	F49033	T-cell receptor ga	210	11	2	PH0891	T-cell receptor be
138	2	18.2	10	2	S71948	matrix metallopro	211	11	2	PH0938	T-cell receptor be
139	2	18.2	10	2	C54823	olfactory receptor	212	11	2	PH0947	T-cell receptor be
140	2	18.2	10	2	PT0632	T-cell receptor be	213	11	2	PH0903	T-cell receptor be
141	2	18.2	10	2	PT0664	T-cell receptor be	214	11	2	PH0904	T-cell receptor be
142	2	18.2	10	2	PT0215	T-cell receptor be	215	11	2	PH0924	T-cell receptor be
143	2	18.2	10	2	B38887	T-cell receptor ga	216	11	2	PH0919	T-cell receptor be
144	2	18.2	10	2	D54823	olfactory receptor	217	11	2	PH0914	T-cell receptor be
145	2	18.2	10	2	S65187	cytochrome-c oxida	218	11	2	PH0922	T-cell receptor be
146	2	18.2	10	2	PK0350	lysosome-associate	219	11	2	PH0906	T-cell receptor be
147	2	18.2	10	2	C10572	T-cell receptor be	220	11	2	A61575	Trimeresurus serin
148	2	18.2	10	2	PH0940	T-cell receptor be	221	11	2	S60294	tubulin 2 beta-3 c
149	2	18.2	10	2	PH0940	T-cell receptor be	222	11	4	PC2390	trichorozin I - fu
150	2	18.2	10	2	PH0944	T-cell receptor be	223	11	4	PC2392	trichorozin III -
151	2	18.2	10	2	PH0934	T-cell receptor be	224	11	4	S52252	hypothetical prote
152	2	18.2	10	2	PH0694	T-cell receptor be	225	11	4	I54081	retinoic acid rece
153	2	18.2	10	2	PH0944	T-cell receptor be	226	11	2	C49215	urease (EC 3.5.1.5
154	2	18.2	10	2	PH0945	T-cell receptor be	227	11	2	A28856	fructose-bisphosph
155	2	18.2	10	2	PH0926	T-cell receptor be	228	11	2	C36201	1-aminocyclopropan
156	2	18.2	10	2	PH0916	T-cell receptor be	229	11	2	S25485	transcription fact
157	2	18.2	10	2	PH0923	T-cell receptor be	230	11	2	S26541	T-cell receptor be
158	2	18.2	10	2	PH0895	T-cell receptor be	231	11	2	S26557	T-cell receptor be
159	2	18.2	10	2	PH0948	T-cell receptor be	232	11	2	S26546	T-cell receptor be
160	2	18.2	10	2	C54226	light-harvesting p	233	11	2	S26547	T-cell receptor be
161	2	18.2	11	1	XASNBA	bradykinin-potenti	234	11	2	S26555	T-cell receptor be
162	2	18.2	11	1	SPH0	substance p - hors	235	11	2	S26556	T-cell receptor be
163	2	18.2	11	1	EA0CC	eledosin - curled	236	11	2	S26553	T-cell receptor be
164	2	18.2	11	1	A60654	substance p - guin	237	11	2	S26558	T-cell receptor be
165	2	18.2	11	1	EXOC	eledosin - musky	238	11	2	S26552	T-cell receptor be
166	2	18.2	11	2	S32575	ribosomal protein	239	11	2	S26549	T-cell receptor be
167	2	18.2	11	2	A38841	rhodopsin homolog	240	11	2	S26559	T-cell receptor be
168	2	18.2	11	2	C53652	rhlR protein - pse	241	11	2	S26548	T-cell receptor be
169	2	18.2	11	2	A25930	ermC leader peptid	242	11	2	S26554	T-cell receptor be
170	2	18.2	11	2	YHR1	morphogenetic neur	243	11	2	S26544	histone H2B - huma
171	2	18.2	11	2	YHHU	morphogenetic neur	244	11	2	S65409	translatlon elonga
172	2	18.2	11	2	YHBO	morphogenetic neur	245	11	2	S01222	tachykinin - Afric
173	2	18.2	11	2	YHXA8	morphogenetic neur	246	11	2	S10059	kassinin - Senegal
174	2	18.2	11	2	YHJFYH	morphogenetic neur	247	11	2	S07206	24K kidney and bla
175	2	18.2	11	2	B26744	medascol-tachinin -	248	11	2	A58501	

249	2	18.2	12	2	G49215	urease (EC 3.5.1.5)	322	2	18.2	13	1	UNOPBT	neurotensin - brus
250	2	18.2	12	2	E45733	hypothetical prote	323	2	18.2	13	1	MTOMAD	melanotropin alpha
251	2	18.2	12	2	S71034	patB protein - Sal	324	2	18.2	13	1	MTOMAD	cytochrome P450 CW
252	2	18.2	12	2	S43013	hypothetical prote	325	2	18.2	13	2	S16874	neurotensin [valid
253	2	18.2	12	2	B28551	hypothetical prote	326	2	18.2	13	2	A28505	neurotensin - comm
254	2	18.2	12	2	T44420	hypothetical prote	327	2	18.2	13	2	A61067	neurotensin - comm
255	2	18.2	12	2	S18722	mark protein - lee	328	2	18.2	13	2	A32734	enkephalin precurs
256	2	18.2	12	2	S77540	agglutinin-III lec	329	2	18.2	13	2	A28953	alpha-conotoxin SI
257	2	18.2	12	2	P00596	1,4-alpha-glucan b	330	2	18.2	13	2	H35245	histone H1.c - mou
258	2	18.2	12	2	PA0098	ribosomal protein	331	2	18.2	13	2	A35245	histone H1a - mou
259	2	18.2	12	2	C60629	hemocyanin - are	332	2	18.2	13	2	S78519	ribosomal protein
260	2	18.2	12	2	E61408	hemocyanin chain 5	333	2	18.2	13	2	S39413	tubulin beta chain
261	2	18.2	12	2	A33900	hydrin 1 - African	334	2	18.2	13	2	A60336	outer membrane pro
262	2	18.2	12	2	S10626	lipovitellin - Bla	335	2	18.2	13	2	E37390	traA protein - Esc
263	2	18.2	12	2	A34859	proteinase E - bla	336	2	18.2	13	2	E39778	lactose phosphotra
264	2	18.2	12	2	A55837	5-aminimidazole r	337	2	18.2	13	2	P80122	OLL protein - vacc
265	2	18.2	12	2	A61504	sterol carrier pro	338	2	18.2	13	2	S21152	tryptophyllin-rela
266	2	18.2	12	2	S29830	dimethylamine mo	339	2	18.2	13	2	A05174	tryptophyllin-13 -
267	2	18.2	12	2	I77529	estrogen receptor	340	2	18.2	13	2	A60458	protocatechuate 3,
268	2	18.2	12	2	S47463	T-cell antigen rec	341	2	18.2	13	2	S12388	argA protein - Sal
269	2	18.2	12	2	S47491	T-cell antigen rec	342	2	18.2	13	2	S70723	lipamide dehydrog
270	2	18.2	12	2	S47393	T-cell antigen rec	343	2	18.2	13	2	B26093	microbial collagen
271	2	18.2	12	2	S47394	T-cell antigen rec	344	2	18.2	13	2	PC1008	40K extracellular
272	2	18.2	12	2	S47395	T-cell antigen rec	345	2	18.2	13	2	S63492	dissimilatory sulf
273	2	18.2	12	2	PH1180	T-cell receptor al	346	2	18.2	13	2	S36668	hypothetical prote
274	2	18.2	12	2	PH1187	T-cell receptor al	347	2	18.2	13	2	A46463	predorsal antige
275	2	18.2	12	2	PH1189	T-cell receptor al	348	2	18.2	13	2	S08575	botulinum neuroto
276	2	18.2	12	2	PH1182	T-cell receptor al	349	2	18.2	13	2	G44644	neurotoxin-associa
277	2	18.2	12	2	PH1185	T-cell receptor al	350	2	18.2	13	2	S36887	ribosomal protein
278	2	18.2	12	2	PH1180	T-cell receptor al	351	2	18.2	13	2	S23103	erythronolide synt
279	2	18.2	12	2	PH1183	T-cell receptor al	352	2	18.2	13	2	S14316	photosystem I 9K c
280	2	18.2	12	2	PH1188	T-cell receptor al	353	2	18.2	13	2	PA0049	protein QA100046 -
281	2	18.2	12	2	PH1172	T-cell receptor al	354	2	18.2	13	2	S28425	20K protein - rape
282	2	18.2	12	2	PH1171	T-cell receptor al	355	2	18.2	13	2	S00316	photosystem I 13K
283	2	18.2	12	2	PH1175	T-cell receptor al	356	2	18.2	13	2	B44957	protein I7 - commo
284	2	18.2	12	2	PH1174	T-cell receptor al	357	2	18.2	13	2	PC1149	equinotoxin 1A - s
285	2	18.2	12	2	PH1179	T-cell receptor al	358	2	18.2	13	2	A61514	glutathione transf
286	2	18.2	12	2	PH1181	T-cell receptor al	359	2	18.2	13	2	P50443	potassium channel
287	2	18.2	12	2	S51737	T-cell receptor be	360	2	18.2	13	2	B56533	CB61 homolog - cha
288	2	18.2	12	2	P80553	glystrophin-associa	361	2	18.2	13	2	A57789	gallbladder stone
289	2	18.2	12	2	A20507	Ig kappa chain J1	362	2	18.2	13	2	B28810	glutathione transf
290	2	18.2	12	2	C20507	Ig kappa-1 chain J	363	2	18.2	13	2	S23638	Ig kappa chain J s
291	2	18.2	12	2	D20507	Ig kappa-1 chain J	364	2	18.2	13	2	S23640	Ig kappa chain J s
292	2	18.2	12	2	E20997	Ig kappa & epsilon J	365	2	18.2	13	2	S47356	T-cell antigen rec
293	2	18.2	12	2	PH0743	T-cell receptor be	366	2	18.2	13	2	S47357	T-cell antigen rec
294	2	18.2	12	2	PH1467	T-cell receptor be	367	2	18.2	13	2	S47358	T-cell antigen rec
295	2	18.2	12	2	PH1468	T-cell receptor be	368	2	18.2	13	2	S47359	T-cell antigen rec
296	2	18.2	12	2	PH1467	T-cell receptor be	369	2	18.2	13	2	S47362	T-cell antigen rec
297	2	18.2	12	2	PH1467	T-cell receptor be	370	2	18.2	13	2	S47365	T-cell antigen rec
298	2	18.2	12	2	PH1470	T-cell receptor be	371	2	18.2	13	2	S47368	T-cell antigen rec
299	2	18.2	12	2	PH1464	T-cell receptor be	372	2	18.2	13	2	S47371	T-cell antigen rec
300	2	18.2	12	2	PH1466	T-cell receptor be	373	2	18.2	13	2	S47372	T-cell antigen rec
301	2	18.2	12	2	PH1461	T-cell receptor be	374	2	18.2	13	2	S47373	T-cell antigen rec
302	2	18.2	12	2	PH1469	T-cell receptor be	375	2	18.2	13	2	S47376	T-cell antigen rec
303	2	18.2	12	2	PH1457	T-cell receptor be	376	2	18.2	13	2	S47377	T-cell antigen rec
304	2	18.2	12	2	PH1459	T-cell receptor be	377	2	18.2	13	2	S47378	T-cell antigen rec
305	2	18.2	12	2	PH0771	T-cell receptor be	378	2	18.2	13	2	S47380	T-cell antigen rec
306	2	18.2	12	2	PH1468	T-cell receptor be	379	2	18.2	13	2	S47381	T-cell antigen rec
307	2	18.2	12	2	PT0216	T-cell receptor be	380	2	18.2	13	2	S47382	T-cell antigen rec
308	2	18.2	12	2	H41946	T-cell receptor ga	381	2	18.2	13	2	S47383	T-cell antigen rec
309	2	18.2	12	2	B32521	hexokinase (EC 2.7	382	2	18.2	13	2	S47384	T-cell antigen rec
310	2	18.2	12	2	PH0930	T-cell receptor be	383	2	18.2	13	2	S47385	T-cell antigen rec
311	2	18.2	12	2	PH0931	T-cell receptor be	384	2	18.2	13	2	S47388	T-cell antigen rec
312	2	18.2	12	2	PH0936	T-cell receptor be	385	2	18.2	13	2	S47389	T-cell antigen rec
313	2	18.2	12	2	PH0920	T-cell receptor be	386	2	18.2	13	2	S47390	T-cell antigen rec
314	2	18.2	12	2	PC4377	telomeric and tetr	387	2	18.2	13	2	S47392	T-cell antigen rec
315	2	18.2	12	2	S71380	lebetin 1 isoform	388	2	18.2	13	2	S47400	T-cell antigen rec
316	2	18.2	12	2	B56049	urinary tract ston	389	2	18.2	13	2	S47474	T-cell antigen rec
317	2	18.2	12	2	S27624	Na+/K+-exchanging	390	2	18.2	13	2	PH0138	T-cell receptor be
318	2	18.2	12	2	S27623	Na+/K+-exchanging	391	2	18.2	13	2	S61798	T-cell-specific tr
319	2	18.2	12	2	A51432	Na+/K+-exchanging	392	2	18.2	13	2	A39846	agrecan - bovine
320	2	18.2	12	4	S49077	frame shifted cys	393	2	18.2	13	2	S78766	ribosomal protein
321	2	18.2	13	1	UNB3	neurotensin - bovi	394	2	18.2	13	2	C53275	Ig kappa-1 chain J

395 2 18.2 13 2 B53275
 396 2 18.2 13 2 B25448
 397 2 18.2 13 2 B34932
 398 2 18.2 13 2 B33933
 399 2 18.2 13 2 B26406
 400 2 18.2 13 2 B40603
 401 2 18.2 13 2 PH1474
 402 2 18.2 13 2 PH0754
 403 2 18.2 13 2 PH0928
 404 2 18.2 13 2 A47630
 405 2 18.2 13 2 C47630
 406 2 18.2 13 2 B47630
 407 2 18.2 13 2 B47630
 408 2 18.2 13 2 B47630
 409 2 18.2 13 2 C131905
 410 2 18.2 13 2 G33488
 411 2 18.2 13 2 C61576
 412 2 18.2 13 2 A86126
 413 2 18.2 13 2 H85575
 414 2 18.2 13 2 S01504
 415 2 18.2 13 2 L70075
 416 2 18.2 14 1 QWAVV
 417 2 18.2 14 1 QWVHM
 418 2 18.2 14 1 QWVHX
 419 2 18.2 14 1 QWVHP
 420 2 18.2 14 1 QWVAP
 421 2 18.2 14 1 LPE76
 422 2 18.2 14 1 LFERW
 423 2 18.2 14 2 P23373
 424 2 18.2 14 2 JN0489
 425 2 18.2 14 2 PH1705
 426 2 18.2 14 2 L51532
 427 2 18.2 14 2 B29743
 428 2 18.2 14 2 A44513
 429 2 18.2 14 2 A61462
 430 2 18.2 14 2 JH032E
 431 2 18.2 14 2 E70858
 432 2 18.2 14 2 S29632
 433 2 18.2 14 2 A52503
 434 2 18.2 14 2 L39753
 435 2 18.2 14 2 FL0142
 436 2 18.2 14 2 S54945
 437 2 18.2 14 2 L54945
 438 2 18.2 14 2 B44854
 439 2 18.2 14 2 B56463
 440 2 18.2 14 2 S60374
 441 2 18.2 14 2 S36442
 442 2 18.2 14 2 S14864
 443 2 18.2 14 2 S29789
 444 2 18.2 14 2 PA0169
 445 2 18.2 14 2 PA0045
 446 2 18.2 14 2 S69721
 447 2 18.2 14 2 G44957
 448 2 18.2 14 2 PS0249
 449 2 18.2 14 2 S35267
 450 2 18.2 14 2 A51306
 451 2 18.2 14 2 B34135
 452 2 18.2 14 2 PC1215
 453 2 18.2 14 2 G61408
 454 2 18.2 14 2 S14336
 455 2 18.2 14 2 S12504
 456 2 18.2 14 2 S62374
 457 2 18.2 14 2 L64815
 458 2 18.2 14 2 S43639
 459 2 18.2 14 2 S41601
 460 2 18.2 14 2 PH1769
 461 2 18.2 14 2 PH0135
 462 2 18.2 14 2 E47039
 463 2 18.2 14 2 A47421
 464 2 18.2 14 2 F46394
 465 2 18.2 14 2 A39764
 466 2 18.2 14 2 P07054
 467 2 18.2 14 2 PH1601

468 2 18.2 14 2 PH1448
 469 2 18.2 14 2 PH0792
 470 2 18.2 14 2 PH0801
 471 2 18.2 14 2 PH1450
 472 2 18.2 14 2 PH1471
 473 2 18.2 14 2 PH0765
 474 2 18.2 14 2 PH0753
 475 2 18.2 14 2 PH0762
 476 2 18.2 14 2 PH0755
 477 2 18.2 14 2 PH0774
 478 2 18.2 14 2 D35141
 479 2 18.2 14 2 C35141
 480 2 18.2 14 2 S55141
 481 2 18.2 14 2 PC7079
 482 2 18.2 14 2 S65392
 483 2 18.2 14 2 A37789
 484 2 18.2 14 2 PH0945
 485 2 18.2 14 2 PH0915
 486 2 18.2 14 2 PC4382
 487 2 18.2 14 2 B83836
 488 2 18.2 14 2 B85761
 489 2 18.2 14 2 B81280
 490 2 18.2 14 2 C39170
 491 2 18.2 14 2 G33160
 492 2 18.2 14 2 A17150
 493 2 18.2 14 4 S00843
 494 2 18.2 15 2 B26597
 495 2 18.2 15 2 B61243
 496 2 18.2 15 2 PA0003
 497 2 18.2 15 2 P00195
 498 2 18.2 15 2 S21240
 499 2 18.2 15 2 S21202
 500 2 18.2 15 2 PC2215

ALIGNMENTS

RESULT 1

S45651
 Probable Na⁺-transporting ATP synthase (EC 3.6.1.-) - Acetobacterium woodii (fragment)
 C:Species: Acetobacterium woodii
 C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
 C:Accession: S45651
 K:Reidlinger, C.; Mueller, V.
 Eur. J. Biochem. 225, 275-284, 1994
 A:Title: Purification of ATP synthase from Acetobacterium woodii and identification
 A:Reference number: S45648; MIMD:94307271; PMID:8033902
 A:Molecule type: protein
 A:Residues: 1-8 <REL>
 A:Experimental source: DSM 1030
 C:Keywords: hydrolase

Query Match 27 38, Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3

DB 4 ASK 6

RESULT 2

J50302
 Xenopsin-related peptide 2 - turkey
 N:Contains: xenopsin-related peptide 1
 C:Species: Meleagris gallopavo (common turkey)
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000
 C:Accession: J50302
 R:Caraway, K.E.; Cochrane, D.E.; Mitra, S.P.
 Regul. Pept. 22, 403-414, 1988
 A:Title: Xenopsin related peptide generated in avian gastric extracts.

A:Reference number: J50302; MUID:89042995; PMID:2463902

A:Accession: J50302

A:Molecule type: protein

A:Residues: 1-9 <CA>

C:Comment: The peptides are present within several tissues primarily in large molecular

C:Suprafamily: yeast coatomer complex alpha chain; WB repeat homology

C:Keywords: neuropeptide

F:1-9/Product: xenopsin-related peptide 2 #status experimental <XP2>

F:2-9/Product: xenopsin-related peptide 1 #status experimental <XP1>

Query Match 27.3% Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7

DB 1 PKR 5

RESULT 3

A60320

xenopsin-related peptide 2 - rat

N:Contains: xenopsin-related peptide 1

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-Nov-1992 #sequence_revision 10 Nov 1992 #text_change 18-Aug-2000

C:Accession: A60320

R:Carraway, R.E.; Mitra, S.P.; Muraki, K.

Regul. Pept. 29, 229-239, 1990

A:Title: Isolation and structures of xenopsin related peptides from rat stomach, liver a

A:Reference number: A60320; MUID:91018491; PMID:2217944

A:Accession: A60320

A:Molecule type: protein

A:Residues: 1-9 <CA>

A:Note: the authors purified these peptides from pepsin-treated extracts of stomach, liv

C:Comment: Xenopsin and xenopsin-related peptides are similar to neurotensin in sequence

C:Suprafamily: yeast coatomer complex alpha chain; WB repeat homology

C:Keywords: neuropeptide

F:1-9/Product: xenopsin-related peptide 2 #status experimental <XP1>

F:2-9/Product: xenopsin-related peptide 1 #status experimental <XP2>

Query Match 27.3% Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7

DB 3 PKR 5

RESULT 4

S70722

65.4K GTP-binding protein (glnA tdkE intergenic region) homolog - Salmonella typhimurium

N:Alternate names: yihK protein homolog

C:Species: Salmonella typhimurium

C>Date: 11-Mar-1998 #sequence_revision 17 Apr 1998 #text_change 24-Apr-1998

C:Accession: S70722

R:Qi, S.Y.; Li, Y.; Szynski, A.; Gilles, L.G.; Weir, A.; Connor, C.D.

Mol. Microbiol. 17, 523-531, 1995

A:Title: Salmonella typhimurium responses to a bacteriophage protein from human neutrophil

A:Reference number: S70719; MUID:96100451; PMID:8559071

A:Accession: S70722

A:Molecule type: protein

A:Residues: 1-10 <QIS>

A:Experimental source: strain SL1344

Query Match 27.3% Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RNI 9

DB 6 RNI 8

RESULT 5

F41839

ribosomal protein L16 - Achleplasma laidlawii (fragment)

C:Species: Achleplasma laidlawii

C>Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 18-Nov-1994

C:Accession: F41839

R:Lim, P.O.; Sears, B.B.

J. Bacteriol. 174, 2606-2611, 1992

A:Title: Evolutionary relationships of a plant-pathogenic mycoplasma-like organism a

A:Reference number: F41839; MUID:92210505; PMID:1556079

A:Accession: F41839

A>Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-10 <LIM>

A:Cross-references: GB:M74471

C:Genetics:

A:Gene: rpl16

C:Keywords: protein biosynthesis; ribosome

Query Match 27.3% Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7

DB 4 PKR 6

RESULT 6

PA0116

ferredoxin:NADP reductase (EC 1.18.1.2) - rice (fragment)

C:Species: Oryza sativa (rice)

C>Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 03-Jun-2002

C:Accession: PA0116

R:Kamo, M.; Tsugita, A.

submitted to JIPID, March 1995

A:Reference number: PA0114

A:Accession: PA0116

A:Molecule type: protein

A:Residues: 1-10 <KAM>

A:Experimental source: iea

C:Keywords: NADP; oxidoreductase

Query Match 27.3% Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4

DB 5 SKK 7

RESULT 7

PS0220

ferredoxin:NADP reductase (EC 1.18.1.2) - rice (fragment)

C:Species: Oryza sativa (rice)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002

C:Accession: PS0220

R:Uchiyama, Y.; Tsugita, A.

submitted to JIPID, August 1991

A:Reference number: PS0205

A:Accession: PS0220

A:Molecule type: protein

A:Residues: 1-10 <UCH>

C:Keywords: NADP; oxidoreductase

Query Match 27.3% Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4

DB 11

Db 5 SKK 7

RESULT 8
S4249
anti protein phage P7
C:Species: Bacillus subtilis
C:Date: 07-Sep-1994 #sequence_revision 26 May 1995 #text_change 08-Oct-1999
C:Accession: S4249
R:Clifton, M.; Schuster, H.
Cell 62, 591-598, 1990
A:Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
A:Reference number: S4249, MUID:90335568; PMID:1696181
A:Accession: S4249
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-11 <CIT>
A:Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KKP 5
III
Db 2 KKP 4

RESULT 9
B41835
translation elongation factor EF-G homolog - Bacillus subtilis (fragment)
C:Species: Bacillus subtilis
C:Date: 30-Sep-1993 #sequence_revision 30 Sep 1994 #text_change 05-Dec-1997
C:Accession: B41835
R:Mitchell, C.; Morris, P.W.; Vary, J.C.
J. Bacteriol. 174, 2474-2477, 1992
A:Title: Identification of proteins phosphorylated by ATP during sporulation of Bacillus
A:Reference number: A41835; MUID:92210469; PMID:1556567
A:Accession: B41835
A:Molecule type: protein
A:Residues: 1-11 <MIT>
A:Note: this protein is phosphorylated during stationary phase but not during exponential
A:Keywords: phosphoprotein

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 KKP 9
III
Db 7 KKP 9

RESULT 10
S19775
wound-induced protein - tomato (fragment)
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Jun-1992 #sequence_revision 30 Jun-1992 #text_change 09-Sep-1997
C:Accession: S19775
R:Parsons, B.L.
submitted to the EMBL Data Library, May 1992
A:Reference number: S19775
A:Accession: S19775
A:Molecule type: mRNA
A:Residues: 1-11 <PAR>
A:Cross-references: EMBL:X59884; NID:g19426; PID:g19424

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SKK 4
III

Db 4 SKK 6

RESULT 11
T08533
hypothetical protein X - Enterobacter aerogenes plasmid R751
C:Species: Enterobacter aerogenes
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T08533
R:Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
Plasmid 36, 95-111, 1996
A:Title: Conservation of the genetic switch between replication and transfer genes (
A:Reference number: 216434; MUID:97118926; PMID:8954881
A:Accession: T08533
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-13 <THO>
A:Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64477.1; PID:g1572582
C:Genetics:
A:Genome: plasmid R751

Query Match 27.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KKP 5
III
Db 7 KKP 9

RESULT 12
S22995
hypothetical protein X (traJ 5' region) - Escherichia coli plasmid R751
C:Species: Escherichia coli
C:Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 08-Oct-1999
C:Accession: S22995
R:Ziegelin, G.; Pansegrau, W.; Strack, B.; Balzer, D.; Kroeger, M.; Kruff, V.; Lank
DNA Seq. 1, 303-327, 1991
A:Title: Nucleotide sequence and organization of genes flanking the transfer origin
A:Reference number: S22992; MUID:92190548; PMID:1665997
A:Accession: S22995
A:Molecule type: DNA
A:Residues: 1-13 <ZIE>
A:Cross-references: EMBL:X54458; NID:g42656; PIDN:CAA38330.1; PID:g581211
C:Genetics:
A:Genome: plasmid
A:Start codon: TTG

Query Match 27.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KKP 5
III
Db 7 KKP 9

RESULT 13
JQ1350
hypothetical protein, 1.3K (rps16 5' region) - Emericella nidulans
C:Species: Emericella nidulans, Aspergillus nidulans
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997
C:Accession: JQ1350
R:Bradshaw, R.E.; Pillar, T.M.
Gene 108, 157-162, 1991
A:Title: Isolation and nucleotide sequence of the ribosomal protein S16-encoding gen
A:Reference number: JQ1349; MUID:92104500; PMID:1761226
A:Accession: JQ1350
A:Molecule type: DNA
A:Residues: 1-13 <BRA>
A:Cross-references: GB:M65259; NID:g168087; PID:g168089
A:Experimental source: strain R153

Query Match 27.3% Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
 DB 10 KKP 12

RESULT 14
 E60396
 antigen 7H8/2 - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C:Date: 10-Sep-1993 #sequence_revision 0 Sep-1993 #text_change 09-Jun-2000
 C:Accession: E60396
 R:Limpitboon, T.; Taylor, D.W.; Jones, G.; Geyse, H.M.; Saul, A.
 Southeast Asian J. Trop. Med. Public Health 21, 458-496, 1990
 A:Title: Characterization of a Plasmodium falciparum epitope recognized by a monoclonal
 A:Reference number: A60396; MUID:91164876; PMID:1706114
 A:Accession: E60396
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-13 <LIM>
 A:Cross-references: GB:M31305

Query Match 27.3% Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKP 9
 DB 11 KKP 13

RESULT 15
 S52456
 hypothetical protein - human
 C:Species: Homo sapiens (man)
 C:Date: 08-May-1995 #sequence_revision 21-Jun-1995 #text_change 05-Nov-1999
 C:Accession: S52456
 R:Agarokastritis, A.; Leversha, M.A.; Ferguson-Smith, M.; Moschonas, M.K.
 submitted to the EMBL Data Library, March 1995
 A:Description: A cosmid clone mapped to human chromosome 11p15 detects a lag 1 restriction
 A:Reference number: S52355
 A:Accession: S52356
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-13 <AGR>
 A:Cross-references: EMBL:X72861; NID:9557002; EMBL:AA51342 1; PID:9557003

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3
 DB 6 ASK 8

RESULT 16
 H64008
 hypothetical protein H10492 - Haemophilus influenzae (strain Rd Kw20)
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
 C:Accession: H64008
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kiehlavag, A.
 ; Gocayne, J.D.; Scott, J.; Shirley, B.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidman, J.
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fritchman, J.L.; Geoghegan, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: H64008

A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-14 <TIGR>
 A:Cross-references: GB:012731; GB:142023; NID:91573465; PID:91573478; TIGR:H10492

Query Match 27.3% Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKP 6
 DB 2 KKP 4

RESULT 17
 PA0013
 photosystem II oxygen-evolving complex protein 2 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
 C:Accession: PA0013
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimen-
 A:Reference number: PA0001
 A:Accession: PA0013
 A:Molecule type: protein
 A:Residues: 1-14 <KAM>
 A:Experimental source: leaf
 C:Keywords: photosynthesis; photosystem II

Query Match 27.3% Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKP 6
 DB 11 KKP 13

RESULT 18
 S33803
 chaperone, TCPI-related - oat
 C:Species: Avena sativa (oat)
 C:Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999
 C:Accession: S33803
 R:Mummett, E.; Grimm, R.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Gatenby, A.A.; Sch
 Nature 453, 644-648, 1993
 A:Title: A TCPI-related molecular chaperone from plants refolds phytochrome to its I
 A:Reference number: S33800; MUID:93288140; PMID:8099715
 A:Accession: S33803
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <NUM>

Query Match 27.3% Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
 DB 8 KKP 10

RESULT 19
 H83778
 hypothetical protein BH1032 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: H83778
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
 A:Reference number: A83650; MUID:20512582; PMID:11058132

C:Accession: H83778
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-14 <STO>
 A:Cross-references: GB:AP001510; GB:BA000004; NID:420174449; PION:BAR04751.1; JSPUB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BHI032

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
 DB 4 PKR 6

RESULT 20
 A54370

Inorganic diphosphatase (EC 3.6.1.1) - vacuolar (fragment)
 C:Species: Cucurbita sp. (cucurbita)
 C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 04-Jun-2002
 C:Accession: A54370
 R:Sato, M.H.; Kasahara, M.; Ishii, N.; Homareda, S.; Matsui, H.; Yoshida, M.
 J. Biol. Chem. 269, 6725-6728, 1994
 A:Title: Purified vacuolar inorganic pyrophosphatase consisting of a 75-kDa polypeptide
 A:Reference number: A54370; MUID:94.65068; PMID:7120031
 A:Accession: A54370
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <SAT>
 C:Keywords: hydrolase

Query Match 27.3% Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RNI 9
 DB 4 RNI 5

RESULT 21
 S3689

Ribosomal protein S26 - Mycobacterium bovis (fragment)
 C:Species: Mycobacterium bovis
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
 C:Accession: S3689
 R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 9-14, 1993
 A:Title: Isolation and amino acid sequence of the 16S ribosomal protein S19 from Mycobac
 A:Reference number: S3689; MUID:94009653; PMID:8404418
 A:Accession: S3689
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <GNA>
 C:Keywords: protein biosynthesis; ribosome

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NIK 10
 DB 2 NIK 4

RESULT 22
 T09463

Ribosomal protein S14 - brown alga (Pylaiella littoralis) mitochondrion (fragment)
 C:Species: mitochondrion Pylaiella littoralis
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999

C:Accession: T09463
 R:Rousvoldi, S.; Oudot, M.; Fontaine, J.; Kloareg, B.; Goer, S.L.
 J. Mol. Biol. 277, 1047-1057, 1998
 A:Title: Witnessing the evolution of transcription in mitochondria: The mitochondria
 A:Reference number: T1668; MUID:98239704; PMID:9571021
 A:Accession: T09463
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-15 <ROU>
 A:Cross-references: EMBL:AF04976; NID:q3243103; PID:q3243104
 A:Experimental source: strain Roscoff
 C:Genetics:
 A:Gene: rps14
 A:Genome: mitochondrion
 C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3
 DB 2 ASK 4

RESULT 23
 PA0046

Protein GAI00044 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C:Accession: PA0046; PA0042
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JPIB, July 1994
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimens
 A:Reference number: PA0001
 A:Accession: PA0046
 A:Molecule type: Protein
 A:Residues: 1-15 <KAM>
 A:Experimental source: stem

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4
 DB 3 SKK 5

RESULT 24
 PT0082

Protein QA00023 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 06-Jun-1997
 C:Accession: PT0082
 R:Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
 submitted to JPIB, December 1995
 A:Reference number: PN0173
 A:Accession: PT0082
 A:Molecule type: protein
 A:Residues: 1-15 <TSU>
 A:Experimental source: leaf

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
 DB 4 KPK 6

RESULT 25

S71300
ICL1 protein - Paramoecium tetraurelia (fragment)
C:Species: Paramoecium tetraurelia
C:Date: 11-Mar-1998 #sequence_revision 17 Apr 1998 #text_change 02-Dec-1999
C:Accession: S71300
R:Madeddu, L.; Klotz, G.; le Caer, J.-P.; Weissman, J.
Eur. J. Biochem. 238, 121-128, 1996

A:Title: Characterization of centrin spots in Paramoecium

A:Reference number: S71298; MUID:96248429; PMID:95656429

A:Accession: S71300

A:Molecule type: protein

A:Residues: 1-15 <MAD>

A:Experimental source: strain d4-2

C:Genetics:

A:Genetic code: SGC5

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0% Pred. No. 3.7e-03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7

III

DB 10 PKR 12

RESULT 26

S77987
cytochrome-c oxidase (EC 1.9.3.1) chain V10.2 - bovine tuna (fragments)
C:Species: Thunnus obesus (bigeye tuna)
C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 04-Sep-1998
C:Accession: S77987
R:Arnold, S.; Lee, J.; Kim, M.; Sund, E.; Linders, D.; Lottspächer, F.; Kadembach, B.

submitted to the Protein Sequence Database, June 1997

A:Reference number: S77980

A:Accession: S77987

A:Molecule type: protein

A:Residues: 18,9-15 <ARN>

A:Experimental source: heart

C:Genetics:

A:Genome: nuclear

C:Function:

A:Pathway: oxidative phosphorylation; respiratory chain

C:Keywords: electron transfer; membrane associated complex; mitochondrial inner membrane

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0% Pred. No. 3.7e-03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5

III

DB 8 KKP 10

RESULT 27

S03955
acidic fibroblast growth factor - dog (fragment)
N:Alternate names: alpha-endothelial cell growth factor
C:Species: Canis lupus familiaris (dog)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C:Accession: S03955
R:Quinkler, W.; Maasberg, M.; Bernotat-Ganicowski, S.; Luethe, N.; Sharma, H.S.; Schape

Eur. J. Biochem. 181, 67-75, 1989

A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea

A:Reference number: S03953; MUID:8921204; PMID:2714282

A:Accession: S03955

A:Molecule type: protein

A:Residues: 1-15 <QU>

C:Keywords: growth factor

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0% Pred. No. 3.7e-03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6

III

DB 4 KPK 6

RESULT 28

PX0031

mixed lymphocyte reaction inhibitor rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Feb-1995

C:Accession: PX0031

R:Shinomiya, T.; Chhara, T.; Wada, N.; Omori, A.; Kamada, N.

J. Biochem. 107, 433-439, 1990

A:Title: Rat liver arginase suppresses mixed lymphocyte reaction.

A:Reference number: PX0031; MUID:90256720; PMID:2140355

A:Accession: PX0031

A:Molecule type: protein

A:Residues: 1-15 <SHI>

A:Experimental source: liver

C:Keywords: lymphocyte

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0% Pred. No. 3.7e-03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6

III

DB 10 KPK 12

RESULT 29

LFSAME

probable msrA leader peptide - Staphylococcus epidermidis

C:Species: Staphylococcus epidermidis

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C:Accession: S11157

R:Ross, J.L.; Eady, E.A.; Cove, J.H.; Cunliffe, W.J.; Baumberg, S.; Wootton, J.C.

Mol. Microbiol. 4, 1207-1214, 1990

A:Title: Inducible erythromycin resistance in staphylococci is encoded by a member c

A:Reference number: S11157; MUID:91041730; PMID:2233255

A:Accession: S11157

A:Molecule type: DNA

A:Residues: 1-8 <ROS>

A:Cross-references: EMBL:X52085; NID:947000; PIDN:CAA36303.1; PID:g58i653

C:Superfamily: probable msrA leader peptide

Query Match 18.2% Score 2; DB 1; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

III

DB 3 AS 4

RESULT 30

A31570

angiotensin-converting enzyme inhibitor - yellowfin tuna

C:Species: Thunnus albacares (yellowfin tuna)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000

C:Accession: A31570

R:Kohama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.

Biochem. Biophys. Res. Commun. 155, 332-337, 1988

A:Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.

A:Reference number: A31570; MUID:88326322; PMID:3415688

A:Accession: A31570

A:Molecule type: protein

A:Residues: 1-8 <ROH>

A>Note: The source is designated as Neothunnus macropterus

C:Superfamily: unassigned animal peptides

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PK 10
 II
 DB 4 PK 5

RESULT 31
 S70727
 IgGF protein - Shigella flexneri (fragment)
 C.Species: Shigella flexneri
 C.Date: 15-Feb-1997 #sequence_revision 15-Mar-1997 #text_change 05-Oct-1999
 C.Accession: S70727
 R.Ailaoui, A.; Sansonetti, P.J.; Menard, R.; Khatz, S.; Mounier, J.; Phalipon, A.; Parso
 Mol. Microbiol. 17, 461-470, 1995
 A.Title: MxiG, a membrane protein required for secretion of Shigella spp. Ipa invasins:
 A.Reference number: S70727; MUID:96100445; PMID:855965
 A.Accession: S70727
 A.Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A.Molecule type: DNA
 A.Residues: 1-8 <ALL>
 A.Cross-references: EMBL:Z48957; NID:q429886; PDB:1AA882;1;1; PMID:3929881
 A.Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995
 C.Genetics:
 A.Gene: 199F

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SK 3
 II
 DB 1 SK 2

RESULT 32
 A39308
 Glycine reductase (EC 1.4.99.1) sulfolipyl protein C, alpha chain - Clostridium sticklandii
 C.Species: Clostridium sticklandii
 C.Date: 19-Jan-1992 #sequence_revision 19-Jun-1992 #text_change 15-Aug-1997
 C.Accession: A39308
 R.Stadman, T.C.; Davis, J.N.
 J. Biol. Chem. 265, 22147-22154, 1991
 A.Title: Glycine reductase protein C, subunit alpha, characterized and its role in the
 A.Reference number: A39308; MUID:9294143; PMID:1392192
 A.Accession: A39308
 A.Status: preliminary
 A.Molecule type: protein
 A.Residues: 1-8 <STA>
 C.Function:
 A.Description: glycine reductase complex catalyzes the reductive decarboxylation of glycine
 C.Keywords: ALP; oxidoreductase

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KP 5
 II
 DB 2 KP 3

RESULT 33
 T10552
 Hypothetical protein 1 - spring vetch
 C.Species: Vicia sativa (spring vetch, faba)
 C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C.Accession: T10552
 R.Christianson, A.; Hansen, A.C.; Vind, J.; Rasmussen, N.; Larsen, K.; Yan, W.; Biss
 submitted to the EMBL Data Library, December 1997
 A.Description: A novel type of DNA binding protein, interacting with a conserved sequence

A:Reference number: Z17228
 A:Accession: T10952
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-8 <CHR>
 A:Cross-references: EMBL:X5995; NID:q1360633; PID:e225824

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SK 4
 II
 DB 7 SK 8

RESULT 34
 S21288
 Lectin - potato (fragment)
 C.Species: Solanum tuberosum (potato)
 C.Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
 C.Accession: S21288
 R.Millar, D.G.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Siabas, A.R.; Bolwell, G.P
 Biochem. J. 283, 813-821, 1992
 A.Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characteriz
 A.Reference number: S21288; MUID:92272683; PMID:1590771
 A.Accession: S21288
 A.Molecule type: protein
 A.Residues: 1-8 <MIL>
 A:Experimental source: var. Ulster Sceptre
 C.Function:
 A.Description: may be involved in defence mechanism of the plant
 C.Keywords: hydroxyproline; lectin

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
 II
 DB 2 AS 3

RESULT 35
 A39892
 Element, P cytotype-determining - fruit fly (Drosophila melanogaster) (fragment)
 C.Species: Drosophila melanogaster
 C.Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Feb-1997
 C.Accession: A39892
 R.Nitakaka, E.; Mukai, T.; Yamazaki, T.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7605-7608, 1987
 A>Title: Repressor of P elements in Drosophila melanogaster: cytotypic determination
 A:Reference number: A39892
 A:Accession: A39892
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-8 <NIT>
 C.Genetics:
 A.Gene: FlyBase:P-element
 A:Cross-references: FlyBase:FBgn0003055

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
 II
 DB 2 PK 3

RESULT 36
 A14583
 aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (f

N:Alternate names: aspartate aminotransferase, mitochondrial
 C:Species: Gallus gallus (chicken)
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31 Mar-2000

C:Accession: A14683
 R:Wilson, K.J.; Hunziker, P.; Hughes, G.J.
 FEBS Lett. 108, 98-102, 1979

A:Title: Microsequence analysis. IV. Automatic liquid-phase sequencing using DABITC.
 A:Reference number: A14683; MUID:80092116; PMID:520566
 A:Accession: A14683
 A:Molecule type: protein
 A:Residues: 1-8 <WL>
 C:Keywords: aminotransferase; mitochondrion

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2 8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
 II
 DB 7 PK 8

RESULT 37

A28719
 Thymic humoral factor gamma-2 bovine (fragment)

C:Species: Bos primigenius taurus (cattle)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1993

C:Accession: A28719
 R:Burstein, Y.; Buchner, V.; Pecht, M.; Trainor, N.
 Biochemistry 27, 4066-4071, 1988

A:Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an immunoreactive protein.
 A:Reference number: A28719; MUID:88326920; PMID:3261954
 A:Accession: A28719
 A:Molecule type: protein
 A:Residues: 1-8 <BUK>

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2 8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
 II
 DB 5 PK 6

RESULT 38

A54823
 Olfactory receptor 17 - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 28-Apr-1995 #sequence_revision 28 Apr 1995 #text_change 17-Mar-1999

C:Accession: A54823
 R:Chess, A.; Simon, I.; Cedar, H.; Axel, R.
 Cell 78, 823-834, 1994

A:Title: Allelic inactivation regulates olfactory receptor gene expression.
 A:Reference number: A54823; MUID:94373818; PMID:808245
 A:Accession: A54823
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-8 <CHS>

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2 8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RN 8
 II
 DB 4 RN 5

RESULT 39

PT0595

T-cell receptor beta chain V-D-J region (100-2AA) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0595
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region

A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0595
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-8 <FE>
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2 8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
 II
 DB 1 AS 2

RESULT 40

PT0627

T-cell receptor beta chain V-D-J region (100-2H) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0627
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0627
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-8 <FE>
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2 8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
 II
 DB 1 AS 2

RESULT 41

PT0530

T-cell receptor beta chain V-D-J region (100-4AK) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0530
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0530
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-8 <FE>
 A:Experimental source: adult thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2 8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
 II
 DB 1 AS 2

RESULT 42

PT0527

T-cell receptor beta chain V-D-J region (100-41) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0527

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0527

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FE>

A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

II

DB 1 AS 2

RESULT 43

PT0522

T-cell receptor beta chain V-D-J region (100-41) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0522

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0522

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FE>

A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

II

DB 1 AS 2

RESULT 44

PT0509

T-cell receptor beta chain V-D-J region (100-4N) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0509

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0509

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FE>

A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

II

DB 1 AS 2

RESULT 45

PT0639

T-cell receptor beta chain V-D-J region (111-1AA) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0639

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0639

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

II

DB 1 AS 2

RESULT 46

PT0631

T-cell receptor beta chain V-D-J region (111-1I) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0631

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0631

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

II

DB 1 AS 2

RESULT 47

PT0613

T-cell receptor beta chain V-D-J region (111-1L) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0613

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0613

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 1 AS 2

RESULT 48

PT0653

T-cell receptor beta chain V-D-J region (126-141) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0653

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Functional sequences of fetal T-cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711556

A:Accession: PT0653

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <P>>

A:Experimental source: day 4 postnatal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 1 AS 2

RESULT 49

PT0547

T-cell receptor beta chain V-D-J region (126-141) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0547

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Functional sequences of fetal T-cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711556

A:Accession: PT0547

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <P>>

A:Experimental source: day 18 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 1 AS 2

RESULT 50

PT0557

T-cell receptor beta chain V-D-J region (126-141) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0557

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Functional sequences of fetal T-cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711556

A:Accession: PT0557

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <P>>

A:Experimental source: day 18 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 1 AS 2

Search completed: September 30, 2003, 10:09:37

Job time : 20.4167 secs

GenCore version 5.1.6
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OM protein - protein search, using SW-Med-1

Run on: September 30, 2003, 11:07:04 : Search time 6.25 Seconds
(without alignment)
#2,767 Million cell updates/sec

Title: US-09-787-443-1

Perfect score: 11

Sequence: : ASKKPRNIKA 11

Scoring table: SLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 707

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	8	B44K_PORGI	P61886 porphyromon
2	4	36.4	11	Q515_BACSU	P61095 bacillus su
3	3	27.3	10	R416_ACHIA	P29221 achioleplasm
4	3	27.3	12	R519_ELXEL	P47681 elm yellows
5	3	27.3	14	R519_PEWPI	P42091 piceon pea
6	3	27.3	15	R519_PEWPI	P42091 piceon pea
7	3	27.3	15	R519_PEWPI	P42091 piceon pea
8	3	27.3	15	R519_PEWPI	P42091 piceon pea
9	3	27.3	15	R519_PEWPI	P42091 piceon pea
10	3	27.3	15	R519_PEWPI	P42091 piceon pea
11	2	18.2	8	A117_CANMA	P41805 carinus ma
12	2	18.2	8	F4K1_PENNO	P41486 penarus aca
13	2	18.2	8	F4K3_HUMAN	P41487 penarus aca
14	2	18.2	8	F4K4_HUMAN	P41487 penarus aca
15	2	18.2	8	LCK4_LETMA	P41143 leucophara
16	2	18.2	8	LPM5_STAPP	P24211 staphylococ
17	2	18.2	8	R57_MYCOT	P41564 mycobacteri
18	2	18.2	9	Q515_BACSU	P61095 bacillus su
19	2	18.2	9	Q515_BACSU	P61095 bacillus su
20	2	18.2	9	Q515_BACSU	P61095 bacillus su
21	2	18.2	9	Q515_BACSU	P61095 bacillus su
22	2	18.2	9	Q515_BACSU	P61095 bacillus su
23	2	18.2	9	Q515_BACSU	P61095 bacillus su
24	2	18.2	9	Q515_BACSU	P61095 bacillus su
25	2	18.2	9	Q515_BACSU	P61095 bacillus su
26	2	18.2	9	Q515_BACSU	P61095 bacillus su
27	2	18.2	9	Q515_BACSU	P61095 bacillus su
28	2	18.2	9	Q515_BACSU	P61095 bacillus su
29	2	18.2	9	Q515_BACSU	P61095 bacillus su
30	2	18.2	9	Q515_BACSU	P61095 bacillus su
31	2	18.2	9	Q515_BACSU	P61095 bacillus su
32	2	18.2	9	Q515_BACSU	P61095 bacillus su
33	2	18.2	9	Q515_BACSU	P61095 bacillus su

34	2	18.2	10	1	AH3_PRUSE	P29261 prunus sero
35	2	18.2	10	1	BPP6_BOTIN	P30426 bothrops in
36	2	18.2	10	1	BRK_ONCMY	P31351 vipera aspi
37	2	18.2	10	1	BRK_ONCMY	Q9prz1 oncorhynch
38	2	18.2	10	1	COXM_RAT	P80431 rattus norv
39	2	18.2	10	1	COXM_RABIT	P80336 oryctolagus
40	2	18.2	10	1	COXM_SHEEP	P80337 ovis aries
41	2	18.2	10	1	FAR7_MACRS	P83280 macrobrachi
42	2	18.2	10	1	FIBH_CERS1	P14537 ceratotheri
43	2	18.2	10	1	G0N1_CHEPR	P80677 chelyosoma
44	2	18.2	10	1	G0N1_PETMA	P04378 petromyzon
45	2	18.2	10	1	G0N1_PETMA	P30946 petromyzon
46	2	18.2	10	1	G0P2_BOVIN	P11180 bos taurus
47	2	18.2	10	1	PNEU_HUMAN	P22103 homo sapien
48	2	18.2	10	1	PNEU_RAT	P21996 rattus norv
49	2	18.2	10	1	SPI_HALRO	Q10997 halocynthia
50	2	18.2	10	1	TKNC_RANCA	P22690 rana catesb
51	2	18.2	10	1	TRP7_LEUMA	P81739 leucophaea
52	2	18.2	10	1	UPA5_HUMAN	P30091 homo sapien
53	2	18.2	10	1	UPA8_HUMAN	P30094 homo sapien
54	2	18.2	10	1	UXA2_CHLTR	P32080 homo sapien
55	2	18.2	10	1	UXA6_CHLTR	P38003 chlamydia t
56	2	18.2	10	1	UXA6_CHLTR	P38007 chlamydia t
57	2	18.2	10	1	XYNB_DICB4	P80712 dictyoglomu
58	2	18.2	11	1	BPPB_AKCHA	P01021 agkistrodon
59	2	18.2	11	1	BRK_MESFL	P12797 megascolla
60	2	18.2	11	1	EFG_CLOPA	P81350 clostridium
61	2	18.2	11	1	LADD_ONCMY	P81018 oncorhynch
62	2	18.2	11	1	MORN_HUMAN	P01163 homo sapien
63	2	18.2	11	1	PVK1_PERAM	P41837 periplaneta
64	2	18.2	11	1	Q20A_COMTE	P80464 comamonas t
65	2	18.2	11	1	RK2_CONAM	P42341 conopholis
66	2	18.2	11	1	TKN7_UPERU	P08616 uperoletia r
67	2	18.2	11	1	TKNA_GADMO	P28498 gadus morhu
68	2	18.2	11	1	TKNA_HORSE	P01290 equus cabal
69	2	18.2	11	1	TKNA_ONCMY	P28499 oncorhynch
70	2	18.2	11	1	TKNA_RANCA	P22688 rana catesb
71	2	18.2	11	1	TKNA_RANCI	P29207 rana ridibu
72	2	18.2	11	1	TKNA_SCYCA	P41333 scyllorhinu
73	2	18.2	11	1	TKND_RANCA	P22891 rana catesb
74	2	18.2	11	1	TKN_ELEMO	P01293 eleodon mos
75	2	18.2	12	1	FAR7_PENNO	P83322 penaeus mon
76	2	18.2	12	1	GRAK_RANRU	P40754 rana rugosa
77	2	18.2	12	1	HCYL_CARMA	P83176 carcinus ma
78	2	18.2	12	1	LOSK_LOCOMI	P47733 locustina mlg
79	2	18.2	12	1	GPS3_DROVI	P17845 drosophila
80	2	18.2	12	1	RR16_GINBI	P36207 ginkgo bilio
81	2	18.2	12	1	RS19_CLYEP	Q46490 clover yell
82	2	18.2	12	1	RS19_TOBBP	Q56251 tomato big
83	2	18.2	12	1	SO15_BACSU	P80863 bacillus su
84	2	18.2	12	1	TKN1_KASMA	P08613 kassina mac
85	2	18.2	12	1	TKN_KASSE	P08611 kassina sen
86	2	18.2	12	1	UHO3_RAT	P56372 rattus norv
87	2	18.2	13	1	ADFB_TENMO	P83109 tenebrio mo
88	2	18.2	13	1	AH4_PRUSE	P29262 prunus sero
89	2	18.2	13	1	AU11_LITRA	P82386 litoria ran
90	2	18.2	13	1	AU12_LITRA	P82387 litoria ran
91	2	18.2	13	1	BRK_PARDI	P42717 parapolybia
92	2	18.2	13	1	EP65_HUMAN	P54963 homo sapien
93	2	18.2	13	1	IDHP_RAT	P56574 rattus norv
94	2	18.2	13	1	ITB5_BOVIN	P80747 bos taurus
95	2	18.2	13	1	MLA_ANOCA	P41589 anolis caro
96	2	18.2	13	1	MLA_CANDR	P01198 camelus dro
97	2	18.2	13	1	NEUT_BUFMA	P81796 bufo marinu
98	2	18.2	13	1	NEUT_CHICK	P13724 gallus gall
99	2	18.2	13	1	NEUT_RANTE	P41536 rana tempor
100	2	18.2	13	1	NEUT_TRIVU	P31745 trichosurus
101	2	18.2	13	1	ODPA_CANFA	P49823 canis famill
102	2	18.2	13	1	PSAE_PEA	P20118 pisum sativ
103	2	18.2	13	1	PSAE_PINS	P81668 pinus pinas
104	2	18.2	13	1	RPOC_MYCPA	P47716 mycoplasma
105	2	18.2	13	1	RS19_ASHYP	Q44592 ash yellows
106	2	18.2	13	1	TEML_RANTE	P57104 rana tempor

107	2	18.2	13	1	TT13_PHYCO	P04095 phyllorhizids	180	1	9.1	8	1	ALL1_CYDPO	P82152 cydia pomon
108	2	18.2	13	1	UBT1_LITEW	P82050 litoria ewi	181	1	9.1	8	1	ALL3_CYDPO	P82154 cydia pomon
109	2	18.2	14	1	EFTU_CANFA	P54835 canis famli	182	1	9.1	8	1	ALL4_CALVO	P41840 calliphora
110	2	18.2	14	1	IF2G_RAT	P81795 rattus norv	183	1	9.1	8	1	ALL4_CYDPO	P82155 cydia pomon
111	2	18.2	14	1	KLPS_SCARA	P58396 scaptoecsa	184	1	9.1	8	1	ALL5_CALVO	P41841 calliphora
112	2	18.2	14	1	LHW_ELFIR	P03055 catrobacter	185	1	9.1	8	1	ALL5_CYDPO	P82156 cydia pomon
113	2	18.2	14	1	LHW_EFOT1	P03055 escherichia	186	1	9.1	8	1	ALL6_CYDPO	P82157 cydia pomon
114	2	18.2	14	1	LHW_RHIME	P18854 rhizobium m	187	1	9.1	8	1	ALL8_CARMA	P81811 carcinus ma
115	2	18.2	14	1	MAST_PALJA	P42715 parapolybia	188	1	9.1	8	1	ALL9_CARMA	P81812 carcinus ma
116	2	18.2	14	1	MAST_PALJA	P42715 parapolybia	189	1	9.1	8	1	ANG2_BOTJA	Q10582 botrops ja
117	2	18.2	14	1	MAST_VESPA	P21654 vespa basai	190	1	9.1	8	1	CAD1_ENTFA	P13268 enterococcu
118	2	18.2	14	1	MAST_VESCR	P41516 vespa crabr	191	1	9.1	8	1	CLP_THICU	P80488 thiobacilli
119	2	18.2	14	1	MAST_VESLE	P41514 vespula lew	192	1	9.1	8	1	COM2_CONPU	P58785 conus purpu
120	2	18.2	14	1	MAST_VESMA	P42205 vespa manda	193	1	9.1	8	1	COM2_CONPU	P58785 conus purpu
121	2	18.2	14	1	MAST_VESOR	P17238 vespa orien	194	1	9.1	8	1	COM2_CONPU	P58785 conus purpu
122	2	18.2	14	1	MAST_VESXA	P01515 vespa xanth	195	1	9.1	8	1	FAR1_PANRE	P13269 enterococcu
123	2	18.2	14	1	MGRX_METTM	P56815 methanobact	196	1	9.1	8	1	FAR2_MACRS	P41872 panagrellus
124	2	18.2	14	1	MGR2_METTM	P56816 methanobact	197	1	9.1	8	1	FAR4_MACRS	P83275 macrobrachi
125	2	18.2	14	1	RS19_CLOPP	Q46228 clover prot	198	1	9.1	8	1	FAR7_ASCSU	P83277 macrobrachi
126	2	18.2	14	1	RS19_CLOPP	Q46228 clover prot	199	1	9.1	8	1	FAR8_CALVO	P41863 calliphora
127	2	18.2	14	1	RS19_FROAP	Q44160 prunus arme	200	1	9.1	8	1	FAR8_CALVO	P41863 calliphora
128	2	18.2	14	1	FAT_RV1W2	P12509 human immun	201	1	9.1	8	1	FUSS_FUSSO	P81010 fusarium so
129	2	18.2	14	1	FAT_RV1W2	P12511 human immun	202	1	9.1	8	1	GLUR_HUMAN	P02729 homo sapien
130	2	18.2	14	1	TKN1_SCHCK	P82470 schistocerc	203	1	9.1	8	1	HIF1_PERAM	P04549 periplaneta
131	2	18.2	14	1	TKNM_CARMA	P40951 rana margar	204	1	9.1	8	1	HIF2_PERAM	P04549 periplaneta
132	2	18.2	14	1	UC04_MALZE	P36610 zea mays (m	205	1	9.1	8	1	HIF_TENNO	P25419 tenebrio mo
133	2	18.2	14	1	UN46_CUJFA	P41362 clostridium	206	1	9.1	8	1	LCK1_LEUMA	P21140 leucophaea
134	2	18.2	15	1	ACEA_ACTCA	P28467 acinetobact	207	1	9.1	8	1	LCK2_LEUMA	P21141 leucophaea
135	2	18.2	15	1	ACT_PINPS	P81085 pinus pinas	208	1	9.1	8	1	LCK3_LEUMA	P21142 leucophaea
136	2	18.2	15	1	AH2_PUSKE	P49260 prunus sero	209	1	9.1	8	1	LCK5_LEUMA	P19987 leucophaea
137	2	18.2	15	1	ASFL_LACSN	P82648 lactobacilli	210	1	9.1	8	1	LCK6_LEUMA	P19988 leucophaea
138	2	18.2	15	1	ATF2_PINPS	P81653 pinus pinas	211	1	9.1	8	1	LCK7_LEUMA	P19989 leucophaea
139	2	18.2	15	1	ATF2_SPHIL	P80983 spinacia ol	212	1	9.1	8	1	LCK8_LEUMA	P19990 leucophaea
140	2	18.2	15	1	CXX_WHEAT	P58763 tritium ae	213	1	9.1	8	1	LMT2_LOCOMI	P22396 locusta mag
141	2	18.2	15	1	DEMM_PSECH	P19917 pseudomonas	214	1	9.1	8	1	LPK_LEUMA	P13049 leucophaea
142	2	18.2	15	1	G10H_PSESE	P80721 pseudomonas	215	1	9.1	8	1	NPB_BOVIN	P15507 bos taurus
143	2	18.2	15	1	EP1A_MIGCK	P82466 macropylis	216	1	9.1	8	1	NS3_MYCTU	P81152 mycobacteri
144	2	18.2	15	1	GR78_HORSE	P76392 equus cabal	217	1	9.1	8	1	ORMY_ORCLI	P82455 oronectes
145	2	18.2	15	1	LEFL_LACTIO	P28588 aximelia po	218	1	9.1	8	1	PLP_BRANA	P81707 brassica na
146	2	18.2	15	1	MAL2_HARTO	P80072 bacillus th	219	1	9.1	8	1	PKK2_PERAM	P82692 periplaneta
147	2	18.2	15	1	MAGX_CHICK	Q42960 gallus gall	220	1	9.1	8	1	PKK3_PERAM	P82618 periplaneta
148	2	18.2	15	1	MILL_PINKR	P81037 oncorhynch	221	1	9.1	8	1	RPKH_PANBO	P08939 pandalus bo
149	2	18.2	15	1	M11_PALKR	P81408 palomedia pr	222	1	9.1	8	1	RS1_ERWCH	P37985 erwinia chr
150	2	18.2	15	1	MK2A_PALPR	P83409 palomedia pr	223	1	9.1	8	1	RT34_BOVIN	P82929 bos taurus
151	2	18.2	15	1	NKSE_PSELE	P83409 palomedia pr	224	1	9.1	8	1	UC26_MALZE	P80632 zea mays (m
152	2	18.2	15	1	NKSE_PSELE	P83409 palomedia pr	225	1	9.1	8	1	UC26_MALZE	P80632 zea mays (m
153	2	18.2	15	1	ORPA_MARIP	P41285 manes tra tr	226	1	9.1	8	1	UC09_RAT	P38644 mus musculu
154	2	18.2	15	1	ORPA_MARIP	P41285 manes tra tr	227	1	9.1	8	1	UPA1_HUMAN	P56575 rattus norv
155	2	18.2	15	1	RIYA_SCH	P84454 spinacia ol	228	1	9.1	8	1	UPAA_HUMAN	P30096 homo sapien
156	2	18.2	15	1	RKS_PSVCA	P80657 physcomitre	229	1	9.1	8	1	VGLG_HSV2B	P81780 herpes simp
157	2	18.2	15	1	RS10_RAT	P59181 lactilios st	230	1	9.1	8	1	WPL_PERAT	P83195 perkinsus a
158	2	18.2	15	1	RT32_BOVIN	P62927 bos taurus	231	1	9.1	8	1	WPL_PERAT	P83195 perkinsus a
159	2	18.2	15	1	SOUP_PINPS	P81082 pinus pinas	232	1	9.1	8	1	ALC1_CARMA	P81813 carcinus ma
160	2	18.2	15	1	TAL_THERR	P34070 tremetia br	233	1	9.1	8	1	ALC1_CARMA	P81814 carcinus ma
161	2	18.2	15	1	UB1_CLOPA	P81347 clostridium	234	1	9.1	8	1	ALC_CHURE	P82678 chlamydomon
162	2	18.2	15	1	UBL1_MONIA	P50103 monodelphis	235	1	9.1	8	1	BS43_SERPL	P83375 serratia pl
163	2	18.2	15	1	UC01_MALZE	P80607 zea mays (m	236	1	9.1	8	1	BUK_CLOPA	P81337 clostridium
164	2	18.2	15	1	UC08_MALZE	P80614 zea mays (m	237	1	9.1	8	1	CCAP_CARMA	P38556 carcinus ma
165	2	18.2	15	1	UC13_MALZE	P80619 zea mays (m	238	1	9.1	8	1	COXE_THUOB	P38556 carcinus ma
166	2	18.2	15	1	UC17_MALZE	P80623 zea mays (m	239	1	9.1	8	1	DI_NEPNO	P80975 thunnus obe
167	2	18.2	15	1	UC23_MALZE	P80629 zea mays (m	240	1	9.1	8	1	DNF1_LOCOMI	P24816 nephrops no
168	2	18.2	15	1	UNC4_FINPS	P81673 pinus pinas	241	1	9.1	8	1	FAR1_CALVO	P41856 calliphora
169	2	18.2	15	1	VORPA_METTM	P80907 methanobact	242	1	9.1	8	1	FAR2_CALVO	P41857 calliphora
170	1	9.1	8	1	ACT_CARMA	P80709 carcinus ma	243	1	9.1	8	1	FAR2_CALVO	P41857 calliphora
171	1	9.1	8	1	AKHG_GRYCH	P14886 gryllus bim	244	1	9.1	8	1	FAR3_CALVO	P41858 calliphora
172	1	9.1	8	1	AKH_LILSAU	P25418 libellula a	245	1	9.1	8	1	FAR3_PENMO	P83319 penaeus mon
173	1	9.1	8	1	AKH_MEMLU	P25423 melolontha	246	1	9.1	8	1	FAR5_CALVO	P41860 calliphora
174	1	9.1	8	1	AKH_TASAL	P14595 tabanus atr	247	1	9.1	8	1	FAR5_PENMO	P83320 penaeus mon
175	1	9.1	8	1	ALI2_CARMA	P81815 carcinus ma	248	1	9.1	8	1	FAR7_CALVO	P41862 calliphora
176	1	9.1	8	1	ALI5_CARMA	P81818 carcinus ma	249	1	9.1	8	1	FAR8_MACRS	P83281 macrobrachi
177	1	9.1	8	1	ALI6_CARMA	P81819 carcinus ma	250	1	9.1	8	1	FAR9_ASCSU	P43172 ascaris suu
178	1	9.1	8	1	ALI7_CARMA	P81820 carcinus ma	251	1	9.1	8	1	FARA_CALVO	P41865 calliphora
179	1	9.1	8	1	ALI8_CARMA	P81821 carcinus ma	252	1	9.1	8	1	FARD_CALVO	P41868 calliphora

253	1	9.1	9	1	FARP_CALSI	P18495	callinectes	326	1	9.1	10	1	FARP_PANRE	P82660	panagrellus
254	1	9.1	9	1	FIBB_ERIPA	P19446	erythrocebu	327	1	9.1	10	1	FARP_CALVO	P41867	calliphora
255	1	9.1	9	1	FIBB_MACFI	P19345	macaca fusc	328	1	9.1	10	1	FARP_LOCHI	P38553	locusta mig
256	1	9.1	9	1	FIBB_PAPPA	P19344	papio anubi	329	1	9.1	10	1	FARP_MANSE	P18523	manduca sex
257	1	9.1	9	1	FIBB_PAPPA	P19343	papio hamad	330	1	9.1	10	1	FARP_MYTED	P42560	mytilus edu
258	1	9.1	9	1	FIBB_THERF	P19342	theropithec	331	1	9.1	10	1	GAJU_HUMAN	P01358	homo sapien
259	1	9.1	9	1	FLA2_TREHY	P80159	treponema h	332	1	9.1	10	1	GLEM_HUMAN	P02728	homo sapien
260	1	9.1	9	1	FRT1_SARBU	P83350	sarcophaga	333	1	9.1	10	1	GONI_ALLUMI	P37041	alligator m
261	1	9.1	9	1	IPR_RHOVI	P82992	rhodopsendo	334	1	9.1	10	1	GONI_CLUPA	P81749	clupea pall
262	1	9.1	9	1	ISOI_CYPCA	P42993	cyprinus ca	335	1	9.1	10	1	GONI_CHEPR	P80678	chelyosoma
263	1	9.1	9	1	KNL3_BOMVA	P83058	bombina var	336	1	9.1	10	1	GON2_CHICK	P37043	gallus gall
264	1	9.1	9	1	LITO_LITAU	P88945	litoria aur	337	1	9.1	10	1	GON3_ONCKE	P20367	oncorhynch
265	1	9.1	9	1	LITR_PHYHO	P88946	phyllomedus	338	1	9.1	10	1	GONL_SQUAC	P27429	squalus aca
266	1	9.1	9	1	LMP1_LOCHI	P31799	locusta mig	339	1	9.1	10	1	GRP_RANKI	P23260	rana ridibu
267	1	9.1	9	1	LMP3_LOCHI	P41489	locusta mig	340	1	9.1	10	1	GS09_BACSU	P80243	bacillus su
268	1	9.1	9	1	MMT1_BCVIN	P29177	bos taurus	341	1	9.1	10	1	HTF1_ROMMI	P18110	romalea mic
269	1	9.1	9	1	MOSF_CLYJA	P19853	clypeaster	342	1	9.1	10	1	HTF2_CARMO	P11385	carausius m
270	1	9.1	9	1	MOSH_CLYJA	P19852	clypeaster	343	1	9.1	10	1	HTF_HELZE	P16353	heliobhis z
271	1	9.1	9	1	NEUX_HUMAN	P04277	homo sapien	344	1	9.1	10	1	HTF_NAUCI	P10939	nauphoeta c
272	1	9.1	9	1	NSK1_SARBU	P41492	sarcophaga	345	1	9.1	10	1	HTF_TABAT	P14596	tabanus atr
273	1	9.1	9	1	OXYA_SCYCA	P42996	scytorhinu	346	1	9.1	10	1	LABA_JATMU	P13270	jatropha mu
274	1	9.1	9	1	OXYA_SQUAC	P42999	squalus aca	347	1	9.1	10	1	LCMS_LEUMA	P21144	leucophaea
275	1	9.1	9	1	OXYF_SCYCA	P42997	scytorhinu	348	1	9.1	10	1	LPK2_LOCHI	P41488	locusta mig
276	1	9.1	9	1	OXYT_BUPFE	P42995	bufo regula	349	1	9.1	10	1	LSK2_LEUMA	P09039	leucophaea
277	1	9.1	9	1	OXYT_CYPCA	P23879	cyprinus ca	350	1	9.1	10	1	MALE_KLEPN	O05564	klebsiella
278	1	9.1	9	1	OXYT_RABTT	P32878	oryctolagus	351	1	9.1	10	1	MOSQ_CLYJA	P19962	clypeaster
279	1	9.1	9	1	OXYT_RAJCL	P42994	raja clavat	352	1	9.1	10	1	MP2_MICOC	P81533	microplitis
280	1	9.1	9	1	OXYV_SQUAC	P43000	squalus aca	353	1	9.1	10	1	NO40_TOBAC	P55962	nicotiana t
281	1	9.1	9	1	PGLR_DIAAB	P81179	diaprepes a	354	1	9.1	10	1	NS1_MYCTU	P81135	mycobacteri
282	1	9.1	9	1	PHH1_LYCES	P83380	lycopersico	355	1	9.1	10	1	PAP1_PARMA	P81863	pardachirus
283	1	9.1	9	1	PKK1_PERAM	P82691	periplaneta	356	1	9.1	10	1	PORB_METIM	P80901	methanobact
284	1	9.1	9	1	PISP_BOMMU	P82063	bombyx mori	357	1	9.1	10	1	PPCK_FASHE	P80525	fasciola he
285	1	9.1	9	1	RS42_LITREJ	P82075	litoria fub	358	1	9.1	10	1	PSBF_CAPAN	Q03367	capsicum an
286	1	9.1	9	1	RS10_SERMA	O68536	serotia ma	359	1	9.1	10	1	PVK_LOCHI	P83382	locusta mig
287	1	9.1	9	1	R733_HOVIN	P82526	bos taurus	360	1	9.1	10	1	Q2OB_COMTE	P80465	comamonas t
288	1	9.1	9	1	SAMP_MUSTA	P19095	mustelus ca	361	1	9.1	10	1	Q2OG_COMTE	P80466	comamonas t
289	1	9.1	9	1	SAP_STOVA	P24047	stomopneute	362	1	9.1	10	1	RCA_PINPS	P81084	pinus pinas
290	1	9.1	9	1	TALI_PICJA	P17440	pichia ladi	363	1	9.1	10	1	RRPL_PHODV	P35946	phocine dis
291	1	9.1	9	1	TAL3_PICJA	P17441	pichia ladi	364	1	9.1	10	1	RT02_BOVIN	P82923	bos taurus
292	1	9.1	9	1	THF_PIG	P01255	sus scrofa	365	1	9.1	10	1	SLAP_BACTG	P49325	bacillus th
293	1	9.1	9	1	TKC1_CAIVO	P41517	calliphora	366	1	9.1	10	1	SP34_DICMG	P81545	dictyosteli
294	1	9.1	9	1	TKL1_LOCHI	P16223	locusta mig	367	1	9.1	10	1	SYK_CAMUP	O46464	campylobact
295	1	9.1	9	1	TRP4_LEUMA	P81736	leucophaea	368	1	9.1	10	1	TEMK_RANTE	P56923	rana tempor
296	1	9.1	9	1	UF02_MOUSE	P18640	mus musculu	369	1	9.1	10	1	TKL2_LOCHI	P16224	locusta mig
297	1	9.1	9	1	ULAH_HUMAN	P31931	homo sapien	370	1	9.1	10	1	TKL3_LOCHI	P30249	locusta mig
298	1	9.1	9	1	ULAH_HUMAN	P31934	homo sapien	371	1	9.1	10	1	TKL4_LOCHI	P30250	locusta mig
299	1	9.1	9	1	ULAK_MOUSE	P99031	mus musculu	372	1	9.1	10	1	TKN1_SCYCA	P08608	scytorhinu
300	1	9.1	9	1	UN19_PAPA	P81355	clostridium	373	1	9.1	10	1	TKNB_CHICK	P19851	gallus gall
301	1	9.1	9	1	UPA3_HUMAN	P32089	homo sapien	374	1	9.1	10	1	TKNB_ONCMY	P22689	oncorhynch
302	1	9.1	9	1	UPA6_HUMAN	P30092	homo sapien	375	1	9.1	10	1	TKNB_RANCA	P22689	oncorhynch
303	1	9.1	9	1	UPA7_HUMAN	P30093	homo sapien	376	1	9.1	10	1	TKNB_RANRI	P29135	rana ridibu
304	1	9.1	9	1	XYLA_SERSU	P19149	streptomyce	377	1	9.1	10	1	TKN1_PHYBI	P08610	phyllomedus
305	1	9.1	9	1	YHFR_AZOV1	P25825	azotobacter	378	1	9.1	10	1	TKS1_AEDAE	P42634	aedes aegypt
306	1	9.1	10	1	AREG1_AGRAE	P34655	agropyre ae	379	1	9.1	10	1	TKS2_AEDAE	P42635	aedes aegypt
307	1	9.1	10	1	AREH_LOCHI	P81626	locusta mig	380	1	9.1	10	1	TKU1_UREUN	P40751	urechis uni
308	1	9.1	10	1	AL19_CARMA	P81822	carcinus ma	381	1	9.1	10	1	TKU2_UREUN	P40752	urechis uni
309	1	9.1	10	1	AMPN_HEYAM	P81731	helicoverpa	382	1	9.1	10	1	TMOF_AEDAE	P19425	aedes aegypt
310	1	9.1	10	1	ANG1_BOLJA	Q10581	bothrops ja	383	1	9.1	10	1	TPIS_NICPL	P19118	nicotiana p
311	1	9.1	10	1	ANGT_BOVIN	P01017	bos taurus	384	1	9.1	10	1	TRP5_LEUMA	P81737	leucophaea
312	1	9.1	10	1	ANGT_CHICK	P01018	gallus gall	385	1	9.1	10	1	TRP6_LEUMA	P81738	leucophaea
313	1	9.1	10	1	ARE_CAPUS	P80474	capnocytoph	386	1	9.1	10	1	TRP8_LEUMA	P81740	leucophaea
314	1	9.1	10	1	BPP2_PCTIN	P30422	bothrops in	387	1	9.1	10	1	TRP9_LEUMA	P81741	leucophaea
315	1	9.1	10	1	BPP2_PCTJA	P01022	bothrops ja	388	1	9.1	10	1	UH05_RAT	P56573	rattus norv
316	1	9.1	10	1	CATB_SHEEP	P83205	ovis aries	389	1	9.1	10	1	UPA3_HUMAN	P40930	homo sapien
317	1	9.1	10	1	COXA_ONCMY	P80328	oncorhynch	390	1	9.1	10	1	UPA2_HUMAN	P30088	homo sapien
318	1	9.1	10	1	COXH_ONCMY	P80331	oncorhynch	391	1	9.1	10	1	UPA4_HUMAN	P30090	homo sapien
319	1	9.1	10	1	COXK_ONCMY	P80332	oncorhynch	392	1	9.1	10	1	UPA9_HUMAN	P30095	homo sapien
320	1	9.1	10	1	COXO_RAT	P80432	rattus norv	393	1	9.1	10	1	UR1_HUMAN	P32118	homo sapien
321	1	9.1	10	1	COXO_HUCB	P80982	thunus obe	394	1	9.1	10	1	UR1_HUMAN	P34990	homo sapien
322	1	9.1	10	1	ESL_LACCA	P81758	lactobacilli	395	1	9.1	10	1	URES_MORMO	P17339	morganella
323	1	9.1	10	1	ESTA_SCHGA	P81012	schizaphis	396	1	9.1	10	1	UXBI_YEAST	P99012	saccharomyc
324	1	9.1	10	1	FAR2_PENMU	P83317	penaeus mon	397	1	9.1	10	1	VEG6_BACSU	P80699	bacillus su
325	1	9.1	10	1	FAR5_MACKS	P83278	macrobrachi	398	1	9.1	11	1	ANGT_CRIGE	P09037	crinia geor

399	1	9.1	11	1	ASL1_BACSE	P83146 bacteroides	472	1	9.1	12	1	TA10_TREME	P01371 tremella me
400	1	9.1	11	1	ASL2_BACSE	P83147 bacteroides	473	1	9.1	12	1	TIN2_HOPTI	P82852 hoplobatrach
401	1	9.1	11	1	BPP3_BOTIN	P30423 bothrops in	474	1	9.1	12	1	TIN3_HOPTI	P82853 hoplobatrach
402	1	9.1	11	1	BPP4_BOTIN	P30424 bothrops in	475	1	9.1	12	1	TKN2_KASMA	P08614 kassina mac
403	1	9.1	11	1	BPP4_AGRIF	P04562 agkistrodon	476	1	9.1	12	1	TKN2_METMA	P80652 methanosarc
404	1	9.1	11	1	CA21_LITFC	P82087 litorea cit	477	1	9.1	12	1	UKA2_HUMAN	P31144 homo sapien
405	1	9.1	11	1	CA22_LITFC	P82088 litorea cit	478	1	9.1	12	1	ULAL_MOUSE	P99032 mus musculu
406	1	9.1	11	1	CA41_LITFC	P82091 litorea cit	479	1	9.1	12	1	UN39_CLOPA	P81359 clostridium
407	1	9.1	11	1	CA42_LITFC	P82092 litorea cit	480	1	9.1	12	1	UP01_CABEL	P55954 caenorhabdi
408	1	9.1	11	1	CEP1_ACHFC	P22790 achatina fu	481	1	9.1	12	1	UR2A_CATCO	P04558 catostomus
409	1	9.1	11	1	GUR2_PERAM	P11496 periplaneta	482	1	9.1	12	1	UR2B_CATCO	P04559 catostomus
410	1	9.1	11	1	GUXA_CANFA	P39501 canis fami	483	1	9.1	12	1	UR2B_CYPCA	P04561 cyprinus ca
411	1	9.1	11	1	CX5A_CANAL	P58848 conus eulic	484	1	9.1	12	1	UR2_GILMI	P01147 gillichthys
412	1	9.1	11	1	CX5B_CANAL	P58849 conus eulic	485	1	9.1	12	1	UR2_POLSP	P81022 polyodon sp
413	1	9.1	11	1	CX11_CONMR	P58807 conus marino	486	1	9.1	12	1	UR2_SCYCA	P35490 scyllorhinu
414	1	9.1	11	1	ESL1_RAI	P55571 rattus norv	487	1	9.1	12	1	V14K_WSSV	P82006 white spot
415	1	9.1	11	1	FAR6_PENMG	P81321 penaeus mon	488	1	9.1	12	1	V23K_WSSV	P82005 white spot
416	1	9.1	11	1	FAR9_CALVO	P41864 calliphora	489	1	9.1	12	1	V25K_WSSV	P82004 white spot
417	1	9.1	11	1	HS70_PINPS	P81572 pinus pinas	490	1	9.1	12	1	XYLA_STRVN	P14405 streptomyce
418	1	9.1	11	1	LPW_THETH	P05624 thernus the	491	1	9.1	12	1	Y2PY_ECOLI	P17776 escherichia
419	1	9.1	11	1	LSK1_LEUMA	P04428 leucophaea	492	1	9.1	13	1	ACT7_SOYBN	P15987 glycine max
420	1	9.1	11	1	LSKP_PERAM	P36885 perip. aneta	493	1	9.1	13	1	BLAC_STRGR	P81173 streptomyce
421	1	9.1	11	1	MHBI_KLEPN	P80580 klebsiella	494	1	9.1	13	1	BOML_PSEGU	P42991 pseudophryn
422	1	9.1	11	1	MLG1_TREIS	P41989 theriozyon	495	1	9.1	13	1	BP37_LEUMA	P81754 leucophaea
423	1	9.1	11	1	NXSM_CANFA	P45820 canis fami	496	1	9.1	13	1	BPPI_BOTJA	P01020 bothrops ja
424	1	9.1	11	1	NXSM_PSELE	P56022 pseudonaja	497	1	9.1	13	1	CD71_LITEA	P82051 litorea ewi
425	1	9.1	11	1	PAC1_CARMO	P82684 parausonia	498	1	9.1	13	1	CH60_CANFA	P49818 canis fami
426	1	9.1	11	1	PQOC_PSEFC	P55173 pseudomonas	499	1	9.1	13	1	CHEP_PARID	P42718 parapolybia
427	1	9.1	11	1	RANC_RANFI	P08951 rana pipien	500	1	9.1	13	1	CPI_APUCA	Q10998 aplisia cal
428	1	9.1	11	1	RE41_LITRO	P82074 litorea rub							
429	1	9.1	11	1	RHPI_CHAV	P31179 chandipura							
430	1	9.1	11	1	RS3G_ONCMY	P81328 encortynchu							
431	1	9.1	11	1	TZPI_PBOVG	P31031 proteus vul							
432	1	9.1	11	1	TIN2_HOPTI	P82651 hoplobatrach							
433	1	9.1	11	1	TIN4_HOPTI	P82654 hoplobatrach							
434	1	9.1	11	1	TKC2_CALVO	P41516 calliphora							
435	1	9.1	11	1	TKN1_PSEGU	P42986 pseudophryn							
436	1	9.1	11	1	TKN1_UPEIN	P82026 upeolelea i							
437	1	9.1	11	1	TKN1_UPEUG	P08622 upeolelea r							
438	1	9.1	11	1	TKN2_PSEGU	P42987 pseudophryn							
439	1	9.1	11	1	TKN3_PSEGU	P42988 pseudophryn							
440	1	9.1	11	1	TKN4_PSEGU	P42989 pseudophryn							
441	1	9.1	11	1	TKN5_PSEGU	P42990 pseudophryn							
442	1	9.1	11	1	TKNA_CHICK	P19850 gallus gall							
443	1	9.1	11	1	TKN2_ZHYLU	P58615 physalaemus							
444	1	9.1	11	1	UF05_MOUSE	P49643 mus musculu							
445	1	9.1	11	1	UXAG_EURAN	P41933 homo sapien							
446	1	9.1	11	1	UXB2_YEAST	P05013 saccharomyce							
447	1	9.1	11	1	CALM_TETTH	P05055 tetrahymena							
448	1	9.1	11	1	CXAL_CANTM	P50983 conus imper							
449	1	9.1	11	1	CX41_CANKR	P58809 conus marino							
450	1	9.1	11	1	CXST_CANTM	P58846 conus texti							
451	1	9.1	11	1	FARI_CANTM	P41869 calliphora							
452	1	9.1	11	1	FIFI_SARHO	P81349 sarcophaga							
453	1	9.1	11	1	FIFI_LITIN	P82021 litorea inf							
454	1	9.1	11	1	H2AX_ONCMY	P83327 encorhynchu							
455	1	9.1	11	1	HCVB_MEGTR	C10584 megathura c							
456	1	9.1	11	1	HEP1_BACSE	P83054 bacteroides							
457	1	9.1	11	1	HS9A_RAI	P82995 rattus norv							
458	1	9.1	11	1	LICH_BACSI	P82907 bacillus li							
459	1	9.1	11	1	LM71_LEUMA	P22395 locusta mig							
460	1	9.1	11	1	N040_LOTJA	Q22426 lotus japon							
461	1	9.1	11	1	N040_SESHC	Q24369 sesbania ro							
462	1	9.1	11	1	N040_SOYBN	P55960 glycine max							
463	1	9.1	11	1	NUDM_CANFA	P54713 canis fami							
464	1	9.1	11	1	PA21_MICPM	P25072 micrurus fu							
465	1	9.1	11	1	PA2B_VIPBO	P31859 vipera beru							
466	1	9.1	11	1	PORD_METTM	P80903 methanobact							
467	1	9.1	11	1	PKK4_PERAM	P82619 periplaneta							
468	1	9.1	11	1	PKK4_PFERU	P82690 periplaneta							
469	1	9.1	11	1	PKP3_PHYPA	P80662 physcomitre							
470	1	9.1	11	1	PKK2_PERAM	P81555 periplaneta							
471	1	9.1	11	1	REL_CONSP	P58805 conus spuri							

ALIGNMENTS

RESULT 1
 B44K_PORGI
 ID B44K_PORGI STANDARD: PRT: 8 AA.
 AC P81886:
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 44 kDa immunogenic protein (Fragment).
 OS Porphyromonas gingivalis (Bacteroides gingivalis).
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonas.
 OX NCBI_TaxID=837;
 RN 111
 RP SEQUENCE.
 RC SIRALIN=VFB 3492;
 RC MEDLINE=20198497; PubMed=10731616;
 RA Norris J.M., Love D.N.;
 RI "Serum antibody responses of cats to soluble whole cell antigens of
 RT feline Porphyromonas gingivalis";
 RL Vet. Microbiol. 73:37-49(2000).
 CC -!- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
 KW Antigen.
 FT NON_TER
 SQ SEQUENCE 8 AA: 989 MW; 9554540326CB476D CRC64;
 Query Match 36.4%; Score 4; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 QY 6 KRNI 9
 Db 5 KRNI 8
 RESULT 2
 CS15_BACSU
 ID CS15_BACSU STANDARD: PRT: 11 AA.
 AC P81095;
 DT 15-JUL-1998 (Rel. 36, Created)

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DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DI Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).
CS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID:1423;
RN 11;
RP SEQUENCE.
RC STRAIN:168 / JH642;
RA Graumann P.L., Schmid R., Marahleh M.A.;
RL Submitted (OCT-1997) to the SWISS-PROT data bank.
[2]
RP CHARACTERIZATION.
RC STRAIN:168 / JH642;
RX MEDLINE:96345629; PubMed-8755921;
RA Graumann P., Schroeder K., Schmid R., Marahleh M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RL J. Bacteriol. 178:4611-4619(1996).
CC 1- SUBCELLULAR LOCATION: Cytoplasmic.
CC 1- INDUCTION: In response to low temperature.
CC 1- CAUTION: Could not be found in the genome of B. subtilis 168.
FT NON_TER 11
SQ SEQUENCE 11 AA: 1360 MW: 156683.632240 kDa
Query Match 36.4%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RNK 10
DB 2 RNK 5

RESULT 3
RLC:ACHLA
ID RS19_ELYEP STANDARD: PRT; 10 AA.
AC P29221;
DT 01-DEC-1992 (Rel. 24, Created)
DI 01-DEC-1992 (Rel. 24, Last sequence update)
DE 01 NOV-1995 (Rel. 32, Last annotation update)
DE 50S ribosomal protein L16 (Fragment)
GN RPL16
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID:2148;
RN 11;
RP SEQUENCE FROM N.A.
RX MEDLINE:12210505; PubMed 1554679.
RA Lim P.C., Sears B.B.;
RT "Evolutionary relationships of a plant ribonuclease-like protein and Acholeplasma laidlawii deduced from two ribosomal protein gene sequences.";
RL J. Bacteriol. 174:2606-2611(1992).
CC 1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.
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EMBL: M74771; AAA21914.1;
DR PIR: F41839;
DR InterPro: IPR000114; Ribosomal L16.
DR PROSITE: PS00586; RIBOSOMAL_L16_2; Partial.
DR PROSITE: PS00701; RIBOSOMAL_L16_2; Partial.
KW Ribosomal protein; rRNA-binding.

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FT NON_TER 10
SQ SEQUENCE 10 AA: 1324 MW: 83386.62184032766 kDa
Query Match 27.3%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 4 PKR 6

RESULT 4
RS19_ELYEP STANDARD: PRT; 12 AA.
AC Q47881;
DT 30-MAY-2000 (Rel. 39, Created)
DI 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19 OR RPS19.
CS Elm yellows phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID:35774;
RN 11;
RP SEQUENCE FROM N.A.
RX MEDLINE:94350802; PubMed-8071198;
RA Gundersen D.E., Lee J.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for their classification.";
RL J. Bacteriol. 176:5244-5254(1994).
CC 1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC 1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
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EMBL: U27022; AAA83942.1;
DR HAMAP: MF_C05122;
DR InterPro: IPR002222; Ribosomal_S19.
DR PROSITE: PS00423; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 11
SQ SEQUENCE 12 AA: 1283 MW: 200478.958333AA8 kDa
Query Match 27.3%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4
DB 10 SKK 12

RESULT 5
RS19_PPWPB STANDARD: PRT; 14 AA.
AC Q52693;
DT 30-MAY-2000 (Rel. 39, Created)
DI 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19 OR RPS19.
CS Pigoon pea yellows' biomon phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.

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KT plastid enzymes.*;
KL Planta_201261-272(1997).
CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate + Asp + 3-
   phospho-D-glyceroyl phosphate.
CC -1- PATHWAY: Calvin cycle.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- SIMILARITY: Belongs to the phosphoglycerate kinase family.
DR InterPro: IPR001576; PKC.
DR PROSITE: PS00111; PGLYCERATE_KINASE; PARTIAL.
KW Transferase; Kinase; Multigene family; Calvin cycle; Chloroplast.
FT NON_TER 15 15
SQ SEQUENCE 15 AA: 1531 MW: 564580;F677E6E 68-64;

Query Match 27.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3
DB 6 ASK 8

RESULT 9
RS20_PACST STANDARD: PRI: 15 AA.
AC P59681;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 30S ribosomal protein S20 (BS20) (Fragment).
GN RPS2.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE.
RC STRAIN=10;
RX PubMed-4507606;
RA Yaguchi M., Matheson A.T., Visentin L.P.;
RT "Prokaryotic ribosomal proteins: N-terminal sequence homologues and
   structural correspondence of 30 S ribosomal proteins from Escherichia
   coli and Bacillus stearothermophilus."
RC FEBS Lett. 46:296-300(1974).
CC -1- FUNCTION: Binds directly to 16S ribosomal RNA (By similarity).
CC -1- SIMILARITY: BELONGS TO THE S20 FAMILY OF RIBOSOMAL PROTEINS.
DR HAMAP; MF_00560; ?; 1.
KW Ribosomal protein; rRNA-binding
FT INIT_MET 0 0
FT NON_TER 15 15
SQ SEQUENCE 15 AA: 1645 MW: 454462;F6472 6-64;

Query Match 27.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NIK 10
DB 2 NIK 4

RESULT 10
ACLTHUAL STANDARD: PRI: 8 AA.
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Macthannus macropterus).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
   Acanthomorpha; Acanthopterygii; Perciformes; Percitormes; Strombroides;

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OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
KX MEDLINE=88326322; PubMed 3415688;
KA Kohama Y., Matsunaga S., Oka H., Teramoto T., Okabe M., Mimura T.;
RT "Isolation of angiotensin converting enzyme inhibitor from tuna
   muscle.";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR: A31570; A31570.
SQ SEQUENCE 8 AA: 953 MW: 6AA863733051F1B7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IK 10
DB 4 IK 5

RESULT 11
ALL7_CARMA STANDARD: PRI: 8 AA.
IC P81809; P81804; P81810;
DI 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Carcinustatin 7 (Contains: Carcinustatin 6; Carcinustatin 1).
OS Carcinus maenas (Common shore crab) (Green crab).
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
   OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed-9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
   RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
   allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT PEPTIDE 1 8 CARCINUSTATIN 7.
FT PEPTIDE 2 8 CARCINUSTATIN 6.
FT PEPTIDE 4 8 CARCINUSTATIN 1.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA: 825 MW: 922879DCB4775BD CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 1 AS 2

RESULT 12
FARL_PENMO STANDARD: PRI: 8 AA.
ID FARL_PENMO
AC P83316;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP1 (GDRNFLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
   Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;

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OC Penaeidae; Penaeus.
 OX NCBI_TaxID:6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigornkul P., Pupem J., Krunkasom C., Lomayart S.,
 RA Chaisetchangkura P., Sithigornkul W., Pitsom A.,
 RT *Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 RT of the giant tiger prawn Penaeus monodon.*
 RL Comp. Biochem. Physiol. 131B:125-137(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW-1024.8; MEISLE-MALLI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 1024 MW: 7204.729C4540A8 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RN 8
 DB 3 RN 4
 RESULT 13
 ID FARP3_HOMAM STANDARD; PRT; 8 AA.
 AC P41487;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE FMRFamide-like neuropeptide 3 (Fli 3) (F2).
 OS Homarus americanus (American lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Nephropoidea; Nephropidae; Homarus.
 OX NCBI_TaxID:6706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE=88116164; PubMed=3429714;
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
 RT *Purification and characterization of FMRFamide-like immunoreactive
 RT substances from the lobster nervous system: Isolation and sequence
 RT analysis of two closely related peptides.*
 RL J. Comp. Neurol. 266:16-26(1987).
 CC -!- MISCELLANEOUS: PERICARDIAL GLANDS RELEASE THIS PEPTIDE WITH 100 NM
 CC POTASSIUM IN THE PRESENCE OF CALCIUM.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 1054 MW: 6304.729C4540A8 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RN 8
 DB 3 RN 4
 RESULT 14
 ID FARP4_HOMAM STANDARD; PRT; 8 AA.
 AC P41487;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide 4 (Fli 4) (F1).
 OS Homarus americanus (American lobster).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 OC Nephropoidea; Nephropidae; Homarus.
 OX NCBI_TaxID:6706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pericardial organs;
 RX MEDLINE=88116164; PubMed=3429714;
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
 RT *Purification and characterization of FMRFamide-like immunoreactive
 RT substances from the lobster nervous system: Isolation and sequence
 RT analysis of two closely related peptides.*
 RL J. Comp. Neurol. 266:16-26(1987).
 CC -!- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC
 CC NEUROMUSCULAR JUNCTIONS.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 1067 MW: DDD40729C4540451 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RN 8
 DB 3 RN 4
 RESULT 15
 ID LCK4_LEUMA STANDARD; PRT; 8 AA.
 AC P21143;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE Leucokinin IV (L-IV).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID:5988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT *Primary structure and synthesis of two additional neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RT cephalomyotropins.*
 RL Comp. Biochem. Physiol. 84C:271-276(1986).
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 CC ACTIVITY OF COCKROACH PROTHODIUM (HINDGUT).
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 906 MW: DC6365B1E9D5BDDA CRC64;
 Query Match 18.2% Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AS 2
 DB 2 AS 3
 RESULT 16
 ID LPMS_STAEP STANDARD; PRT; 8 AA.
 LPMS_STAEP

AC P23121;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last annotation update)
 DE Probable msrA leader peptide.
 OS Staphylococcus epidermidis.
 OG Plasmid pUL5050.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=968;
 RX MEDLINE=91041730; PubMed-2233255;
 RA Ross J.J., Eady E.A., Cove J.H., Gublitte W.J., Baumbert S.,
 RA Wootton J.C.;
 RT "Inducible erythromycin resistance in staphylococci is encoded by a
 RT member of the ATP-binding transport super-gene family.";
 RL Mol. Microbiol. 4:1207-1214(1990).
 CC -!- FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE
 CC PROTEIN.
 CC
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 CC
 DR PIR: X520H5; CAA36303.1;
 DR EMBL: S11157; IFSAME.
 KW Leader peptide; Plasmid.
 SQ SEQUENCE 8 AA: 937 MW: FA37340685HEC1A6 CRK64;

 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 AS 2
 DB 1
 3 AS 4

 RESULT 17
 RS7_MYCIT STANDARD; PRT; b AA.
 AC P33564;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S7 (fragment).
 GN RPS3.
 OS Mycobacterium intracellulare.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1767;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=93197130; PubMed-8451173;
 RA Nair J., Rouse D.A., Morris S.L.;
 RT "Nucleotide sequence analysis of the ribosomal S12 gene of
 RT Mycobacterium intracellulare.";
 RL Nucleic Acids Res. 21:1039-1049(1993)
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center, probably blocks exit of the E-site
 CC tRNA (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
 CC and S11 (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
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 CC
 DR EMBL: L08171; AAA25476.1;
 DR PIR: S35538; S35538.
 DR HAMAP: MF_00480; 1.
 DR InterPro: IPR000235; Ribosomal_S7.
 DR PROSITE: PS00052; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; rRNA-binding; tRNA-binding; tRNA-binding.
 FT INIT-MET 0 0 BY SIMILARITY.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 850 MW: 63276DC768732417 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 PK 6
 DB 7 PK 8

 RESULT 18
 CONO_CONGE STANDARD; PRT; 9 AA.
 ID AC P05486;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lys-conopressin G.
 OS Conus geographus (Geography cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88058932; PubMed-3680228;
 RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
 RA Gray W.R., Olivera B.M.;
 RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
 RT peptides from Conus geographus and Conus straitus venoms.";
 RL J. Biol. Chem. 262:15821-15824(1987).
 RN [2]
 RP REVIEW.
 RX MEDLINE=89024586; PubMed-3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails.";
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR: A28495; A28495.
 DR InterPro: IPR000981; Neurhyp_horm.
 DR Pfam: PF00220; hormoned4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHTYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA: 1037 MW: D4FC276EB4540059 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 PK 6
 DB 7 PK 8


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RESULT 19
CONG_CONST          STANDARD:          PRT:          9 AA.
AC  P05487:
DT  01-NOV-1988 (Rel. 09, Created)
DT  01-NOV-1988 (Rel. 09, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Arg-conopressin S.
OS  Conus striatus (Striated cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sordariata; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus
OX  NCBI_TaxID=6493;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=89058532; PubMed=3680228;
RA  Cruz L.J., de Santos V., Zafaralla G.C., Kamilo C.A., Zeikos R.D.,
RA  Gray W.R., Olivera B.M.;
*Invertebrate vasopressin/oxytocin homologs. Characterization of
*peptides from Conus geographus and Conus striatus venoms."
RT  J. Biol. Chem. 262:15821-15824 (1987).
RN  [2]
RP  REVIEW.
RX  MEDLINE=89024586; PubMed=3052286;
RA  Gray W.R., Olivera B.M., Cruz L.J.;
*Peptide toxins from venomous Conus snails."
RT  Annu. Rev. Biochem. 57:665-700 (1988).
OC  1- FUNCTION: Targets vasopressin-oxytocin related receptors.
OC  1- SUBCELLULAR LOCATION: Secreted.
CC  1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR  EIR: B28495; B28495.
DR  InterPro: IPR000981; Neurohyp_borm.
DR  Pfam: PF00220; Hormoned_1.
LP  PROSITE: PS00264; NEUROHYPOPHYS_HORM.
KW  Hormone; Amidation.
FT  DISULFID 1 6
FT  MOD_RES 9 9  AMIDATION
SQ  SEQUENCE 9 AA: 1031 MW: 178376.454 Da; GCS:4;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RN 8
DB 11
   4 RN 5

RESULT 20
CONG_CONST          STANDARD:          PRT:          9 AA.
AC  P84647;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Contryphan Vn.
OS  Conus ventricosus (Mediterranean cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sordariata; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus.
OX  NCBI_TaxID=117992;
RN  [1]
RP  SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RX  TISSUE-Venom;
RA  Massilia G.R., Schinina M.E., Asenjo P., Pedraza J.F.;
*Contryphan-Vn: a novel peptide from the venom of the Mediterranean
*snail Conus ventricosus."
RT  Biochem. Biophys. Res. Commun. 289:906-913 (2001).
OC  1- SUBCELLULAR LOCATION: Secreted
CC  1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  1- MASS SPECTROMETRY: MW=1088.6; METHOD MAINT.

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 11
   6 AS 7

RESULT 22
FAR4_CALVO
1D  FAR4_CALVO          STANDARD:          PRT:          9 AA.

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CC  1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW  Toxin; Amidation; D-amino acid.
FT  DISULFID 3 9
FT  MOD_RES 5 5  D-TRYPTOPHAN.
FT  MOD_RES 9 9  AMIDATION.
SQ  SEQUENCE 9 AA: 1091 MW: 8038676323676EBA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KP 5
DB 6 KP 7

RESULT 21
DISIP_RABIT          STANDARD:          PRT:          9 AA.
AC  P01158;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Delta sleep-inducing peptide (DSIP).
OS  Oryctolagus cuniculus (Rabbit).
OC  Eukaryota; Metazoa; Chordata; Cniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX  NCBI_TaxID=9986;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=77185324; PubMed=862769;
RA  Monnier M., Dudier L., Gachter R., Maier P.F., Tobler H.J.,
RA  Schoenenberger G.A.;
*The delta sleep inducing peptide (DSIP). Comparative properties of
*the original and synthetic nonapeptide."
RT  Experientia 33:548-552 (1977).
RN  [2]
RP  SEQUENCE AND SYNTHESIS.
RX  MEDLINE=79054421; PubMed=568769;
RA  Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
RT  *The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
RT  analysis, sequence, synthesis and activity of the nonapeptide."
RT  Pflugers Arch. 376:119-129 (1978).
RN  [3]
RP  REVIEW.
RX  MEDLINE=87175129; PubMed=3550726;
RA  Gray M.V., Kastin A.J.;
*Delta-sleep-inducing peptide (DSIP): an update."
RT  Peptides 7:1165-1187 (1986).
CC  1- FUNCTION: WHEN INFUSED INTO THE MESODIENCEPHALIC VENTRICLE OF
CC  RECIPIENT RABBITS INDUCES SPINDLE AND DELTA EEG ACTIVITY AND
CC  REDUCED MOTOR ACTIVITIES.
CC  1- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM DIALYSATES OF
CC  OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC
CC  STIMULATION OF THE THALAMUS.
CC  1- DATABASE: NAME-Protein Spotlight;
CC  NOTE-Issue 8 of March 2001;
CC  WWW=http://www.expasy.org/spotlight/articles/sptlt008.html".
DR  PIR: A01422; QDRB.
SQ  SEQUENCE 9 AA: 849 MW: DDD365BDDAA8787D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 11
   6 AS 7

RESULT 22
FAR4_CALVO
1D  FAR4_CALVO          STANDARD:          PRT:          9 AA.

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13  FARG_MACRS          STANDARD:          PRI:          9 AA
14  AC  PB1279,
15  DT  28-FEB-2003 (Rel. 41, Last sequence update)
16  DT  26-FEB-2003 (Rel. 41, Last annotation update)
17  DT  26-FEB-2003 (Rel. 41, Last annotation update)
18  DE  PMSFamide-like neuropeptide FLP6 (EGSRNHLRF-amide).
19  OS  Macrobrachium rosenbergii (Giant Fresh Water Prawn).
20  EC  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
21  EC  Eumalacostraca; Decapoda; Decapoda; Pterygota; Arthropoda;
22  EC  Malacostraca; Palaemonidae; Macrobrachium.
23  NCBI_TaxID=79674;
24  RN  [1]
25  PP  SEQUENCE, AND MASS SPECTROMETRY.
26  RC  TISSUE: Eye stalk.
27  RX  MEDLINE=22107394; PubMed=11179812;
28  RA  Sithigorngul P., Saralithongkum W., Lonyant S., Panchan N.,
29  RA  Sithigorngul P., Petson A.;
30  RT  *Three more novel PMSFamide-like neuropeptide sequences from the
31  RT  eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.*
32  RL  Peptides 22:191-197(2001).
33  RL  1- MASS SPECTROMETRY: MH=1080.7; METHOD=MALDI.
34  CC  1- SIMILARITY: BELONGS TO THE FARG (PMSFAMIDE-RELATED PEPTIDE)
35  CC  FAMILY.
36  CR  GO: GO:0007218; P:neuropeptide signaling pathway; IDA;
37  KW  Neuropeptide; Amidation.
38  FT  Mol. Res. 9 AM:tail N.
39  SQ  SEQUENCE 9 AA: 1081 MW: 268007295454.878 AS:64;
40
41  Query Match 18.2% Score 2; DB 1; Length 9;
42  Best Local Similarity 100.0%; Pred. No. 1.3e-05;
43  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
44
45  QY 7 RN 8
46  LB 4 RN 5
47
48  RESULT 27
49  HUIU_KLEAE
50  ID  HUIU_KLEAE          STANDARD:          PRI:          9 AA.
51  AC  P12381,
52  DT  01-OCT-1989 (Rel. 12, Created)
53  DT  01-OCT-1989 (Rel. 12, Last sequence update)
54  DT  28-FEB-2003 (Rel. 41, Last annotation update)
55  DE  Glycerate hydratase (EC 4.2.1.49) (Glycerate) (indole-3-methylpropanoate
56  DE  hydrolase) (fragment).
57  OS  HUIU.
58  OS  Klebsiella aerogenes.
59  CC  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
60  CC  Enterobacteriaceae; Klebsiella.
61  NCBI_TaxID=28451;
62  RN  [1]
63  PP  SEQUENCE FROM N.A.
64  RX  MEDLINE=86198618; PubMed=2834335;
65  RA  Nieuwkoop A.J., Baldauf S.A., Hudspett M.E.S., Bender R.A.;
66  RT  *Bidirectional promoter in the hui(p) region: The histidine
67  RT  utilization (hut) operons from Klebsiella aerogenes.*
68  RL  J. Bacteriol. 170:2240-2246(1988).
69  RN  [2]
70  PP  SEQUENCE FROM N.A.
71  RX  MEDLINE=90368611; PubMed=2203754;
72  RA  Schwacha A., Bender R.A.;
73  RT  *Nucleotide sequence of the gene encoding the repressor for the
74  RT  histidine utilization genes of Klebsiella aerogenes.*
75  RL  J. Bacteriol. 172:5477-5481(1990).
76  CC  1- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-1H-imidazol-4-
77  CC  yl)propanoate + uracinate -> H(2)O
78  CC  1- COFACTOR: Binds 1 NAD per subunit (95% similarity).
79  CC  1- PATHWAY: Histidine degradation; Second step.
80  CC  1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
81  CC  1- SIMILARITY: BELONGS TO THE Glycerate FAMILY
82  CC  This SWISS-PROT entry is copyrighted by the Swiss Institute of Bioinformatics.
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90
91  DR  EMBL: M19665; AAA25078.1;
92  DR  EMBL: M34604; AAA25076.1;
93  DR  HAMAP: MF_00577;
94  DR  InterPro: IPR00193; Glycerate.
95  DR  PROSITE: PS01233; URACINASE; PARTIAL.
96  KW  Histidine metabolism; Lyase; NAD.
97  FT  Non-Ter. 9
98  SQ  SEQUENCE 9 AA: 1140 MW: 970FC41B5325A6C5 CRC64;
99
100  Query Match 18.2% Score 2; DB 1; Length 9;
101  Best Local Similarity 100.0%; Pred. No. 1.3e-05;
102  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
103
104  QY 2 SK 3
105  LB 4 SK 5
106
107  RESULT 28
108  LPCA_STAAU
109  ID  LPCA_STAAU          STANDARD:          PRI:          9 AA.
110  AC  P36884;
111  DT  01-JUN-1994 (Rel. 29, Created)
112  DT  01-JUN-1994 (Rel. 29, Last sequence update)
113  DT  01-OCT-1994 (Rel. 30, Last annotation update)
114  DE  Chloramphenicol resistance leader peptide.
115  OS  Staphylococcus aureus, and
116  OS  Streptococcus agalactiae.
117  CC  Plasmid pSCS6, Plasmid pSCS7, Plasmid pUB112, and Plasmid pIP501.
118  CC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
119  NCBI_TaxID=1280, 1311;
120  RN  [1]
121  PP  SEQUENCE FROM N.A.
122  KC  SPECIES STRAIN: STRAIN-415; PLASMID=pSCS7;
123  RX  MEDLINE=92027652; PubMed=1929326;
124  RA  Schwarz S., Cardoso M.;
125  RT  *Nucleotide sequence and phylogeny of a chloramphenicol
126  RT  acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
127  RT  aureus.*
128  RL  Antimicrob. Agents Chemother. 35:1551-1556(1991).
129  RN  [2]
130  PP  SEQUENCE FROM N.A.
131  KC  SPECIES-S. aureus; PLASMID=pSCS6;
132  RX  MEDLINE=92388047; PubMed=1517170;
133  RA  Cardoso M., Schwarz S.;
134  RT  *Nucleotide sequence and structural relationships of a
135  RT  chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
136  RT  Staphylococcus aureus.*
137  RL  J. Appl. Bacteriol. 72:289-293(1992).
138  RN  [3]
139  PP  SEQUENCE FROM N.A.
140  KC  SPECIES-S. aureus; PLASMID=pUB112;
141  RX  MEDLINE=86081739; PubMed=3865770;
142  RA  Brueckner R., Matzura H.;
143  RT  *Regulation of the inducible chloramphenicol acetyltransferase gene
144  RT  of the Staphylococcus aureus plasmid pUB112.*
145  RL  EMBO J. 4:2295-2300(1985).
146  RN  [4]
147  PP  SEQUENCE FROM N.A.
148  KC  SPECIES-S. agalactiae; PLASMID=pIP501;
149  RX  MEDLINE=93096867; PubMed=1461942;
150  RA  Trica-Cuot P., de Cespedes G., Horad T.;
151  RT  *Nucleotide sequence of the chloramphenicol resistance determinant of
152  RT  the streptococcal plasmid pIP501.*
153  RL  Plasmid 28:272-276(1992).
154  CC  This SWISS-PROT entry is copyrighted by the Swiss Institute of Bioinformatics.
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CC -----
 DR EMBL: M58155; AAA26612.1; -
 DR EMBL: M58156; AAA16528.1; -
 DR EMBL: X02872; CAA26630.1; -
 DR EMBL: X60827; CAA43217.1; -
 DR EMBL: X65462; CAA46454.1; -
 DR PIR: B24362; B24362.
 DR PIR: S30494; S30494.
 KW Leader peptide: Antibiotic resistance; Plasmid.
 SQ SEQUENCE 9 AA: 1074 MW: 50945AAR5H5H53 CRC64;

Query Match 18.2% Score 2: 25 1: Length: 9;
 Best Local Similarity 100.0% Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KK 4
 II
 DB 2 KK 3

RESULT: 29
 NEF_HV128
 ID NEF_HV128 STANDARD; PRT; 9 AA.
 AC P12481.
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Negative factor (F-protein) (27 kDa protein) (FusF) (Fragment).
 GN NEF.
 OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviridae.
 OX NCBI_TaxID=11681;
 RN II
 RP SEQUENCE FROM N.A.
 RX MEDLINE 88281278; PubMed=3395517;
 RA Yoon J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
 RA Gallo R.C.;
 RT "Nucleotide sequence analysis of the env gene of a new Zairian
 RT isolate of HIV-1.";
 RL AIDS Res. Hum. Retroviruses 4:165-174 (1988).
 CC -!- FUNCTION: NEF has GTPase, GTP-binding and a tyrosine phosphorylating
 CC activities. It seems to downregulate the CD4/32 antigen.
 CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR OLD
 CC ZAIREAN MALE.
 CC -----

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CC -----
 DR EMBL: J03653; AAA44687.1; -
 DR HIV; J03653; NEFSJY1.
 KW AIDS; Myristate; GTP-binding.
 FT LIPID 2
 FT NON_TER 9 2 MYRISTATE (HY SIMILARITY).
 SQ SEQUENCE 9 AA: 967 MW: 319C8325A73H76 CRC64;

Query Match 18.2% Score 2: DB 1: Length: 9;
 Best Local Similarity 100.0% Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SK 3
 II

DB 6 SK 7
 RESULT 30
 NEUU_CAVPO
 ID NEUU_CAVPO STANDARD; PRT; 9 AA.
 AC P34966;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuromedin U-9 (NMU-9).
 GN NMU.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN II
 RP SEQUENCE.

CC TISSUE=Small intestine;
 RX MEDLINE=90341105; PubMed=2381877;
 RA Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
 RT "Isolation and microsequence analysis of a novel form of neuromedin U
 RT from guinea pig small intestine.";
 RL Peptides 11:613-617(1990).
 CC -!- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES
 CC SELECTIVE VASOCONSTRICTION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE NMU FAMILY.
 DR InterPro: IPR001942; NMU.
 DR Pfam: PF02070; NMU; 1.
 DR PROSITE: PS00967; NMU; 1.
 KW Amidation; Hormone.
 FT MOD_RES 5 9 AMIDATION.
 SQ SEQUENCE 9 AA: 1169 MW: 1ECF17409C729DB CRC64;

Query Match 18.2% Score 2: DB 1: Length: 9;
 Best Local Similarity 100.0% Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RN 8
 II
 DB 8 RN 9

RESULT 31
 OXYT_EISFO
 ID OXYT_EISFO STANDARD; PRT; 9 AA.
 AC P42994;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE Annetocin.
 DE Annetocin.
 OS Eisenia foetida (Common brandling worm) (Common dung-worm).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
 OC Lumbricina; Lumbricidae; Eisenia.
 OX NCBI_TaxID=6396;
 RN II

CC TISSUE=Pituitary;
 RX MEDLINE=94121660; PubMed=8292046;
 RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
 RA Nomoto K.;
 RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
 RT Eisenia foetida.";
 RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
 CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
 CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE ANIMAL THROUGH
 CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 CC PIR: PC2021; PC2021.
 DR InterPro: IPR000981; Neuhyp_horm.
 DR Pfam: PF00220; Hormone4; 1.

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DR PROSITE: PS00264: NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 5 9 AMIDATION.
SQ SEQUENCE 9 AA: 996 MW: 145EB7AEH4541209 CRC64:

Query Match: 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RN 8
II
DB 4 RN 5

RESULT 32
OXYT_OCTVU
ID OXYT_OCTVU STANDARD: PRT: 9 AA.
AC P80027;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Cephalotoxin.
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidae; Naucoroidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopas.
OX NCBI_TaxID=6645;
RN [1]
RP SEQUENCE.
RC TISSUE Nerve endings.
RX MEDLINE=92270139; PubMed=1599145;
RA Reich G.;
RT "A new peptide of the oxytocin/vasopressin family isolated from
RV nerves of the cephalopod Octopus vulgaris."
RL Neurosci. Lett. 134:191-194(1992).
CC -! FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA
CC CAVA.
CC -! SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurohyp-form.
DR Pfam: PF00220; Hormone4.1.
DR PROSITE: PS00264: NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 5 9 AMIDATION.
SQ SEQUENCE 9 AA: 1072 MW: 17FF47AEH4541209 CRC64:

Query Match: 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RN 8
II
DB 4 RN 5

RESULT 33
ULAB_HUMAN
ID ULAB_HUMAN STANDARD: PRT: 9 AA.
AC P31929;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94114769; PubMed=813870;
RA Hughes G.J., Frutiger S., Paguet N., Pasquati G., Sanchez J.-C.,
RA Tissot J.-D., Balroch A., Appel R.D., Hochstrasser D.F.;

DR PROSITE: PS00264: NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 5 9 AMIDATION.
SQ SEQUENCE 9 AA: 996 MW: 145EB7AEH4541209 CRC64:

Query Match: 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RN 8
II
DB 4 RN 5

RESULT 34
AH3_PROSE
ID AH3_PROSE STANDARD: PRT: 10 AA.
AC P29261;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II) (AH 11) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
RL Plant Physiol. 100:282-290(1992).
CC -! CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O -> (R)-prunasin + D-
CC glucose.
CC -! SUBUNIT: Monomer.
CC -! DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COITLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -! PTM: GLYCOSYLATED.
KW Glucosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1C33 MW: 3331B8D051E04777 CRC64:

Query Match: 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
II
DB 8 AS 9

RESULT 35
BPP8_BOTIN
ID BPP8_BOTIN STANDARD: PRT: 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroqlossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]

```

RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE-90351557; PubMed-2386615;
RA Cintra A.C.O., Vieira C.A., Gaglioli J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: H37196; H37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid
FT MOD_RES 1 1
SQ SEQUENCE 10 AA; 1173 MW; 2FFB354576F6F6B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NI 9
DB 7 NI 8

RESULT 35
BPP_VIPAS
ID BPP_VIPAS STANDARD; PRT: 10 AA.
AC P31351;
DI 01-JUL-1993 (Rel. 26, Created)
DI 01-FEB-1994 (Rel. 28, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin converting
DE enzyme inhibitor).
OS Vipera aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
RX MEDLINE-90382616; PubMed-2169439;
RA Komori Y., Suihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
RT enzyme from the venom of Vipera aspis aspic."
RL Int. J. Biochem. 22:767-771(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: A60377; XASNPC.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
SQ SEQUENCE 10 AA; 1062 MW; 3DAB27C427636734 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
DB 6 PK 7

RESULT 37
BRK_ONCMY
ID BRK_ONCMY STANDARD; PRT: 10 AA.
AC Q9PRZ1;
DI 16-OCT-2001 (Rel. 40, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.

OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE-94039817; PubMed-8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
RT trout plasma."
RL FEBS Lett. 334:75-78(1993).
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
CC THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR: S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KR 7
DB 1 KR 2

RESULT 38
COXM_RAT
ID COXM_RAT STANDARD; PRT: 10 AA.
AC P80431;
DI 01-NOV-1995 (Rel. 32, Created)
DI 01-NOV-1995 (Rel. 32, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)
DE (Fragment).
GN COX7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE-95324529; PubMed-7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform."
RL Eur. J. Biochem. 230:235-241(1995).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) -> 4 ferricyclochrome
CC c + 2 H(2)O;
DR PIR: S65387; S65387.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KK 4
DB 4 KK 5

RESULT 39


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QDP2_BOVIN
ID QDP2_BOVIN STANDARD PRT 10 AA
AC P11180
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2) (Fragment).
GN DLAI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Artiodactyla; Primates; Ruminantia;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=88024154; PubMed=3117054;
RA Bradford A.P., Howell S., Aitken A., James L.A., Yeaman S.J.
RI "Primary structure around the lipoyl-attachment site on the E2
RI component of bovine heart pyruvate dehydrogenase complex.";
RL Biochem. J. 245:919-922(1987).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydropyrimidine acetyltransferase (E2) and
CC lipoyl dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydropyrimidine CoA + S
CC acetylthiodihydropyrimidine.
CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BINDING LIPOYL
CC COFACTOR.
CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH 12-ATHETRAL
CC SYMMETRY.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
DR InterPro: IPR004016; Lipoyl.
DR PROSITE: PS00189; LIPOYL PARTIAL.
KW Glycolysis; Transferase; Acyltransferase. Repeat: Mitochondrion;
KW Lipoyl.
FT N-TER 1 10
FT BINDING 5 5 LIPOYL.
FT N-TER 10 10
SQ SEQUENCE 10 AA; 1066 MW; 889BE7D4A533AB1 (RC654);

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e-04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KA 11
QZ 5 KA 6

RESULT 47
PNEU_HUMAN STANDARD PRT 10 AA
AC P22103;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=91110910; PubMed=2274581;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RI "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: ANTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.

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DR PIR: B33143; B33143;
DR CO: G0:0030103; P.vasopressin secretion; NAS.
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e-04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
QZ 4 PK 5

RESULT 48
PNEU_RAT STANDARD PRT 10 AA
AC P21996;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNN).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID:10116;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RI "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.
DR PIR: A33143; A33143;
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e-04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
QZ 4 PK 5

RESULT 49
SPI_HAIRO STANDARD PRT 10 AA
AC G10947;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (Fragment).
OS Haicynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyrosoma; Haicynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE.
RX TISSUE=Hemolymph; PubMed=8759245;
RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
RI "Purification and characterization of a 58,000-Da proteinase
RI inhibitor from the hemolymph of a solitary ascidian, Haicynthia
RI roretzi.";
RL Comp. Biochem. Physiol. 114B:1-9(1996).
CC -!- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

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DR InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 4225C73B1B1R7AA; CR64;

Query Match 18.2%; Score 2; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1; 20-04;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KK 4
 II
 DB 2 KK 3

RESULT 50

TKNC_RANCA
 ID TKNC_RANCA STANDARD; PRI; 10 AA.
 AC P22690;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Rana tachykinin C (RTK C).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE: Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kagaawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:558-564(1991).
 RN [2]
 RP SEQUENCE
 RC TISSUE=Intestine;
 RX MEDLINE=94523216; PubMed=8212586;
 RA Kagaawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC !- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC !- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: C61033; C61033.
 DR InterPro: IPR002040; Tachykinin.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA: 1086 MW: 3A3A407C59D5BDC / CR64;

Query Match 18.2%; Score 2; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1; 20-04;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
 II
 DB 4 AS 5

Search completed: September 30, 2003, 10:25:56
 Job time : 20.25 secs

GenCore version 5.1.6
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OM protein - protein search, using SW method

Run on: September 30, 2003, 10:07:04 : Search time 31.6667 seconds
(without alignments)
89.639 Million cell updates/sec

Title: US-09-787-443-1

Perfect score: 11

Sequence: 1 ASKKPKRNIKA 11

Scoring table: OLICO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3459

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database :

- 1: SPTREMBL_23:*
- 2: sp_archaea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mammal:*
- 8: sp_mhc:*
- 9: sp_organella:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteria:*
- 17: sp_archaea:*

Errol, N. is the number of hits per 1000000 sequences based on a score greater than or equal to the given value. Results being printed, and is derived by analysis of the data score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	8	8	Q900W5 gossypium
2	4	36.4	9	4	Q90X14 homo sapien
3	4	36.4	10	12	Q900W9 gossypium
4	4	36.4	10	12	Q900W3 gossypium
5	4	36.4	10	12	Q900W1 gossypium
6	4	36.4	10	12	Q900W2 gossypium
7	4	36.4	10	12	Q900W4 gossypium
8	4	36.4	10	12	Q900W6 gossypium
9	4	36.4	10	12	Q900W7 gossypium
10	4	36.4	10	12	Q900W8 gossypium
11	4	36.4	10	12	Q900W9 gossypium
12	4	36.4	10	12	Q900W10 gossypium
13	4	36.4	10	12	Q900W11 gossypium
14	4	36.4	10	12	Q900W12 gossypium
15	4	36.4	10	12	Q900W13 gossypium
16	4	36.4	10	12	Q900W14 gossypium
17	4	36.4	10	12	Q900W15 gossypium

17	4	36.4	10	12	Q900W5
18	4	36.4	10	12	Q900X3
19	4	36.4	10	12	Q900X5
20	4	36.4	10	12	Q900M3
21	4	36.4	10	12	Q900X1
22	4	36.4	10	12	Q900X0
23	4	36.4	10	12	Q900X9
24	4	36.4	10	12	Q900X7
25	3	27.3	8	2	Q93S80
26	3	27.3	8	2	Q56759
27	3	27.3	8	2	Q521H9
28	3	27.3	8	8	Q19961
29	3	27.3	8	8	Q19958
30	3	27.3	8	8	Q19960
31	3	27.3	8	8	Q19959
32	3	27.3	8	8	Q19956
33	3	27.3	8	4	Q16605
34	3	27.3	9	4	Q900W0
35	3	27.3	9	8	Q902L0
36	3	27.3	9	8	Q902L1
37	3	27.3	9	12	Q71067
38	3	27.3	9	12	Q71068
39	3	27.3	10	2	Q9JN49
40	3	27.3	10	4	Q81Z42
41	3	27.3	10	8	Q8HUB4
42	3	27.3	10	10	Q8LPT7
43	3	27.3	10	13	Q73594
44	3	27.3	11	2	Q9S618
45	3	27.3	11	5	Q95PX6
46	3	27.3	11	5	Q25916
47	3	27.3	11	6	Q9TQ50
48	3	27.3	11	9	Q38415
49	3	27.3	11	10	Q04131
50	3	27.3	11	12	Q86866
51	3	27.3	11	12	Q86864
52	3	27.3	11	12	Q86868
53	3	27.3	12	2	Q8VLX8
54	3	27.3	12	4	Q9HBU4
55	3	27.3	12	5	Q61574
56	3	27.3	12	8	Q8MEM1
57	3	27.3	12	8	Q8HU93
58	3	27.3	12	10	Q8LPT6
59	3	27.3	12	10	Q8LPT3
60	3	27.3	13	2	Q9R3R6
61	3	27.3	13	6	Q9GJU2
62	3	27.3	13	11	Q8CIW3
63	3	27.3	13	13	Q83338
64	3	27.3	14	2	Q50268
65	3	27.3	14	3	Q8J1G2
66	3	27.3	14	4	Q16232
67	3	27.3	14	10	Q8LAP5
68	3	27.3	14	11	Q99PB8
69	3	27.3	14	11	Q8CFB6
70	3	27.3	14	12	Q8V3U6
71	3	27.3	14	16	Q9KE26
72	3	27.3	15	2	Q9R546
73	3	27.3	15	2	Q9ZF32
74	3	27.3	15	2	Q9R4T2
75	3	27.3	15	4	Q81ZK4
76	3	27.3	15	6	Q83444
77	3	27.3	15	8	Q9TQ22
78	3	27.3	15	8	Q78794
79	2	18.2	8	2	Q9AGP4
80	2	18.2	8	2	Q8KJ10
81	2	18.2	8	2	Q44463
82	2	18.2	8	2	Q77556
83	2	18.2	8	2	Q6R8R3
84	2	18.2	8	2	Q87471
85	2	18.2	8	2	Q56429
86	2	18.2	8	2	Q9R9E0
87	2	18.2	8	2	Q9R5R0
88	2	18.2	8	2	Q8G940
89	2	18.2	8	4	Q158H9

Q90W5	polyomaviru
Q90X3	polyomaviru
Q90X5	polyomaviru
Q90W3	polyomaviru
Q8J80	polyomaviru
Q90X1	polyomaviru
Q90X9	polyomaviru
Q8J72	polyomaviru
Q53R0	staphylococ
Q56759	xanthobacte
Q521H9	neisseria m
Q19961	gossypium d
Q19958	gossypium b
Q19960	gossypium m
Q19959	gossypium t
Q19956	gossypium a
Q16605	homo sapien
Q90W0	homo sapien
Q902L0	spinacia ol
Q902L1	spinacia ol
Q71067	canine dist
Q71068	canine dist
Q9JN49	staphylococ
Q81Z42	homo sapien
Q8HUB4	anomobryum
Q8LPT7	zea mays (m
Q73594	gallus gall
Q9S618	prochloroco
Q95PX6	caenorhabdi
Q25916	plasmodium
Q9TQ50	bos taurus
Q38415	bacterioph
Q04131	lycopersico
Q86866	lymphocytic
Q86864	lymphocytic
Q86868	lymphocytic
Q8VLX8	thermus the
Q9HBU4	homo sapien
Q61574	ostertagia
Q8MEM1	maiva negle
Q8HU93	bryum donia
Q8LPT6	zea mays (m
Q8LPT3	pisum sativ
Q9R3R6	prochloroco
Q9GJU2	ovis aries
Q8CIW3	mus musculus
Q83338	oncorhynch
Q50268	phytoplasm
Q8J1G2	ashbya goss
Q16232	homo sapien
Q8LAP5	zea mays (m
Q99PB8	mus musculus
Q8CFB6	mus musculus
Q8V3U6	tomato yell
Q9KE26	bacillus ha
Q9R546	mycobacteri
Q9ZF32	saimonella
Q9R4T2	bacillus in
Q81ZK4	homo sapien
Q83444	ovis aries
Q9TQ22	chlamydomon
Q78794	pylalella 1
Q9AGP4	arthrobacte
Q8KJ10	streptomyce
Q44463	rhizobiales
Q77556	escherichia
Q87471	lactobacilli
Q56429	haemophilus
Q9R9E0	thermus the
Q9R5R0	bacillus su
Q8G940	shigella dy
Q158H9	borrelia bu
Q158H9	homo sapien

90	2	18.2	8	4	Q15900	Q15900 homo sapien	163	2	18.2	8	9	Q8H9H6	Q8H9H6 bacterioph
91	2	18.2	8	4	Q9JHK1	Q9JHK1 homo sapien	164	2	18.2	8	9	Q8H9H5	Q8H9H5 bacterioph
92	2	18.2	8	4	Q15888	Q15888 homo sapien	165	2	18.2	8	9	Q8H9H3	Q8H9H3 bacterioph
93	2	18.2	8	4	Q9J350	Q9J350 homo sapien	166	2	18.2	8	10	Q42507	Q42507 triticum ae
94	2	18.2	8	4	Q16468	Q16468 homo sapien	167	2	18.2	8	10	Q8G135	Q8G135 lycopersico
95	2	18.2	8	4	Q9JCN4	Q9JCN4 homo sapien	168	2	18.2	8	11	Q99N10	Q99N10 pedetes cap
96	2	18.2	8	4	Q9J285	Q9J285 homo sapien	169	2	18.2	8	11	Q99NT1	Q99NT1 castor cana
97	2	18.2	8	4	Q8JVK3	Q8JVK3 homo sapien	170	2	18.2	8	11	Q99NS6	Q99NS6 erethizon d
98	2	18.2	8	5	Q9K6M5	Q9K6M5 toxif-asma	171	2	18.2	8	11	Q99NS8	Q99NS8 rattus norv
99	2	18.2	8	5	Q8Z686	Q8Z686 perit-asma	172	2	18.2	8	11	Q99NS5	Q99NS5 dipodomys h
100	2	18.2	8	6	Q9HFA7	Q9HFA7 macroscellid	173	2	18.2	8	11	Q99NS2	Q99NS2 myocastor c
101	2	18.2	8	6	Q9HFB4	Q9HFB4 ursus arcto	174	2	18.2	8	11	Q99NS3	Q99NS3 hydrochoeru
102	2	18.2	8	6	Q9HFC2	Q9HFC2 macrofys en	175	2	18.2	8	11	Q99NT2	Q99NT2 tamias stri
103	2	18.2	8	6	Q9HFC0	Q9HFC0 tiagetaphus	176	2	18.2	8	11	Q99ND2	Q99ND2 mus musculu
104	2	18.2	8	6	Q9HFX8	Q9HFX8 bos tauru	177	2	18.2	8	11	Q99NS1	Q99NS1 dinomys bra
105	2	18.2	8	6	Q9HFR1	Q9HFR1 echinops te	178	2	18.2	8	11	Q9K1U6	Q9K1U6 mus musculu
106	2	18.2	8	6	Q18854	Q18854 canis fami-	179	2	18.2	8	11	Q99NS7	Q99NS7 cricetus
107	2	18.2	8	6	Q9HFA7	Q9HFA7 aelurus tusc	180	2	18.2	8	11	Q99NS0	Q99NS0 agouti taex
108	2	18.2	8	6	Q9HFB7	Q9HFB7 lepus lad	181	2	18.2	8	11	Q99NS9	Q99NS9 mus musculu
109	2	18.2	8	6	Q9HFB9	Q9HFB9 euphractus	182	2	18.2	8	11	Q99NS4	Q99NS4 cavia tschu
110	2	18.2	8	6	Q9HFB8	Q9HFB8 chaetophrac	183	2	18.2	8	11	Q62528	Q62528 mus spretus
111	2	18.2	8	6	Q9HFA8	Q9HFA8 toxodonta a	184	2	18.2	8	12	Q63977	Q63977 influenzavi
112	2	18.2	8	6	Q9HFX1	Q9HFX1 canis fami	185	2	18.2	8	12	Q84271	Q84271 human papill
113	2	18.2	8	6	Q9HFA9	Q9HFA9 procavia ca	186	2	18.2	8	12	Q84273	Q84273 human papill
114	2	18.2	8	6	Q9HFB2	Q9HFB2 sorex arane	187	2	18.2	8	13	Q902V5	Q902V5 fulica leuc
115	2	18.2	8	6	Q9HFB5	Q9HFB5 erinaceus e	188	2	18.2	8	13	Q8JFN8	Q8JFN8 gallus gall
116	2	18.2	8	6	Q9HFB6	Q9HFB6 myrmecophag	189	2	18.2	9	2	Q9K3T0	Q9K3T0 borrelia af
117	2	18.2	8	6	Q9HFB3	Q9HFB3 condylura c	190	2	18.2	9	2	Q9E214	Q9E214 sodalis glo
118	2	18.2	8	6	Q9HFB4	Q9HFB4 equus cabal	191	2	18.2	9	2	Q9E5R1	Q9E5R1 shigella dy
119	2	18.2	8	6	Q9HFB5	Q9HFB5 reusettus l	192	2	18.2	9	2	Q45852	Q45852 clostridium
120	2	18.2	8	6	Q9HFB4	Q9HFB4 panthera on	193	2	18.2	9	2	Q9JN16	Q9JN16 streptococ
121	2	18.2	8	6	Q9HFB3	Q9HFB3 adelphis m	194	2	18.2	9	2	Q31363	Q31363 borrelia ga
122	2	18.2	8	6	Q9HFA4	Q9HFA4 tupia aiuro	195	2	18.2	9	2	Q51349	Q51349 pseudomonas
123	2	18.2	8	6	Q9HFA2	Q9HFA2 tarsius bat	196	2	18.2	9	2	Q9K735	Q9K735 sireptomyc
124	2	18.2	8	6	Q9HFA2	Q9HFA2 tarsius p	197	2	18.2	9	2	Q9K792	Q9K792 borrelia bu
125	2	18.2	8	6	Q9HFB1	Q9HFB1 leopoldus p	198	2	18.2	9	2	Q30790	Q30790 erwinia amy
126	2	18.2	8	6	Q9HFB4	Q9HFB4 oxapia ichu	199	2	18.2	9	2	Q9K4M6	Q9K4M6 streptococ
127	2	18.2	8	6	Q9HFB6	Q9HFB6 pteropus gi	200	2	18.2	9	2	Q93E20	Q93E20 streptococ
128	2	18.2	8	6	Q9HFB7	Q9HFB7 trichechus	201	2	18.2	9	2	Q9K9C4	Q9K9C4 borrelia bu
129	2	18.2	8	6	Q9HFB5	Q9HFB5 felis silve	202	2	18.2	9	2	Q8GL26	Q8GL26 borrelia bu
130	2	18.2	8	6	Q9HFB2	Q9HFB2 tarsius tr	203	2	18.2	9	3	Q9UR18	Q9UR18 sclerotium
131	2	18.2	8	6	Q9HFB7	Q9HFB7 tamandua te	204	2	18.2	9	4	Q16276	Q16276 homo sapien
132	2	18.2	8	6	Q9HFB1	Q9HFB1 hippopotam	205	2	18.2	9	4	Q2BQQ2	Q2BQQ2 homo sapien
133	2	18.2	8	6	Q9HFB4	Q9HFB4 taipia alta	206	2	18.2	9	4	Q9H4B1	Q9H4B1 homo sapien
134	2	18.2	8	6	Q9HFC0	Q9HFC0 choloepus d	207	2	18.2	9	4	Q15896	Q15896 homo sapien
135	2	18.2	8	6	Q9HFA8	Q9HFA8 callimico a	208	2	18.2	9	4	Q9H326	Q9H326 homo sapien
136	2	18.2	8	6	Q9HFA4	Q9HFA4 lemur catia	209	2	18.2	9	4	Q9UMA0	Q9UMA0 homo sapien
137	2	18.2	8	6	Q9HFA7	Q9HFA7 oryctolopus	210	2	18.2	9	4	Q9UCN5	Q9UCN5 homo sapien
138	2	18.2	8	6	Q9HFA7	Q9HFA7 canis fami	211	2	18.2	9	5	Q28112	Q28112 bos taurus
139	2	18.2	8	6	Q9HFA7	Q9HFA7 ailurus ta	212	2	18.2	9	5	Q9TUY0	Q9TUY0 monodelphis
140	2	18.2	8	6	Q9HFA7	Q9HFA7 cynocephala u	213	2	18.2	9	6	Q9T777	Q9T777 bos taurus
141	2	18.2	8	6	Q9HFA7	Q9HFA7 cynocephala th	214	2	18.2	9	6	Q95DS5	Q95DS5 magnolia sa
142	2	18.2	9	8	Q9H9H8	Q9H9H8 nicotiana gl	215	2	18.2	9	8	Q95DS0	Q95DS0 magnolia tr
143	2	18.2	8	8	Q8H9J7	Q8H9J7 lewis hirta	216	2	18.2	9	8	Q9TNF0	Q9TNF0 magnolia tr
144	2	18.2	8	8	Q94PX6	Q94PX6 felis silve	217	2	18.2	9	8	Q8HEM3	Q8HEM3 howittia tr
145	2	18.2	8	8	Q34909	Q34909 locusta mig	218	2	18.2	9	8	Q95DS1	Q95DS1 manglietia
146	2	18.2	8	8	Q94PX7	Q94PX7 felis silve	219	2	18.2	9	8	Q9TNE9	Q9TNE9 magnolia co
147	2	18.2	8	8	Q94PX6	Q94PX6 felis libyc	220	2	18.2	9	8	Q9TNF4	Q9TNF4 magnolia sc
148	2	18.2	8	9	Q37854	Q37854 bacterioph	221	2	18.2	9	8	Q9THL7	Q9THL7 magnolia si
149	2	18.2	8	9	Q8SBJ3	Q8SBJ3 bacterioph	222	2	18.2	9	8	Q9TNE0	Q9TNE0 michelia co
150	2	18.2	8	9	Q8H9K4	Q8H9K4 bacterioph	223	2	18.2	9	8	Q9TND8	Q9TND8 liriodendro
151	2	18.2	8	9	Q8H9K1	Q8H9K1 bacterioph	224	2	18.2	9	8	Q95GN1	Q95GN1 pelargonium
152	2	18.2	8	9	Q8H9J5	Q8H9J5 bacterioph	225	2	18.2	9	8	Q9TNE4	Q9TNE4 magnolia sa
153	2	18.2	8	9	Q8H9J7	Q8H9J7 bacterioph	226	2	18.2	9	8	Q95DS6	Q95DS6 magnolia w
154	2	18.2	8	9	Q8H9J5	Q8H9J5 bacterioph	227	2	18.2	9	8	Q9TNF6	Q9TNF6 magnolia gr
155	2	18.2	8	9	Q8H9J3	Q8H9J3 bacterioph	228	2	18.2	9	8	Q9THL5	Q9THL5 magnolia li
156	2	18.2	8	9	Q8H9J1	Q8H9J1 bacterioph	229	2	18.2	9	8	Q9TNF1	Q9TNF1 magnolia he
157	2	18.2	8	9	Q8H9I9	Q8H9I9 bacterioph	230	2	18.2	9	8	Q95DT3	Q95DT3 magnolia il
158	2	18.2	8	9	Q8H9I8	Q8H9I8 bacterioph	231	2	18.2	9	8	Q9THM0	Q9THM0 magnolia fr
159	2	18.2	8	9	Q8H9I6	Q8H9I6 bacterioph	232	2	18.2	9	8	Q95DS2	Q95DS2 magnolia ov
160	2	18.2	8	9	Q8H9I4	Q8H9I4 bacterioph	233	2	18.2	9	8	Q9T3P4	Q9T3P4 magnolia ma
161	2	18.2	8	9	Q8H9I3	Q8H9I3 bacterioph	234	2	18.2	9	9	Q9TND7	Q9TND7 liriodendro
162	2	18.2	8	9	Q8H9I2	Q8H9I2 bacterioph	235	2	18.2	9	9	Q9THL8	Q9THL8 magnolia of

382	2	18.2	11	8	Q8ME62	Q8me62 porphyra ca	455	2	18.2	12	7	077877	077877 oreochromis
383	2	18.2	11	8	Q8ME17	Q8me17 sida hooker	456	2	18.2	12	7	077882	077882 oreochromis
384	2	18.2	11	8	Q8C5Y0	Q8c5y0 pseudotrache	457	2	18.2	12	8	Q8SER7	Q8seb7 grateloupia
385	2	18.2	11	8	Q8HEM2	Q8hem2 lagunaria p	458	2	18.2	12	8	Q8MEP4	Q8meP4 hibiscus ni
386	2	18.2	11	8	Q8MES5	Q8mes5 abelmoschus	459	2	18.2	12	8	Q8MES0	Q8mes0 anoda crist
387	2	18.2	11	8	Q8MEP0	Q8nep0 hibiscus fe	460	2	18.2	12	8	Q8MEQ6	Q8meq6 hibiscus en
388	2	18.2	11	8	Q8MEF8	Q8mer8 dombeya til	461	2	18.2	12	8	Q8MEM5	Q8men5 hibiscus wa
389	2	18.2	11	8	Q82704	Q82704 nicotiana t	462	2	18.2	12	8	Q8MEN4	Q8men4 hibiscus sc
390	2	18.2	11	8	Q8MES1	Q8mes1 alyogyne pi	463	2	18.2	12	8	Q8MER4	Q8mer4 gossypium s
391	2	18.2	11	8	Q8MEP3	Q8nep3 hibiscus no	464	2	18.2	12	8	Q8MEQ1	Q8meq1 hibiscus in
392	2	18.2	11	8	Q8MEQ7	Q8meq7 hibiscus dr	465	2	18.2	12	8	Q8MES6	Q8mes6 abelmoschus
393	2	18.2	11	8	Q8ME13	Q8me13 pavienia has	466	2	18.2	12	8	Q8MEQ8	Q8meq8 hibiscus do
394	2	18.2	11	8	Q8MEF0	Q8mer0 hibiscus co	467	2	18.2	12	8	Q8MES2	Q8mes2 alyogyne hu
395	2	18.2	11	8	Q8MES3	Q8mes3 alyogyne cr	468	2	18.2	12	8	Q8MEP7	Q8meP7 hibiscus me
396	2	18.2	11	8	Q8MEP5	Q8nep5 hibiscus mi	469	2	18.2	12	8	Q8MEN5	Q8men5 hibiscus sa
397	2	18.2	11	8	Q8MER1	Q8mer1 hibiscus ca	470	2	18.2	12	8	Q8MER9	Q8mer9 decaschisti
398	2	18.2	11	8	Q8SKP8	Q8skp8 ctenophorus	471	2	18.2	12	8	Q8MEM6	Q8mem6 hibiscus tr
399	2	18.2	11	8	Q8MER7	Q8mer7 tiaria viti	472	2	18.2	12	8	Q8MEP1	Q8meP1 hibiscus pe
400	2	18.2	11	8	Q8HQX5	Q8hqx5 rhabdohamn	473	2	18.2	12	8	Q8MEQ4	Q8meq4 hibiscus fr
401	2	18.2	11	9	Q37925	Q37925 bacterioph	474	2	18.2	12	8	Q8MEQ0	Q8meq0 hibiscus lu
402	2	18.2	11	10	Q06626	Q06626 solanum tub	475	2	18.2	12	8	Q8MEM0	Q8mem0 malvaviscus
403	2	18.2	11	10	Q65901	Q65901 leavenworth	476	2	18.2	12	8	Q8MEP2	Q8nep2 hibiscus pe
404	2	18.2	11	10	Q8RV30	Q8rv30 zea mays (m	477	2	18.2	12	8	Q8MEQ2	Q8meq2 hibiscus he
405	2	18.2	11	10	Q8RDE7	Q8rue7 zea mays (m	478	2	19.2	12	8	Q8MER3	Q8mer3 hibiscus br
406	2	18.2	11	10	P82436	P82436 nicotiana t	479	2	18.2	12	8	Q8MEL6	Q8mel6 thespesia t
407	2	18.2	11	10	P82336	P82336 pisum sativ	480	2	18.2	12	8	Q8MER2	Q8mer2 hibiscus bu
408	2	18.2	11	11	Q9QXN6	Q9qxn6 mus musculu	481	2	18.2	12	8	Q8MEF7	Q8meF7 hibiscus tl
409	2	18.2	11	11	Q9QXN1	Q9qn1 mus musculu	482	2	18.2	12	8	Q9MS50	Q9ms50 brassica na
410	2	18.2	11	11	Q9JLE6	Q9jle6 rattus norv	483	2	18.2	12	8	Q8MEP8	Q8nep8 hibiscus ma
411	2	18.2	11	11	Q8R207	Q8r217 mesocricetu	484	2	18.2	12	8	Q8MEM9	Q8mem9 hibiscus su
412	2	18.2	11	11	Q9QXN6	Q9qxn6 mus musculu	485	2	18.2	12	8	Q31851	Q31851 arabidopsis
413	2	18.2	11	12	P89263	P89269 xestia c-ni	486	2	18.2	12	8	Q8MEN8	Q8men8 hibiscus ra
414	2	18.2	11	12	Q99701	Q99701 east africa	487	2	18.2	12	8	Q8MEP6	Q8meP6 hibiscus me
415	2	18.2	11	12	Q69264	Q69269 equine herp	488	2	18.2	12	8	Q8SEB8	Q8seb8 grateloupia
416	2	18.2	11	12	Q86565	Q86565 var cella-2	489	2	18.2	12	8	Q8LU67	Q8lu67 macrostelia
417	2	18.2	11	13	Q8AXF4	Q8axf9 oreochromis	490	2	18.2	12	8	Q8MEP9	Q8nep9 hibiscus ma
418	2	18.2	11	13	Q8AXF6	Q8axf6 oreochromis	491	2	18.2	12	8	Q8MEQ9	Q8meq9 hibiscus di
419	2	18.2	11	15	Q85620	Q85620 moloney mur	492	2	18.2	12	8	Q8SEB9	Q8seb9 grateloupia
420	2	18.2	12	2	Q50959	Q50959 neissoria q	493	2	18.2	12	8	Q03816	Q03816 metasequoia
421	2	18.2	12	2	Q50342	Q50342 mycoplasma	494	2	18.2	12	8	Q6S142	Q6s142 aeonium sim
422	2	18.2	12	2	Q93205	Q93208 acinetobact	495	2	18.2	12	8	Q8MEM8	Q8mem8 hibiscus sy
423	2	18.2	12	2	Q9K5F7	Q95517 helicobacte	496	2	18.2	12	8	Q8MEN0	Q8men0 hibiscus sa
424	2	18.2	12	2	Q9K5F7	Q95515 helicobacte	497	2	18.2	12	8	Q8MEN6	Q8men6 hibiscus sa
425	2	18.2	12	2	Q54579	Q54579 rhodobacter	498	2	18.2	12	8	Q03815	Q03815 abies alba
426	2	18.2	12	2	Q50303	Q50303 bacillus st	499	2	18.2	12	8	Q8MEQ3	Q8meq3 hibiscus fu
427	2	18.2	12	2	P97144	P97144 rhizobium i	500	2	18.2	12	8	Q8MEN1	Q8men1 hibiscus st
428	2	18.2	12	2	Q9K5R4	Q93364 helicobacte							
429	2	18.2	12	2	Q9K5R4	Q93364 helicobacte							
430	2	18.2	12	2	Q52112	Q52112 acinetobact							
431	2	18.2	12	2	Q858V1	Q85m1 acinetobact							
432	2	18.2	12	2	Q858V1	Q85m1 acinetobact							
433	2	18.2	12	2	Q858V1	Q85m1 acinetobact							
434	2	18.2	12	3	Q858V1	Q85m1 acinetobact							
435	2	18.2	12	4	Q9QMK0	Q8146 asibya goss							
436	2	18.2	12	4	Q9QMK0	Q9umr0 homo sapien							
437	2	18.2	12	4	Q9QC17	Q9uq1 homo sapien							
438	2	18.2	12	4	Q16452	Q16452 homo sapien							
439	2	18.2	12	4	Q9QMK0	Q9umg9 homo sapien							
440	2	18.2	12	4	Q16405	Q16405 homo sapien							
441	2	18.2	12	4	Q9QMK0	Q9epk0 homo sapien							
442	2	18.2	12	4	Q9QMK0	Q9umz0 homo sapien							
443	2	18.2	12	5	Q8MY01	Q8my01 drosophila							
444	2	18.2	12	5	Q8T0Y4	Q8t0y6 apis mellif							
445	2	18.2	12	6	Q91QW3	Q91qW3 bos taurus							
446	2	18.2	12	6	Q9XS31	Q9xs31 sus scrofa							
447	2	18.2	12	6	Q8WNR9	Q8wnr9 ovis aries							
448	2	18.2	12	6	Q9TRT8	Q9trt8 bos taurus							
449	2	18.2	12	6	Q9M2S4	Q9m2s4 canis famil							
450	2	18.2	12	6	P83127	P83127 bos indicus							
451	2	18.2	12	7	Q77878	Q77878 oreochromis							
452	2	18.2	12	7	Q77879	Q77879 oreochromis							
453	2	18.2	12	7	Q77881	Q77881 oreochromis							
454	2	18.2	12	7	Q77909	Q77904 oreochromis							

ALIGNMENTS

RESULT 1

019957
 ID 019957 PRELIMINARY: PRT: 8 AA.
 AC 019957;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ribosomal protein L16 (Fragment).
 GN RPL16.
 OS Gossypium hirsutum (Upland cotton).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 OX NCBI_taxid-3635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
 RI "the tortoise and the hare: choosing between noncoding plastome and
 RI nuclear adh sequences for phylogeny reconstruction in a recently
 RI diverged plant group";
 RL Am. J. Bot. 85:1301-1315(1998).

```

EMBL: AF031452; AAC63546.1;
KW Chloroplast. 1 1
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA: 971 MW: 718587340454.527 CRC64:

Query Match 36.4% Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8;e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKRN 8
    ||||
Db 1 PKRN 4

RESULT 2
Q9BX14
ID Q9BX14 PRELIMINARY: PRI: 9 AA.
AC Q9BX14 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE BA254M3.1 (Novel protein) (Fragment).
GN DJ09425.1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Milne S.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL353599; CAC34530.1;
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA: 1009 MW: 691801890.132563 CRC64:

Query Match 36.4% Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8;e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASKK 4
    ||||
Db 2 ASKK 5

RESULT 3
Q9Q0W1
ID Q9Q0W1 PRELIMINARY: PRI: 10 AA.
AC Q9Q0W1 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=DMFA3;
RC MEDLINE=20087544; PubMed=10618230;
RA Hofilli-Mas S.; Pina S.; Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119350; AAF24106.1;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64:

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7;e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKPK 6
    ||||
Db 2 KKPK 5

RESULT 4
Q8JV70
ID Q8JV70 PRELIMINARY: PRI: 10 AA.
AC Q8JV70 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21465052; PubMed=11581397;
RA Hofilli-Mas S.; Formiga-Cruz M.; Clemente-Casares P.; Calafell P.;
RT "Potential transmission of human polyomaviruses through the
RT gas:rointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL; AF304387; AAM97804.1;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64:

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7;e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKPK 6
    ||||
Db 2 KKPK 5

RESULT 5
Q9Q0W1
ID Q9Q0W1 PRELIMINARY: PRI: 10 AA.
AC Q9Q0W1 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CSFB;
RC MEDLINE=20087544; PubMed=10618230;
RA Hofilli-Mas S.; Pina S.; Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119354; AAF24114.1;
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64:

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7;e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKPK 6
    ||||
Db 2 KKPK 5

RESULT 6
Q8JV68
ID Q8JV68 PRELIMINARY: PRI: 10 AA.
AC Q8JV68;

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-USA 6;
RX MEDLINE-21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT *Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.*;
RL J. Virol. 75:10290-10299(2001);
DR EMBL; AF304388; AAM97806.1;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 7
Q9Q0W7 PRELIMINARY; PRT; 10 AA.
ID Q9Q0W7
AC Q9Q0W7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CSFE;
RX MEDLINE-2087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT *Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.*;
RL Appl. Environ. Microbiol. 66:238-245(2000);
DR EMBL; AF119355; AAF24116.1;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 8
Q8JV84 PRELIMINARY; PRT; 10 AA.
ID Q8JV84
AC Q8JV84
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CSF K;
RX MEDLINE-21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT *Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.*;
RL J. Virol. 75:10290-10299(2001);

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RP SEQUENCE FROM N.A.
RC STRAIN-G1;
RX MEDLINE-21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT *Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.*;
RL J. Virol. 75:10290-10299(2001);
DR EMBL; AF303943; AAM97790.1;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1180 MW; 4CD6A97771A32763 CRC64;

Query Match 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 9
Q9Q0W7 PRELIMINARY; PRT; 10 AA.
ID Q9Q0W7
AC Q9Q0W7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NANCY2;
RX MEDLINE-2087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT *Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.*;
RL Appl. Environ. Microbiol. 66:238-245(2000);
DR EMBL; AF119351; AAF24108.1;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 10
Q8JV66 PRELIMINARY; PRT; 10 AA.
ID Q8JV66
AC Q8JV66
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CSF K;
RX MEDLINE-21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT *Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.*;
RL J. Virol. 75:10290-10299(2001);

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DR EMBL: AF194389; AAM97808.1; -
 FT NON_TER 1
 SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match 36.4%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKPK 6
 IIII
 DB 2 KKPK 5

RESULT 11

Q9QGV7 PRELIMINARY: PRI: 10 AA;
 AC Q9QGV7
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DI 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 CX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SFJ;
 RX MEDLINE=20087544; PubMed=19618239;
 RA Rofill-Mas S., Pina S., Girones R.;
 RT "documenting the epidemiologic patterns of polyomaviruses in human
 populations by studying their presence in urban sewage";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL: AF194389; AAF24118.1;
 FT NON_TER 1
 SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match 36.4%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKPK 6
 IIII
 DB 2 KKPK 5

RESULT 12

Q8JV82 PRELIMINARY: PRI: 10 AA;
 AC Q8JV82
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DI 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 CX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FI;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Rofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 gastrointestinal tract after exposure to virions of viral DNA";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL: AF303944; AAM97792.1;
 FT NON_TER 1
 SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match 36.4%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKPK 6
 IIII
 DB 2 KKPK 5

RESULT 13

Q8JV76 PRELIMINARY: PRI: 10 AA;
 AC Q8JV76
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DI 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 CX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USA2;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Rofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 gastrointestinal tract after exposure to virions of viral DNA";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL: AF303944; AAM97798.1;
 FT NON_TER 1
 SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;
 Query Match 36.4%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKPK 6
 IIII
 DB 2 KKPK 5

RESULT 14

Q8JV74 PRELIMINARY: PRI: 10 AA;
 AC Q8JV74
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DI 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 CX NCBI_TaxID=10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USA3;
 RX MEDLINE=21465052; PubMed=11581397;
 RA Rofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 gastrointestinal tract after exposure to virions of viral DNA";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL: AF303946; AAM97800.1;
 FT NON_TER 1
 SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;
 Query Match 36.4%; Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKPK 6
 IIII
 DB 2 KKPK 5

RESULT 15

Q9QGX7

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IQ Q90X7 PRELIMINARY: PRI: 10 AA
AC Q90X7
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment)
OS Polyomavirus JC
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus
OX NCBI_TaxID:10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCN2;
RX MEDLINE-20087544; PubMed-10618230;
RA Botill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RI Appl. Environ. Microbiol. 66:238-245(2000).
RL EMBL: AF119146; AAF24398.1;
DR EMBL: AF119146; AAF24398.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1180 MW: 4036447771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 16
IQ Q90X7 PRELIMINARY: PRI: 10 AA
AC Q90X7
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment)
OS Polyomavirus JC
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus
OX NCBI_TaxID:10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCN2;
RX MEDLINE-20087544; PubMed-10618230;
RA Botill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RI Appl. Environ. Microbiol. 66:238-245(2000).
RL EMBL: AF119146; AAF24102.1;
DR EMBL: AF119146; AAF24102.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4036497771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 19
IQ Q90X5 PRELIMINARY: PRI: 10 AA
AC Q90X5
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment)
OS Polyomavirus JC
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus
OX NCBI_TaxID:10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCN16;
RX MEDLINE-20087544; PubMed-10618230;
RA Botill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RI Appl. Environ. Microbiol. 66:238-245(2000).
RL EMBL: AF119146; AAF24102.1;
DR EMBL: AF119146; AAF24102.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4036497771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 17
IQ Q90W5 PRELIMINARY: PRI: 10 AA
AC Q90W5
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment)
OS Polyomavirus JC
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus
OX NCBI_TaxID:10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCN2;
RX MEDLINE-20087544; PubMed-10618230;
RA Botill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.";
RI Appl. Environ. Microbiol. 66:238-245(2000).
RL EMBL: AF119146; AAF24398.1;
DR EMBL: AF119146; AAF24398.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1180 MW: 4036447771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

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DR EMBL: AF119347; AAF24100.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match: 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
   III
Db 2 KKPK 5

RESULT 20
Q900W3 ID Q900W3 PRELIMINARY; PRT: 10 AA.
AC Q900W3:
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRETORIAL;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119345; AAF24112.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match: 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
   III
Db 2 KKPK 5

RESULT 21
Q8JV80 ID Q8JV80 PRELIMINARY; PRT: 10 AA.
AC Q8JV80:
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F2;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente Casares F., Catalaell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
   gastrointestinal tract after exposure to viruses of viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL: AF303945; AAM97794.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match: 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
   III
Db 2 KKPK 5

RESULT 22
Q900X1 ID Q900X1 PRELIMINARY; PRT: 10 AA.
AC Q900X1:
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN15;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119349; AAF24104.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match: 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
   III
Db 2 KKPK 5

RESULT 23
Q900X9 ID Q900X9 PRELIMINARY; PRT: 10 AA.
AC Q900X9:
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCND;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119345; AAF24096.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match: 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
   III
Db 2 KKPK 5

RESULT 24
Q8JV72 ID Q8JV72 PRELIMINARY; PRT: 10 AA.
AC Q8JV72:

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 CC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 OX NCBI_TaxID:10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-USA 4;
 RX MEDLINE-21465052; PubMed:11581397;
 RA Botill-Mas S., Formiga-Cruz M., Clemente Casares P., Salazar P.,
 RA Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 RT gastrointestinal tract after exposure to virions of viral DNA";
 RL J. Virol. 75:10290-10299(2001);
 DR EMBL: AF304386; AAM97802.1;
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1167 MW; 4CUGAG777AA2763 CR64;

 Query Match 36.4%; Score 4; DB 12; Length 10;
 Best local Similarity 100.0%; Pred. No. 8.3e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 KKKK 6
 Db 2 KKKK 5

 RESULT 25
 Q93SR0
 ID Q93SR0 PRELIMINARY; PRT; 8 AA.
 AC Q93SR0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Beta-lactamase repressor Bial (Fragment).
 GN BIAL.
 OS Staphylococcus epidermidis.
 CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID:1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-6;
 RA Sidhu M.S., Heir E., Sorum H., Holck A.L.;
 RT "Genetic linkage between quaternary ammonium compound and beta-lactam
 RT resistance in Staphylococcus isolated from food";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY028779; AAK38454.1;
 KW Plasmid.
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 930 MW; 4E442580AA4424 CR64;

 Query Match 27.3%; Score 3; DB 2; Length 8;
 Best local Similarity 100.0%; Pred. No. 8.3e-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 SKK 4
 Db 6 SKK 8

 RESULT 26
 Q56759
 ID Q56759 PRELIMINARY; PRT; 8 AA.
 AC Q56759;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE Haloacid dehalogenase (Fragment).
 GN DHB.
 OS Xanthobacter autotrophicus.

OX Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OX Rhodnomicrobacteraceae; Xanthobacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GJ10, and CV. K50;
 RX MEDLINE-95171113; PubMed:7868610;
 RA Van der Ploeg J., Willemson M., van Hall G., Janssen D.B.;
 RT "Adaptation of Xanthobacter autotrophicus GJ10 to bromoacetate due to
 RT activation and mobilization of the haloacetate dehalogenase gene by
 RT insertion element IS1247";
 RL J. Bacteriol. 177:1348-1356(1995).
 DR EMBL: X84038; CAA58857.1;
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 922 MW; F3A9D2DCDD33056 CR64;

 Query Match 27.4%; Score 3; DB 2; Length 8;
 Best local Similarity 100.0%; Pred. No. 8.3e-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 9 IKA 11
 Db 2 IKA 4

 RESULT 27
 Q921E9
 ID Q921E9 PRELIMINARY; PRT; 8 AA.
 AC Q921E9;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DE Carbamoyl-phosphate synthase subunit B (Fragment).
 GN CARB.
 OS Neisseria meningitidis.
 CC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OX Neisseriaceae; Neisseria.
 OX NCBI_TaxID:487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1527;
 RX MEDLINE-95291461; PubMed:7773412;
 RA Lawson F.S., Billowes F.M., Dillon J.A.;
 RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
 RT gonorrhoeae includes a large, variable intergenic sequence which is
 RT also present in other Neisseria species";
 RL Microbiology 141:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1527;
 RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
 RT "Complexity of the variable sequence between the carbamoyl-phosphate
 RT synthase genes of Neisseria species";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF029361; AAC78449.1;
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 988 MW; FA372AB1B4032766 CR64;

 Query Match 27.3%; Score 3; DB 2; Length 8;
 Best local Similarity 100.0%; Pred. No. 8.3e-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 PKR 7
 Db 2 PKR 4

 RESULT 28
 O19961
 ID O19961 PRELIMINARY; PRT; 8 AA.
 AC O19961;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein L16 (Fragment).
GN RPL16.
OS Gossypium darwini (Darwin's cotton).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34276;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.:
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL: AF031456; AAC63549.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 958 MW; 71B5B73411B40327 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 1 PKR 3

RESULT 29
OL19958
ID OL19958 PRELIMINARY: PRT: 8 AA.
DT 01 JAN-1998 (TrEMBLrel. 05, Created)
DT 01 JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01 DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein L16 (Fragment).
GN RPL16.
OS Gossypium barbadense (Sea-island cotton) (Egyptian cotton).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3634;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.:
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL: AF031453; AAC63547.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 958 MW; 71B5B73411B40327 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 1 PKR 3

RESULT 30
OL19960
ID OL19960 PRELIMINARY: PRT: 8 AA.
DT 01 JAN-1998 (TrEMBLrel. 05, Created)
DT 01 JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01 DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein L16 (Fragment).
GN RPL16.
OS Gossypium mustelinum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34275;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.:
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL: AF031455; AAC63549.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 958 MW; 71B5B73411B40327 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 1 PKR 3

RESULT 32
OL19956
ID OL19956 PRELIMINARY: PRT: 8 AA.
AC OL19956;
DT 01 JAN-1998 (TrEMBLrel. 05, Created)

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01 JAN 1998 (TrEMBLrel. 05, Created)
01 JAN 1998 (TrEMBLrel. 05, Last sequence update)
01 MAR 2002 (TrEMBLrel. 20, Last annotation update)
Ribosomal protein L16 (Fragment)
GN RPL16.
OS Gossypium arboreum (Tree cotton).
OC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
CC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
GX NCBI_taxid:29723;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Hyburn J.A., Cronin K.G., Swickard L., Wendel J.F.,
RT "The tortoise and the hare: choosing between recombining plasmids and
RT nuclear AAT sequences for phylogeny reconstruction in a recently
RT diverged plant group."
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL: AF031451; AAC63545.1;
KW Chloroplast.
FT NCN_TER 1 1
FT NCN_TER 8 8
SQ SEQUENCE 8 AA: 958 MW: 71658734.11846323 CRC64;
Query Match: 27.3%; Score 3; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 KKK 7
DB 1 KKK 3
RESULT 33
Q16605 PRELIMINARY; PRT; 9 AA.
AC Q16605;
DT 01-NOV-1996 (TrEMBLrel. 05, Created);
DT 01-NOV-1996 (TrEMBLrel. 05, Last sequence update);
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Glutathione S-transferase 2 (Fragment).
GN GSTA2 (R GST2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
GX NCBI_taxid:9606;
RP SEQUENCE FROM N.A.
RA Chow N.W., Whang-Peng J., Kao-Shan C., Chen C., Fan H., Chen D., Chou P.,
RT "Human glutathione S-transferases: cDNA clones, complementary DNAs,
RT products of different but overlapping cDNA and cDNA populations."
RL J. Biol. Chem. 263:12797-12803(1988).
DR EMBL: M21867; AAA52617.1;
DR EMBL: M21866; AAA35938.1;
FT NCN_TER 9 9
FT NCN_TER 9 9
SQ SEQUENCE 9 AA: 1116 MW: 118852.42363431 CRC64;
Query Match: 27.3%; Score 3; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 KKK 6
DB 4 KKK 6
RESULT 34
Q90QW0 PRELIMINARY; PRT; 9 AA.
AC Q90QW0;
DT 01-MAY-2000 (TrEMBLrel. 19, Created);
DI 01-MAY-2000 (TrEMBLrel. 19, Last sequence update);

DT 01-MAY 2000 (TrEMBLrel. 13, Last annotation update)
DE Prolactin precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
GX NCBI_taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Truong A.T., Puez G., Belayew A., Kenard A., Pictet R., Sell G.I.,
RT Martial J.A.,
RT "Isolation and characterization of the human prolactin gene."
RL EMBO J. 3:429-437(1984).
RN [2]
RP SEQUENCE FROM N.A.
RA Peers B., Naidu A.M., Mondet P., Voz M.L., Belayew A., Martial J.A.,
RT "Binding of a 100-kDa ubiquitous factor to the human prolactin
RT promoter is required for its basal and hormone-regulated activity."
RL Eur. J. Biochem. 210:53-58(1992).
DR EMBL: X00366; CAA25108.1;
KW Signal.
FT SIGNAL 1 8 POTENTIAL.
FT NCN_TER 9 9
SQ SEQUENCE 9 AA: 1060 MW: 0A1A5775B8733054 CRC64;
Query Match: 27.3%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 NIK 10
DB 2 NIK 4
RESULT 35
Q912L0 PRELIMINARY; PRT; 9 AA.
AC Q912L0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created);
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE EUC 11-113H1 harvesting chlorophyll protein II (fragment).
OS Spinacia oleracea (Spinach).
CC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
GX NCBI_taxid:4562;
RN [1]
RP SEQUENCE;
RA Meeche H., Griffin P.R., Shabanowitz J., Hunt D.F., Bennett J.,
RT "Target mass spectrometry identifies sites of three post-translational
RT modifications of spinach light harvesting chlorophyll protein II.
RT Proteolytic cleavage, acetylation, and phosphorylation."
RL J. Biol. Chem. 266:17684-17691(1991).
FT NCN_TER 1 1
FT NCN_TER 9 9
SQ SEQUENCE 9 AA: 999 MW: 54U927633875C1A3 CRC64;
Query Match: 27.3%; Score 3; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 KKK 6
DB 4 KKK 6
RESULT 36
Q912L1 PRELIMINARY; PRT; 9 AA.
AC Q912L1;
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update);

AC Q9T2L1:
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE LHC II-LIGHT-harvesting chlorophyll protein II (Fragment)
 OS Spinacia oleracea (Spinach)
 OG Chloroplast
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia
 CX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=9137386; PubMed=1894441;
 RA Michel H., Griffin P.R., Shabachviz Z., Bonn D.F., Bogenhoff J.
 RT "Random mass spectrometry identifies sites of three post-translational
 RT modifications of spinach light-harvesting chlorophyll protein II.
 RT Proteolytic cleavage, acetylation, and phosphorylation".
 RL J. Biol. Chem. 266:17584-17591(1991).
 FT NON_TER 1 9
 FT NON_TER 9 1
 SQ SEQUENCE 9 AA: 985 MW: 549276338750bps (8-64)

 Query Match 27.3%; Score 3; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 PKR 6
 DB 6 PKR 8

 RESULT 37
 Q71067
 ID Q71067 PRELIMINARY: PRI: 9 AA:
 AC Q71067
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Fusion protein (Fragment)
 OS F.
 OS Canine distemper virus.
 OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OS Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 CX NCBI_TaxID=11232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN Fitch #174/91;
 RA Liemann H., Harder T., Haas L.;
 RT "Genetic analysis of the central untranslated genome region and the
 RT proximal coding part of the F gene of wild-type and vaccine distemper
 RT morbilliviruses".
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF026215; AAC09165.1;
 FT NON_TER 9 9
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA: 1088 MW: 10900327605B1444 CRC64;

 Query Match 27.3%; Score 3; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 PKR 7
 DB 5 PKR 8

 RESULT 38
 Q71068
 ID Q71068 PRELIMINARY: PRI: 9 AA:
 AC Q71068
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Fusion protein (Fragment)
 OS F.
 OS Canine distemper virus.
 OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OS Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 CX NCBI_TaxID=11232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Marten #1;
 RA Liemann H., Harder T., Haas L.;
 RT "Genetic analysis of the central untranslated genome region and the
 RT proximal coding part of the F gene of wild-type and vaccine distemper
 RT morbilliviruses".
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF026215; AAC09166.1;
 FT NON_TER 9 9
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA: 1088 MW: 10900327605B1444 CRC64;

 Query Match 27.3%; Score 3; DB 12; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 5 PKR 7
 DB 6 PKR 8

 RESULT 39
 Q9JN49
 ID Q9JN49 PRELIMINARY: PRI: 10 AA:
 AC Q9JN49
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Plasmid pEl94 ermC leader region (Fragment).
 OS Staphylococcus aureus.
 CX Plasmid pEl94
 OG Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041917; PubMed=3904662;
 RA Narayanan C.S., Dubnau D.;
 RT "Evidence for the translational attenuation model: ribosome-binding
 RT studies and structural analysis with an in vitro run-off transcript
 RT of ermC".
 RL Nucleic Acids Res. 13:7307-7326(1985).
 DR EMBL: X03057; CAA26884.1;
 KW Plasmid
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1228 MW: 586088E33054433B CRC64;

 Query Match 27.3%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 8 NIK 10
 DB 5 NIK 7

 RESULT 40
 Q81ZA2
 ID Q81ZA2 PRELIMINARY: PRI: 10 AA:
 AC Q81ZA2
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Cardiac troponin T (Fragment).
 GN TNNT2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.


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SQ SEQUENCE 11 AA: 1297 MW: 5CC38013B7633337 CRC64;
Query Match: 27.3% Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
DB 5 KKP 7

RESULT 45
Q95PX6 PRELIMINARY; PRT; 11 AA.
AC Q95PX6.
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 1.3 kDa protein.
GN ZK1236.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RX MEDLINE=99069613; PubMed=9851516;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Favallo A.;
RT "Ibe sequence of C. elegans cosmid ZK1236."
RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Waterston R.;
RT "Direct Submission."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
SR EMBL; L13209; AAL11108.1;
DR WormPep; ZK1236.8; CE29629.
KW Hypothetical protein.
SQ SEQUENCE 11 AA: 1304 MW: DFAF510A25A76422 CRC64;

Query Match: 27.3% Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4
DB 7 SKK 9

RESULT 46
Q25916 PRELIMINARY; PRT; 11 AA.
AC Q25916.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Malaria antigen (7H8/2) (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91164876; PubMed=1706114;
RA Limpitboon T., Taylor D., Jones G., Geyson H.M., Saul A.;

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RT *Characterization of a Plasmodium falciparum epitope recognized by a
monoclonal antibody with broad isolate and species specificity.*;
RL Southeast Asian J. Trop. Med. Public Health 21:388-396(1990).
DR EMBL; M31305; AAA29645.1;
FT NON_TER 1
SQ SEQUENCE 11 AA: 1415 MW: DB03D3BC42C33699 CRC64;

Query Match: 27.3% Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RNI 9
DB 9 RNI 11

RESULT 47
Q9TQSO PRELIMINARY; PRT; 11 AA.
AC Q9TQSO.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE C-KIT (Fragment).
GN KIT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsen H.G., Vage D.I., Lien S., Klungland H.;
RT "A polymorphism in the bovine c-kit gene."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ243424; CAB60775.1;
DR EMBL; AJ243066; CAB60774.1;
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA: 1126 MW: DD785FF8A2D2D772 CRC64;

Query Match: 27.3% Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IKA 11
DB 1 IKA 3

RESULT 48
Q38415 PRELIMINARY; PRT; 11 AA.
AC Q38415.
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti protein (Fragment).
OS Bacteriophage P7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC P1-like viruses.
OX NCBI_TaxID=10682;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90335968; PubMed=1696181;
RA Citron M., Schuster H.;
RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs."
RL Cell 62:591-598(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92319637; PubMed=1620606;
RA Citron M., Schuster H.;
RT "The c4 repressor of bacteriophage P1 is a processed 77 base antisense

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RT RNA:";
 AC Nucleic Acids Res. 20:3065-3090(1992).
 DR EMBL: M35139; AAA32437.1;
 FT NON_TER 11
 SQ SEQUENCE 11 AA: 1315 MW: 38A50C6D11B20737 CRC64;

Query Match 27.3% Score 4; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKP 5
 DB 2 KKP 4

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 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Wound induced protein (Fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4391;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=pi8-rod; TISSUE=Pericarp;
 RX MEDLINE=9155536; PubMed-1715767;
 RA Parsons B.L., Mattoo A.K.;
 RT "Wound regulated accumulation of specific transcripts in tomato fruit:
 RT interactions with fruit development, ethylene and light.";
 RL Plant Mol. Biol. 17:453-464(1991).
 DR EMBL: X59864; CAA42539.1;
 FT NON_TER 1
 SQ SEQUENCE 11 AA: 1278 MW: 92CB25762H733425 CRC64;

Query Match 27.3% Score 4; DB 10; Length 11;
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 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 4 SKK 6

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 AC Q86866;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE S-RNA product protein (Fragment).
 OS S-RNA PRODUCT.
 OC Lymphocytic choriomeningitis virus.
 OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
 OX NCBI_TaxID=11623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=9519090; PubMed-7534851;
 RA Moskephidis D., Zinkernagel R.M.;
 RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
 RT choriomeningitis virus.";
 RL J. Virol. 69:2187-2193(1995).
 DR EMBL: S75748; AAB33668.1;
 FT NON_TER 1
 SQ SEQUENCE 11 AA: 1200 MW: 54245C80C9C45B57 CRC64;

Query Match 27.3% Score 3; DB 12; Length 11;

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QY 9 IKA 11
 DB 1 IKA 3

Search completed: September 30, 2003, 10:16:23
 Job time : 59.6667 secs

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CM proteins - protein search, using sw mode.

K.n on: September 30, 2003, 10:27:05: Search time 11:43.3 Seconds
(without alignments)
19,443 Million cells updated/sec

Title: US-09-787-443-1
Perfect score: 11
Sequence: 1 ASKPKRNKA 11

Scoring table: GLLGO
Gapop 60.0, Gapext 60.0

Searched: 328717 seqs, 423,0658 residues

Word size: 0

Total number of hits satisfying chosen parameters: 7845

Minimum LB seq length: 8
Maximum LB seq length: 15

Post-Processing: listing first 500 summaries

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2: /cgn2_6/ptodata/1/aa/FA_00MB.pat
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

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2	4	46.4	8	2	US-09-664-614-1	Sequence 12, Appl
3	4	46.4	8	5	US-07-281-617-2	Sequence 45, Appl
4	4	46.4	9	1	US-08-156-626-11	Sequence 14, Appl
5	4	46.4	9	1	US-08-156-626-11	Sequence 14, Appl
6	4	46.4	9	1	US-08-156-626-11	Sequence 14, Appl
7	4	46.4	9	1	US-08-156-626-11	Sequence 14, Appl
8	4	46.4	9	1	US-08-156-626-11	Sequence 14, Appl
9	4	46.4	10	1	US-08-401-112-53	Sequence 57, Appl
10	4	46.4	10	1	US-08-242-630-1	Sequence 6, Appl
11	4	46.4	10	2	US-04-406-600-12	Sequence 19, Appl
12	4	46.4	10	2	US-07-885-609-27	Sequence 27, Appl
13	4	46.4	10	2	US-08-506-617-27	Sequence 19, Appl
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241	3	27.3	9	1	US-08-454-207A-77	Sequence 77, Appl	224	3	27.3	9	3	US-09-112-206-188	Sequence 188, App
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Sequence 12, Application: US/08266514
Patent No. 5594105
GENERAL INFORMATION:
APPLICANT: COMOGGIO, PAOLO
APPLICANT: PONZELO, CAROLA
TITLE OF INVENTION: PEPTIDE INHIBITORS OF MITOGENESIS AND
TITLE OF INVENTION: MITOGENESIS
NUMBER OF SEQUENCE: 31
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ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,514
FILING DATE: 27-JUN-1994
CLASSIFICATION: 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9313528
FILING DATE: 30-JUN-1994
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APPLICATION NUMBER: GB 9407673.4
FILING DATE: 18-APR-1994

RESULT 1
US-08-266-514-12
Sequence 12, Application: US/08266514
Patent No. 5594105
GENERAL INFORMATION:
APPLICANT: COMOGGIO, PAOLO
APPLICANT: PONZELO, CAROLA
TITLE OF INVENTION: PEPTIDE INHIBITORS OF MITOGENESIS AND
TITLE OF INVENTION: MITOGENESIS
NUMBER OF SEQUENCE: 31
CORRESPONDENCE ADDRESS:
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STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,514
FILING DATE: 27-JUN-1994
CLASSIFICATION: 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9313528
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APPLICATION NUMBER: GB 9407673.4
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 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /note= "The Tyr residue at position 1 may be phosphorylated."
 US-08 266-514-12

Query Match: 36.4%; Score 4; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : ASKK 4
 Db : ASKK 5

RESULT 2
 US-08-654-604-12
 : Sequence 12, Application US/08654604
 : Patent No. 5912183
 : GENERAL INFORMATION:
 : APPLICANT: COMOGGIO, PAOLO
 : APPLICANT: PONZETTO, CAROLA
 : TITLE OF INVENTION: PEPTIDE INHIBITORS OF MITOGENESIS AND
 : NUMBER OF SEQUENCES: 31
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
 : ADDRESS: P.C.
 : STREET: 1755 S. Jefferson Davis Highway, Suite 400
 : CITY: Arlington
 : STATE: Virginia
 : COUNTRY: U.S.A.
 : ZIP: 22202
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/654,604
 : FILING DATE: 29-MAY-1996
 : CLASSIFICATION: 436
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/266,514
 : FILING DATE: 27-JUN-1994
 : APPLICATION NUMBER: GB 931352A
 : FILING DATE: 30-JUN-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: GB 9407673.4
 : FILING DATE: 18-APR-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Oblon, No. 5912183man F.
 : REGISTRATION NUMBER: 24,618
 : REFERENCE/DOCKET NUMBER: 769-123-0
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (703) 413-3000
 : TELEFAX: (703) 413-2220
 : TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /note= "The Tyr residue at position 1 may be phosphorylated."
 US-08-654-604-12

Query Match: 36.4%; Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : ASKK 4
 Db : ASKK 6

RESULT 3
 PCT-US93-12679-25
 : Sequence 25, Application PC/US9312679
 : GENERAL INFORMATION:
 : APPLICANT: Rath, Matthias
 : TITLE OF INVENTION: SYNTHETIC OLIGOPEPTIDES ANALOGOUS TO
 : TITLE OF INVENTION: PROTEIN SIGNAL SEQUENCES -METHODS OF IDENTIFICATION AND
 : NUMBER OF SEQUENCES: 41
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: SHELDON & MAK
 : STREET: 401 Florence Street
 : CITY: Palo Alto
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94301
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US93/12679
 : FILING DATE: 30-DEC-1993
 : CLASSIFICATION:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Cranfill, Raymond B
 : REGISTRATION NUMBER: 32,845
 : REFERENCE/DOCKET NUMBER: RATH-10016PC
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 415-322-5333
 : TELEFAX: 415-322-5499
 : INFORMATION FOR SEQ ID NO: 25:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 8 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : PCT-US93-12679-25

Query Match: 36.4%; Score 4; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : ASKK 6
 Db : ASKK 5

RESULT 4
 US-08-156-552A-14

Sequence 14, Application US/08156552A
Patent No. 5726155
GENERAL INFORMATION:
APPLICANT: Bokoch, Gary M
TITLE OF INVENTION: REGULATION OF OXIDATIVE PESTICIDE USING
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5726155th Torrey Pines Road, 10666
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/156,552A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,944
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: SCRF 281.1
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-156-552A-14

Query Match 36.4% Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 3 KKPK 6

RESULT 6
US-09-156-552A-14
Sequence 14, Application US/09035249A
Patent No. 6294663
GENERAL INFORMATION:
APPLICANT: Bokoch, Gary M
TITLE OF INVENTION: REGULATION OF OXIDATIVE PESTICIDE USING
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 618420th Torrey Pines Road, 10666
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,249A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,552
FILING DATE: 15-NOV-1993
APPLICATION NUMBER: US 08/102,944
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: SCRF 281.1
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-035-249A-14

Query Match 36.4% Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 3 KKPK 6

RESULT 6
US-09-518-046-86
Sequence 86, Application US/09518046
Patent No. 6294663
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Transmembrane Sorine Protease Overexpressed
TITLE OF INVENTION: An Ovarian Carcinoma and Uses Thereof
FILE REFERENCE: D619201P
CURRENT APPLICATION NUMBER: US/09/518,046
CURRENT FILING DATE: 2003-04-02
EARLIER APPLICATION NUMBER: 09/251,416
EARLIER FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 153
SEQ ID NO 86
LENGTH: 9
TYPE: PPT
ORGANISM: Homo sapiens
FEATURE:
LOCATION: 290...304
OTHER INFORMATION: TAB0012 peptide
US-09-518-046-86

Query Match 36.4% Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKPK 7
DB 3 KKPK 6

RESULT 7
US-09-518-046-109
Sequence 109, Application US/09518046
Patent No. 6294663
GENERAL INFORMATION:

1 APPLICANT: O'Brien, Timothy J.
 2 APPLICANT: Underwood, Lowell J.
 3 TITLE OF INVENTION: Transmembrane Surface Protein-Expressed
 4 TITLE OF INVENTION: In Ovarian Carcinoma and Uses Thereof
 5 FILE REFERENCE: D6192CIP
 6 CURRENT APPLICATION NUMBER: US/09/518,045
 7 CURRENT FILING DATE: 2000-03-02
 8 EARLIER APPLICATION NUMBER: 09/261,416
 9 EARLIER FILING DATE: 1999-03-03
 10 NUMBER OF SEQ ID NOS: 153
 11 SEQ ID NO 109
 12 LENGTH: 9
 13 TYPE: EST
 14 ORGANISM: Homo sapiens
 15 FEATURE:
 16 LOCATION: 298...306
 17 OTHER INFORMATION: TAGG-12 peptide
 18 US 09-518 045-109

Query Match: 36.4%, Score 4; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred No. 2 Seq 5;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPR 7
 1 1 1
 1 KPR 4

RESULT 8

1 US-09-518-045-112
 2 Sequence 112, Application US/095,8945
 3 Patent No. 6294663
 4 GENERAL INFORMATION:
 5 APPLICANT: O'Brien, Timothy J.
 6 APPLICANT: Underwood, Lowell J.
 7 TITLE OF INVENTION: Transmembrane Surface Protein-Expressed
 8 TITLE OF INVENTION: In Ovarian Carcinoma and Uses Thereof
 9 FILE REFERENCE: D6192CIP
 10 CURRENT APPLICATION NUMBER: US/09/518,045
 11 CURRENT FILING DATE: 2000-03-02
 12 EARLIER APPLICATION NUMBER: 09/261,416
 13 EARLIER FILING DATE: 1999-03-03
 14 NUMBER OF SEQ ID NOS: 153
 15 SEQ ID NO 112
 16 LENGTH: 9
 17 TYPE: EST
 18 ORGANISM: Homo sapiens
 19 FEATURE:
 20 LOCATION: 294...302
 21 OTHER INFORMATION: TAGG-12 peptide
 22 US 09-518-045-112

Query Match: 36.4%, Score 4; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred No. 2 Seq 5;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPR 7
 1 1 1
 5 KPR 8

RESULT 9

1 US 09-401 512-57
 2 Sequence 57, Application US/08461512
 3 Patent No. 559673
 4 GENERAL INFORMATION:
 5 APPLICANT: Keating, Mark T.
 6 APPLICANT: Curran, Mark E.
 7 APPLICANT: Wang, Qing
 8 TITLE OF INVENTION: Long Qc Sync And Gaps
 9 NUMBER OF SEQUENCES: 81
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESSEE: Venable, Baetjer, Howard & Givens LLP

1 STREET: 1201 New York Avenue, Suite 1000
 2 CITY: Washington
 3 STATE: DC
 4 COUNTRY: USA
 5 ZIP: 20005-3917
 6 COMPUTER RELEASABLE FORM:
 7 MEDIUM TYPE: Floppy disk
 8 COMPUTER: IBM PC compatible
 9 OPERATING SYSTEM: PC-DOS/MS-DOS
 10 SOFTWARE: Patent In Release #1.0, Version #1.25
 11 CURRENT APPLICATION DATA:
 12 APPLICATION NUMBER: US/08/401,512
 13 FILING DATE: 09-MAR-1995
 14 CLASSIFICATION: 435
 15 ATTORNEY/AGENT INFORMATION:
 16 NAME: Sako, Stephen A.
 17 REGISTRATION NUMBER: 38,509
 18 REFERENCE/DOKET NUMBER: 19780-113879
 19 TELECOMMUNICATION INFORMATION:
 20 TELEPHONE: 202-962-4848
 21 TELEFAX: 202-962-9100
 22 INFORMATION FOR SEQ ID NO: 57:
 23 SEQUENCE CHARACTERISTICS:
 24 LENGTH: 10 amino acids
 25 TYPE: amino acid
 26 TOPOLOGY: linear
 27 MOLECULE TYPE: peptide
 28 HYPOTHETICAL: NO
 29 US-08-401-512-57

Query Match: 36.4%, Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred No. 1 Seq 02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKKP 5
 1 1 1
 2 SKKP 5

RESULT 10

1 US 08-242-678D 6
 2 Sequence 6, Application US/08242678D
 3 Patent No. 5760300
 4 GENERAL INFORMATION:
 5 APPLICANT: HABIBI, RALPH R.
 6 TITLE OF INVENTION: INHIBITION OF LIVER CANCER BY THE USE OF
 7 TITLE OF INVENTION: GNRH AND GNRH ANALOGS
 8 NUMBER OF SEQUENCES: 12
 9 CORRESPONDENCE ADDRESS:
 10 ADDRESSEE: BURNS, DVANE, SWECKER & MATHIS
 11 STREET: P.O. Box 1404
 12 CITY: Alexandria
 13 STATE: Virginia
 14 COUNTRY: United States
 15 ZIP: 22303 1404
 16 COMPUTER RELEASABLE FORM:
 17 MEDIUM TYPE: Floppy disk
 18 COMPUTER: IBM PC compatible
 19 OPERATING SYSTEM: PC-DOS/MS-DOS
 20 SOFTWARE: Patent In Release #1.0, Version #1.30
 21 CURRENT APPLICATION DATA:
 22 APPLICATION NUMBER: US/08/242,678D
 23 FILING DATE: 13-MAY-1994
 24 CLASSIFICATION: 514
 25 ATTORNEY/AGENT INFORMATION:
 26 NAME: Dadio, Susan M.
 27 REGISTRATION NUMBER: 40,373
 28 REFERENCE/DOKET NUMBER: 028722-103
 29 TELECOMMUNICATION INFORMATION:
 30 TELEPHONE: (703) 836-8620
 31 TELEFAX: (703) 836-2021
 32 INFORMATION FOR SEQ ID NO: 6:
 33 SEQUENCE CHARACTERISTICS:

```

: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 1
: OTHER INFORMATION: /label AA1
: OTHER INFORMATION: /note "AA1 is A-ETV, beta 2 NACHTHL D ALA, AA2 is
: OTHER INFORMATION: D-P CHLORO THR, AA3 is beta 2-PYR-GLY-D-ALA"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /label AA5
: OTHER INFORMATION: /note "AA5 is alpha case N PESTION-NCO-LEU-YE-LYS, AA6 is also
: OTHER INFORMATION: D-LYS"
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 8
: OTHER INFORMATION: /label AA8
: OTHER INFORMATION: /note "AA8 is N PESTION N IS PROPY-LYS"
: FEATURE:
: NAME/KEY: Modified site
: LOCATION: 10
: OTHER INFORMATION: /label AA10
: OTHER INFORMATION: /note "AA10 is D-ALA"
: US-08-406-330-19
: Query Match 36.4% Score 4 DB 1 Length 10
: Best Local Similarity 100.0% Pred. No. 1.5e+02
: Matches 4: Conservative 0 Mismatches 0 Gaps 0
:
: QY 1 ASKX 4
: DB 3 ASKX 6
:
: RESULT 11
: US-08-406-330-19
: Sequence 19, Application US/08406330
: Patent No. 5817748
: GENERAL INFORMATION:
: APPLICANT: Miller, Jonathan L.
: APPLICANT: Lyle, Vicki A.
: TITLE OF INVENTION: MIMOTOPES AND ANTIMIMOTOPES
: TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IIb/IIIa
: NUMBER OF SEQUENCES: 81
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nixon, Benjamin, David & Associates
: STREET: Clinton Square 100, Park Ave.
: CITY: Rochester
: STATE: New York
: COUNTRY: USA
: ZIP: 14604
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/406-330
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Timian, Susan J.
: REGISTRATION NUMBER: 34,163
: REFERENCE/DOCKET NUMBER: 20884/100
: TELEPHONE: (716) 263-1636
: TELEFAX: (716) 263-1600
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:

```

```

: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-406-330-19
: Query Match 36.4% Score 4 DB 2 Length 10
: Best Local Similarity 100.0% Pred. No. 1.5e+02
: Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0
:
: QY 2 SKKP 5
: DB 2 SKKP 5
:
: RESULT 12
: US-07-885-089B-27
: Sequence 27, Application: US/07885089B
: Patent No. 5830955
: GENERAL INFORMATION:
: APPLICANT: Shoyab, Mohammed
: APPLICANT: McDonald, Vicki L.
: APPLICANT: Bradley, James G.
: APPLICANT: Plowman, Gregory D.
: TITLE OF INVENTION: AMPHIREGULINS: A FAMILY OF
: TITLE OF INVENTION: HEPARIN-BINDING EPITHELIAL CELL GROWTH FACTORS
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds LLP
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/885,089B
: FILING DATE: 18-MAY-1992
: CLASSIFICATION: 540
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 5624-174
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 790-9090
: TELEFAX: 212 799-9741
: TELEX: 6614 PENNIE
: INFORMATION FOR SEQ ID NO: 27:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-885-089B-27
: Query Match 36.4% Score 4 DB 2 Length 10
: Best Local Similarity 100.0% Pred. No. 1.5e+02
: Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0
:
: QY 4 KPKR 7
: DB 3 KPKR 4
:
: RESULT 13
: US-08-556-597-19
: Sequence 19, Application: US/08556597

```

```

: Patent No. 5877155
: GENERAL INFORMATION:
: APPLICANT: Miller, Jonathan L.
: APPLICANT: Ly-e, Vicki A.
: TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
: NUMBER OF SEQUENCES: 173
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
: STREET: Clinton Square, P.O. Box 1051
: CITY: Rochester
: STATE: New York
: COUNTRY: USA
: ZIP: 14603
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/556,597
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/406,310
: FILING DATE: 17-MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Timian, Susan J.
: REGISTRATION NUMBER: 44,103
: REFERENCE/DOCKET NUMBER: 20884/103
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (716) 263-1635
: TELEFAX: (716) 263-1600
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US 08/556-597-19

```

```

Query Match 36.4%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 SKKP 5
DB 1 1
2 SKKP 5

```

```

RESULT 14
US-08-416-035-8
: Sequence 8, Application US/08416035
: Patent No. 5739278
: GENERAL INFORMATION:
: APPLICANT: Baum, Gantler
: APPLICANT: Cool, Deborah E.
: TITLE OF INVENTION: Methods and Compositions for Proteins
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed and Berry
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/416,035
: FILING DATE: 30-MAR-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/059,949
: FILING DATE: 10-MAY-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Sharkley, Richard G.
: REGISTRATION NUMBER: 32,629
: REFERENCE/DOCKET NUMBER: 940010.531
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 622-6031
: TELEX: 3721836
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-416-035-8

```

```

Query Match 36.4%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 ASKK 4
DB 7 ASKK 10

```

```

RESULT 15
PCT-US93-05325-7
: Sequence 7, Application PC/TUS9305325
: GENERAL INFORMATION:
: APPLICANT: SKI, INTERNATIONAL
: TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
: NUMBER OF SEQUENCES: 39
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SKI, INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
: ADDRESSEE: COUNSEL
: STREET: 333 Ravenswood Avenue
: CITY: Menlo Park
: STATE: California
: COUNTRY: USA
: ZIP: 94025
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/05325
: FILING DATE: 19930603
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/894,497
: FILING DATE: 05-JUN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: CLARK, JANET P.
: REGISTRATION NUMBER: 34,799
: REFERENCE/DOCKET NUMBER: PCT-2679
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 859-2446
: TELEFAX: (415) 859-3880
: TELEX: 334486
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 13 amino acids
: TYPE: AMINO ACID

```

1 TOPOLOGY: linear
2 MOLECULE TYPE: peptide
3 PRT US99-05425-7

Query Match 36.4% Score 4: DB 5: Length 12:
Best Local Similarity 100.0% Pred. No. 2e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKKK 5
DB 9 KKKK 12

RESULT 16

US-08-314-172A-5
1 Sequence 5, Application US/08314172A
2 Patent No. 5650194
3 GENERAL INFORMATION:
4 APPLICANT: Meenese, Etica
5 APPLICANT: Bowles, Vernon
6 APPLICANT: Brandon, Malcolm
7 APPLICANT: Walker, John
8 TITLE OF INVENTION: VACCINE COMPOSITION
9 NUMBER OF SEQUENCES: 13
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Merchant & Gould
12 STREET: 4130 No. 5650154west Center, 90 S. 7th Street
13 CITY: Minneapolis
14 STATE: Minnesota
15 COUNTRY: USA
16 ZIP: 55402

17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Diskette
19 COMPUTER: IBM Compatible
20 OPERATING SYSTEM: DOS
21 SOFTWARE: FASTSEQ Version 1.5
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/314.172A
24 FILING DATE: 28-SEP-1994
25 CLASSIFICATION: 435
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 08/070.652
28 FILING DATE: 01-JUN-1993
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Mark T. Skoog
31 REGISTRATION NUMBER: 40,178
32 REFERENCE/DOCKET NUMBER: 4159-180801
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE:
35 TELEFAX:
36 INFORMATION FOR SEQ ID NO: 5:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 15 amino acids
39 TYPE: amino acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42 MOLECULE TYPE: peptide
43 HYPOTHETICAL: NO
44 ANTI-SENSE: NO
45 FRAGMENT TYPE: internal
46 ORIGINAL SOURCE:
47 US-08-314-172A-5

Query Match 36.4% Score 4: DB 5: Length 15:
Best Local Similarity 100.0% Pred. No. 2e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 SKKP 5
DB 9 SKKP 12

RESULT 17
US-08-637-418-9
1 Sequence 9, Application US/08637418
2 Patent No. 5891848
3 GENERAL INFORMATION:
4 APPLICANT: OOMURA, Yutaka
5 TITLE OF INVENTION: PEPTIDE FRAGMENTS
6 NUMBER OF SEQUENCES: 20
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Fisher, Christen & Sabol
9 STREET: 1019 19th St., N.W., Suite 300
10 CITY: Washington
11 STATE: D.C.
12 COUNTRY: U.S.A.
13 ZIP: 20036

14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.30
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/637.418
21 FILING DATE: 25-APR-1996
22 CLASSIFICATION: 514
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: JP 125,947/1995
25 FILING DATE: 25-APR-1995
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Hollander, Barry L.
28 REGISTRATION NUMBER: 28,566
29 REFERENCE/DOCKET NUMBER: NZK-116
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (202) 659-2000
32 TELEFAX: (202) 659-2015
33 INFORMATION FOR SEQ ID NO: 9:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 15 amino acids
36 TYPE: amino acid
37 STRANDEDNESS:
38 TOPOLOGY: linear
39 MOLECULE TYPE: peptide
40 HYPOTHETICAL: NO
41 ANTI-SENSE: NO
42 FRAGMENT TYPE: N-terminal
43 ORIGINAL SOURCE:
44 ORGANISM: Homo sapiens
45 US-08-637-418-9

Query Match 36.4% Score 4: DB 2: Length 15:
Best Local Similarity 100.0% Pred. No. 2e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKKK 5
DB 9 KKKK 12

RESULT 18

US-08-637-418-10
1 Sequence 10, Application US/08637418
2 Patent No. 5891848
3 GENERAL INFORMATION:
4 APPLICANT: OOMURA, Yutaka
5 TITLE OF INVENTION: PEPTIDE FRAGMENTS
6 NUMBER OF SEQUENCES: 20
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Fisher, Christen & Sabol
9 STREET: 1019 19th St., N.W., Suite 300
10 CITY: Washington
11 STATE: D.C.
12 COUNTRY: U.S.A.
13 ZIP: 20036
14 COMPUTER READABLE FORM:

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1 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC-DOS/MS-DOS
4 SOFTWARE: Patent In Release #1.0, Version #1.30
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/09/637,418
7 FILING DATE: 25-APR-1996
8 CLASSIFICATION: 514
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: JP 125,947/1995
11 FILING DATE: 25-APR-1995
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Hollander, Barry I.
14 REGISTRATION NUMBER: 28,566
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (202) 659-2000
17 TELEFAX: (202) 659-2015
18 INFORMATION FOR SEQ ID NO: 10:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 15 amino acids
21 TYPE: amino acid
22 STRANDEDNESS:
23 TOPOLOGY: linear
24 MOLECULE TYPE: peptide
25 HYPOTHETICAL: NO
26 ANTI-SENSE: NO
27 FRAGMENT TYPE: N-terminal
28 ORIGINAL SOURCE:
29 ORGANISM: Homo sapiens
30 FEATURE:
31 NAME/KEY: Modified-site
32 LOCATION: 15
33 OTHER INFORMATION: /product "Xaa is the amino form of
34 (OTHER INFORMATION: Tyrosine."
35 US-09-637 418-19
36
37 Query Match 36.4%; Score 4; IP 2; Length 15;
38 Best Local Similarity 100.0%; Pred. No. 2e+27
39 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
40
41 QY 3 KKPK 6
42 III
43 DB 9 KKPK 12
44
45 RESULT 19
46 US-08-637 418-19
47 Sequence 19, Application US/08/637418
48 Patent No. 5891848
49 GENERAL INFORMATION:
50 APPLICANT: OOMURA, Yutaka
51 TITLE OF INVENTION: PEPTIDE FRAGMENTS
52 NUMBER OF SEQUENCES: 20
53 CORRESPONDENCE ADDRESS:
54 ADDRESSEE: Fisher, Christen & Sabol
55 STREET: 1019 19th St., N.W., Suite 300
56 CITY: Washington
57 STATE: D.C.
58 COUNTRY: U.S.A.
59 ZIP: 20036
60 COMPUTER READABLE FORM:
61 MEDIUM TYPE: Floppy disk
62 COMPUTER: IBM PC compatible
63 OPERATING SYSTEM: PC-DOS/MS-DOS
64 SOFTWARE: Patent In Release #1.0, Version #1.30
65 CURRENT APPLICATION DATA:
66 APPLICATION NUMBER: US/08/637,418
67 FILING DATE: 25-APR-1996
68 CLASSIFICATION: 514
69 PRIOR APPLICATION DATA:
70 APPLICATION NUMBER: JP 125,947/1995
71 FILING DATE: 25-APR-1995
72 ATTORNEY/AGENT INFORMATION:
73 NAME: Hollander, Barry I.
74 REGISTRATION NUMBER: 28,566
75 TELECOMMUNICATION INFORMATION:
76 TELEPHONE: (202) 659-2000
77 TELEFAX: (202) 659-2015
78 INFORMATION FOR SEQ ID NO: 10:
79 SEQUENCE CHARACTERISTICS:
80 LENGTH: 15 amino acids
81 TYPE: amino acid
82 STRANDEDNESS:
83 TOPOLOGY: linear
84 MOLECULE TYPE: peptide
85 HYPOTHETICAL: NO
86 ANTI-SENSE: NO

```

```

1 ATTORNEY/AGENT INFORMATION:
2 NAME: Hollander, Barry I.
3 REGISTRATION NUMBER: 28,566
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: (202) 659-2000
6 TELEFAX: (202) 659-2015
7 INFORMATION FOR SEQ ID NO: 19:
8 SEQUENCE CHARACTERISTICS:
9 LENGTH: 15 amino acids
10 TYPE: amino acid
11 STRANDEDNESS:
12 TOPOLOGY: linear
13 MOLECULE TYPE: peptide
14 HYPOTHETICAL: NO
15 ANTI-SENSE: NO
16 FRAGMENT TYPE: N-terminal
17 ORIGINAL SOURCE:
18 ORGANISM: Bos taurus
19 US-08-637-418-19
20
21 Query Match 36.4%; Score 4; DB 2; Length 15;
22 Best Local Similarity 100.0%; Pred. No. 2e+02;
23 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
24
25 QY 3 KKPK 6
26 IIII
27 DB 9 KKPK 12
28
29 RESULT 20
30 US-08-637-418-20
31 Sequence 20, Application US/08637418
32 Patent No. 5891848
33 GENERAL INFORMATION:
34 APPLICANT: OOMURA, Yutaka
35 TITLE OF INVENTION: PEPTIDE FRAGMENTS
36 NUMBER OF SEQUENCES: 20
37 CORRESPONDENCE ADDRESS:
38 ADDRESSEE: Fisher, Christen & Sabol
39 STREET: 1019 19th St., N.W., Suite 300
40 CITY: Washington
41 STATE: D.C.
42 COUNTRY: U.S.A.
43 ZIP: 20036
44 COMPUTER READABLE FORM:
45 MEDIUM TYPE: Floppy disk
46 COMPUTER: IBM PC compatible
47 OPERATING SYSTEM: PC-DOS/MS-DOS
48 SOFTWARE: Patent In Release #1.0, Version #1.30
49 CURRENT APPLICATION DATA:
50 APPLICATION NUMBER: US/08/637,418
51 FILING DATE: 25-APR-1996
52 CLASSIFICATION: 514
53 PRIOR APPLICATION DATA:
54 APPLICATION NUMBER: JP 125,947/1995
55 FILING DATE: 25-APR-1995
56 ATTORNEY/AGENT INFORMATION:
57 NAME: Hollander, Barry I.
58 REGISTRATION NUMBER: 28,566
59 TELECOMMUNICATION INFORMATION:
60 TELEPHONE: (202) 659-2000
61 TELEFAX: (202) 659-2015
62 INFORMATION FOR SEQ ID NO: 20:
63 SEQUENCE CHARACTERISTICS:
64 LENGTH: 15 amino acids
65 TYPE: amino acid
66 STRANDEDNESS:
67 TOPOLOGY: linear
68 MOLECULE TYPE: peptide
69 HYPOTHETICAL: NO
70 ANTI-SENSE: NO

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1 FRAGMENT TYPE: N-terminal
 2 ORIGINAL SOURCE: Bos taurus
 3 ORGANISM: Bos taurus
 4 FEATURE:
 5 NAME/KEY: Modified-site
 6 LOCATION: 15
 7 OTHER INFORMATION: /Product: "Xaa is the amino terminus
 8 OTHER INFORMATION: Tyrosine."
 9 US 08-637-416-20

1 Query Match 36.4% Score 41 DB 3 Length 15
 2 Best Local Similarity 100.0% Pred. No. 2e-02
 3 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QY 4 KKK 6
 2 111
 3 9 KKK 12

1 RESULT 21
 2 US 09-041-889-17
 3 Sequence 17, Application: US/09041889
 4 Patent No. 603864
 5 GENERAL INFORMATION:
 6 APPLICANT: Braun, Jonathan
 7 TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
 8 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
 9 TITLE OF INVENTION: Microbial UC PANCA antigens
 10 NUMBER OF SEQUENCES: 41
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: Campbell & Flores LLP
 13 STREET: 4370 La Jolla Village Drive, Suite 700
 14 CITY: San Diego
 15 STATE: California
 16 COUNTRY: USA
 17 ZIP: 92122
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: Floppy disk
 20 OPERATING SYSTEM: IBM PC compatible
 21 SOFTWARE: Patent In Release #1.0, Version #1.25
 22 CURRENT APPLICATION DATA:
 23 FILING DATE:
 24 CLASSIFICATION:
 25 PRIOR APPLICATION DATA:
 26 APPLICATION NUMBER: US 08/847,058
 27 FILING DATE: 11 APR-1997
 28 ATTORNEY/AGENT INFORMATION:
 29 NAME: Campbell, Cathryn A.
 30 REGISTRATION NUMBER: 41,815
 31 REFERENCE/DOCKET NUMBER: P-PM 3006
 32 TELECOMMUNICATION INFORMATION:
 33 TELEPHONE: (619) 535-9001
 34 TELEFAX: (619) 535-8949
 35 INFORMATION FOR SEQ ID NO: 17:
 36 SEQUENCE CHARACTERISTICS:
 37 LENGTH: 15 amino acids
 38 TYPE: amino acid
 39 TOPOLOGY: linear
 40 US 09-041-889-17

1 Query Match 36.4% Score 41 DB 3 Length 15
 2 Best Local Similarity 100.0% Pred. No. 2e-02
 3 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QY 4 KKK 6
 2 111
 3 9 KKK 12

1 RESULT 22
 2 US 09-041-889-17
 3 Sequence 17, Application: US/09041889
 4 Patent No. 603864
 5 GENERAL INFORMATION:
 6 APPLICANT: Braun, Jonathan
 7 TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
 8 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
 9 TITLE OF INVENTION: Microbial UC PANCA antigens
 10 NUMBER OF SEQUENCES: 41
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: Campbell & Flores LLP
 13 STREET: 4370 La Jolla Village Drive, Suite 700
 14 CITY: San Diego
 15 STATE: California
 16 COUNTRY: USA
 17 ZIP: 92122
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: Floppy disk
 20 OPERATING SYSTEM: IBM PC compatible
 21 SOFTWARE: Patent In Release #1.0, Version #1.25
 22 CURRENT APPLICATION DATA:
 23 FILING DATE:
 24 CLASSIFICATION:
 25 PRIOR APPLICATION DATA:
 26 APPLICATION NUMBER: US 08/847,058
 27 FILING DATE: 11 APR-1997
 28 ATTORNEY/AGENT INFORMATION:
 29 NAME: Campbell, Cathryn A.
 30 REGISTRATION NUMBER: 41,815
 31 REFERENCE/DOCKET NUMBER: P-PM 3006
 32 TELECOMMUNICATION INFORMATION:
 33 TELEPHONE: (619) 535-9001
 34 TELEFAX: (619) 535-8949
 35 INFORMATION FOR SEQ ID NO: 17:
 36 SEQUENCE CHARACTERISTICS:
 37 LENGTH: 15 amino acids
 38 TYPE: amino acid
 39 TOPOLOGY: linear
 40 US 09-041-889-17

1 QY 4 KKK 6
 2 111
 3 9 KKK 12

1 Query Match 36.4% Score 41 DB 3 Length 15
 2 Best Local Similarity 100.0% Pred. No. 2e-02
 3 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QY 4 KKK 6
 2 111
 3 9 KKK 12

1 US 09-041-889-17
 2 Sequence 17, Application: US/09041889
 3 Patent No. 603864
 4 GENERAL INFORMATION:
 5 APPLICANT: Braun, Jonathan
 6 TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
 7 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
 8 TITLE OF INVENTION: Microbial UC PANCA antigens
 9 NUMBER OF SEQUENCES: 41
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESSEE: Campbell & Flores LLP
 12 STREET: 4370 La Jolla Village Drive, Suite 700
 13 CITY: San Diego
 14 STATE: California
 15 COUNTRY: USA
 16 ZIP: 92122
 17 COMPUTER READABLE FORM:
 18 MEDIUM TYPE: Floppy disk
 19 OPERATING SYSTEM: IBM PC compatible
 20 SOFTWARE: Patent In Release #1.0, Version #1.25
 21 CURRENT APPLICATION DATA:
 22 FILING DATE:
 23 CLASSIFICATION:
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: US 08/847,058
 26 FILING DATE: 11 APR-1997
 27 ATTORNEY/AGENT INFORMATION:
 28 NAME: Campbell, Cathryn A.
 29 REGISTRATION NUMBER: 41,815
 30 REFERENCE/DOCKET NUMBER: P-PM 3006
 31 TELECOMMUNICATION INFORMATION:
 32 TELEPHONE: (619) 535-9001
 33 TELEFAX: (619) 535-8949
 34 INFORMATION FOR SEQ ID NO: 17:
 35 SEQUENCE CHARACTERISTICS:
 36 LENGTH: 15 amino acids
 37 TYPE: amino acid
 38 TOPOLOGY: linear
 39 US 09-041-889-17

1 Query Match 36.4% Score 41 DB 3 Length 15
 2 Best Local Similarity 100.0% Pred. No. 2e-02
 3 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QY 4 KKK 6
 2 111
 3 9 KKK 12

1 RESULT 21
 2 US 09-041-889-17
 3 Sequence 17, Application: US/09041889
 4 Patent No. 603864
 5 GENERAL INFORMATION:
 6 APPLICANT: Braun, Jonathan
 7 TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
 8 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
 9 TITLE OF INVENTION: Microbial UC PANCA antigens
 10 NUMBER OF SEQUENCES: 41
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: Campbell & Flores LLP
 13 STREET: 4370 La Jolla Village Drive, Suite 700
 14 CITY: San Diego
 15 STATE: California
 16 COUNTRY: USA
 17 ZIP: 92122
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: Floppy disk
 20 OPERATING SYSTEM: IBM PC compatible
 21 SOFTWARE: Patent In Release #1.0, Version #1.25
 22 CURRENT APPLICATION DATA:
 23 FILING DATE:
 24 CLASSIFICATION:
 25 PRIOR APPLICATION DATA:
 26 APPLICATION NUMBER: US 08/847,058
 27 FILING DATE: 11 APR-1997
 28 ATTORNEY/AGENT INFORMATION:
 29 NAME: Campbell, Cathryn A.
 30 REGISTRATION NUMBER: 41,815
 31 REFERENCE/DOCKET NUMBER: P-PM 3006
 32 TELECOMMUNICATION INFORMATION:
 33 TELEPHONE: (619) 535-9001
 34 TELEFAX: (619) 535-8949
 35 INFORMATION FOR SEQ ID NO: 17:
 36 SEQUENCE CHARACTERISTICS:
 37 LENGTH: 15 amino acids
 38 TYPE: amino acid
 39 TOPOLOGY: linear
 40 US 09-041-889-17

1 Query Match 36.4% Score 41 DB 3 Length 15
 2 Best Local Similarity 100.0% Pred. No. 2e-02
 3 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QY 4 KKK 6
 2 111
 3 9 KKK 12

1 RESULT 22
 2 US 09-041-889-17
 3 Sequence 17, Application: US/09041889
 4 Patent No. 603864
 5 GENERAL INFORMATION:
 6 APPLICANT: Braun, Jonathan
 7 TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
 8 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
 9 TITLE OF INVENTION: Microbial UC PANCA antigens
 10 NUMBER OF SEQUENCES: 41
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: Campbell & Flores LLP
 13 STREET: 4370 La Jolla Village Drive, Suite 700
 14 CITY: San Diego
 15 STATE: California
 16 COUNTRY: USA
 17 ZIP: 92122
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: Floppy disk
 20 OPERATING SYSTEM: IBM PC compatible
 21 SOFTWARE: Patent In Release #1.0, Version #1.25
 22 CURRENT APPLICATION DATA:
 23 FILING DATE:
 24 CLASSIFICATION:
 25 PRIOR APPLICATION DATA:
 26 APPLICATION NUMBER: US 08/847,058
 27 FILING DATE: 11 APR-1997
 28 ATTORNEY/AGENT INFORMATION:
 29 NAME: Campbell, Cathryn A.
 30 REGISTRATION NUMBER: 41,815
 31 REFERENCE/DOCKET NUMBER: P-PM 3006
 32 TELECOMMUNICATION INFORMATION:
 33 TELEPHONE: (619) 535-9001
 34 TELEFAX: (619) 535-8949
 35 INFORMATION FOR SEQ ID NO: 17:
 36 SEQUENCE CHARACTERISTICS:
 37 LENGTH: 15 amino acids
 38 TYPE: amino acid
 39 TOPOLOGY: linear
 40 US 09-041-889-17

1 QY 4 KKK 6
 2 111
 3 9 KKK 12

1 Query Match 36.4% Score 41 DB 3 Length 15
 2 Best Local Similarity 100.0% Pred. No. 2e-02
 3 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QY 4 KKK 6
 2 111
 3 9 KKK 12

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,058
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 2438
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-837-058 17

Query Match: 36.4% Score 4: DB 3: Length 15:
Best local Similarity 100.0%: Pred. No. 2e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKPK 6
DB 12 KKPK 15

US-08-837-058 18
Sequence 18: Application US/08837058
Patent No. 6074835
GENERAL INFORMATION:
APPLICANT: Braum, Jonathan
APPLICANT: Targan, Stephan R.
APPLICANT: Eggena, Mark
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,058
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 2438
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-837-058 18

Query Match: 36.4% Score 4: DB 3: Length 15:

Best local Similarity 100.0%: Pred. No. 2e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 3 KKPK 6
DB 2 KKPK 5
US-09-537-357 2
Sequence 2: Application US/09537357
Patent No. 6271018
GENERAL INFORMATION:
APPLICANT: Alais, Arash
APPLICANT: Nathalie Tillet
TITLE OF INVENTION: MUSKELON (CUCUMIS MELO) HYDROPEROXIDE
FILE REFERENCE: 06027-0002
CURRENT APPLICATION NUMBER: US/09/537,357
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 15
TYPE: PKT
ORGANISM: Cucumis melo
US-09-537-357 2

Query Match: 36.4% Score 4: DB 3: Length 15:
Best local Similarity 100.0%: Pred. No. 2e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 6 KRNI 9
DB 10 KRNI 13

US-09-417-264 17

Sequence 17: Application US/09417264
Patent No. 6537768
GENERAL INFORMATION:
APPLICANT: Braum, Jonathan
APPLICANT: Cohavy, Ofer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/041,889
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

```

: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-09-417-264-17

Query Match: 36.4%, Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKKK 6
ID 12 KKKK 15

RESULT 27
US-09-417-264-18
: Sequence 18, Application US/09417264
: Patent No. 6537768
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: TITLE OF INVENTION: Microbial UC pANA antigens
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores Ltd
: STREET: 4370 La Jolla Village Drive, Suite 750
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/417,264
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/041,489
: FILING DATE:
: FILING DATE:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 41,816
: REFERENCE/DOCKET NUMBER: P 18
: INFORMATION INFORMATION:
: TELEPHONE: (619) 535-8949
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-09-417-264-18

Query Match: 36.4%, Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKKK 6
ID 2 KKKK 5

RESULT 28
US-07-717-052-1
: Sequence 3, Application US/07717052

```

```

: Patent No. 5243027
: GENERAL INFORMATION:
: APPLICANT: Mimura, Tsutomu
: APPLICANT: Kohama, Yasuhiko
: APPLICANT: Nagata, Kazuhiko
: APPLICANT: Tsurutani, Ryochi
: TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME
: TITLE OF INVENTION: INHIBITOR
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Squibb, Mich, Zinn, Macpeak & Seas
: STREET: 2109 Pennsylvania Avenue
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A
: ZIP: 20037-4202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/737,852
: FILING DATE: 19910731
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 02-45975
: FILING DATE: 25-FEB-1990
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)293-7060
: TELEFAX: (202)293-7860
: TELEX: 6491103
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: AMINO ACIDS
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Bacillus stearothermophilus
: STRAIN: NCA 150;
US-07-737-852-3

Query Match: 27.4%, Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 ASK 3
ID 4 ASK 6

RESULT 29
US-07-920-697-1
: Sequence 1, Application US/07920597
: Patent No. 5447915
: GENERAL INFORMATION:
: APPLICANT: Schreiber, Stuart
: APPLICANT: Hatakey, Steven
: TITLE OF INVENTION: terminally-blocked Antiviral Peptides
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Allaretti & Witcoff, Ltd.
: STREET: 16 South Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/920,597
: FILING DATE: 19920828
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO pct/us91/01142
: FILING DATE: 28-FEB-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5447915nan, Kevin E
: REGISTRATION NUMBER: 35,303
: REFERENCE/DOCKET NUMBER: 91,174-E
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-715-1000
: TELEFAX: 312-715-1234
: TELEX: 910-221-5317
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-07 920-597-1
:
: Query Match 27.3%; Score 3; DB 1; Length 8;
: Best Local Similarity 100.0%; Pred. No. 2.5e+05;
: Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 4 KPK 6
: DB 1
:
: RESULT 30
: US-07-920-597-2
: Sequence 2, Application US/07920597
: Patent No. 5447915
: GENERAL INFORMATION:
: APPLICANT: Schreiber, Stuart
: TITLE OF INVENTION: Terminally-Blocked Antiviral Peptides
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Allgretti & Wilcott, Ltd.
: STREET: 10 South Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC DOS/MS DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/920,597
: FILING DATE: 19920828
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO pct/us91/01142
: FILING DATE: 28-FEB-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5447915nan, Kevin E
: REGISTRATION NUMBER: 35,303
: REFERENCE/DOCKET NUMBER: 91,174 E
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-715-1000
: TELEFAX: 312-715-1234
: TELEX: 910-221-5317
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
:
: US-09-787-443-1
:
: Query Match 27.3%; Score 3; DB 1; Length 8;
: Best Local Similarity 100.0%; Pred. No. 2.5e+05;
: Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 4 KPK 6
: DB 1
:
: RESULT 31
: US-08-432-617-2
: Sequence 2, Application US/08432617
: Patent No. 5495000
: GENERAL INFORMATION:
: APPLICANT: Krstiansky, John L.
: TITLE OF INVENTION: Anticoagulant Peptides
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marion Merrell Dow Inc.
: STREET: 2110 East Galbraith Rd.
: CITY: Cincinnati P. O. Box 156300
: STATE: Ohio
: COUNTRY: USA
: ZIP: 45215-6300
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/432,617
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/971,909
: FILING DATE: 18-DEC-1992
: APPLICATION NUMBER: US 07/557,288
: FILING DATE: 24-JUL-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/US91/04658
: FILING DATE: 28-JUN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Boudreaux, William R
: REGISTRATION NUMBER: 35,796
: REFERENCE/DOCKET NUMBER: M01556 US-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (513) 948-6566
: TELEFAX: (513) 948-7961
: TELEX: 214320
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-432-617-2
:
: Query Match 27.3%; Score 3; DB 1; Length 8;
: Best Local Similarity 100.0%; Pred. No. 2.5e+05;
: Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 5 PKR 7
: DB 1
:
: RESULT 32
: US-08-261-525A-3

```

Sequence 3, Application US/08261525A
Patent No. 5569598
GENERAL INFORMATION:
APPLICANT: PARK, Soon Jae
APPLICANT: LEE, Young Mee
APPLICANT: WON, Teug Yeon
APPLICANT: KWON, Soon Chang
APPLICANT: LEE, Seung Joo
APPLICANT: KIM, Jung Ho
APPLICANT: KIM, Bum Joon
TITLE OF INVENTION: NOVEL AMINOPEPTIDASE, PROCESSES FOR
THE PREPARATION OF THE PREPARATION OF AMINOPEPTIDASE AND
TITLE OF INVENTION: THE PREPARATION OF AMINOPEPTIDASE AND
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARK, Soon Jae
STREET: Lucky Apt. 6-101, Doryong-dong, Yuseong-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-340
ADDRESSEE: LEE, Young Mee
STREET: Shinsung Apt. 3-306, 28 4, Nae-dong, Seo-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 302-181
ADDRESSEE: WON, Teug Yeon
STREET: Gongjak Hanyang Apt. 4-1201, 85b,
STREET: Tanbang-dong, Seo-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 302-223
ADDRESSEE: KWON, Soon Chang
STREET: Shinsung Apt. 3-107, 28 4, Nae-dong, Seo-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 302-181
ADDRESSEE: LEE, Seung Joo
STREET: Lucky Apt. 8-107, 45b-4, Doryong-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-340
ADDRESSEE: KIM, Jung Ho
STREET: Lucky Dormitory 511, 60b-1, Doryong-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-340
ADDRESSEE: KIM, Bum Joon
STREET: Lucky Dormitory 502, 48b-1, Doryong-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-340
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44MB STORAGE
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,525A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 93-11107
FILING DATE: 17-JUN-1993

ATTORNEY/AGENT INFORMATION:
NAME: Shahan Islam
REGISTRATION NUMBER: 32,507
REFERENCE/DOCKET NUMBER: A-9883
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-1000
TELEFAX: (212) 953-7249
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Streptomyces thermotritificans
US-08-261-525A-3
Query Match 27.3%, Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 2 SKK 4
Db 3 SKK 5
RESULT 33
US-08-240-514-39
Sequence 39, Application US/08240514
Patent No. 5670347
GENERAL INFORMATION:
APPLICANT: GOPAL, T. Venkat
TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,514
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 73521/102/CLIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904135
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-240-514-39
Query Match 27.3%, Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 4 KPK 6
Db 3

100 0: KKK 8

RESULT 14

US-08-249-387-5
 : Sequence 5, Application US/08249387
 : Patent No. 5681700
 : GENERAL INFORMATION:
 : APPLICANT: Reichlin, Morris
 : TITLE OF INVENTION: Assay for Pathogenicity of Ant. DNA
 : NUMBER OF SEQUENCES: 6
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Patricia L. Parist
 : STREET: 1100 Peachtree Street, Suite 2800
 : CITY: Atlanta
 : STATE: Georgia
 : COUNTRY: USA
 : ZIP: 30309-4530
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: Patent In Release #1.0, Version #1.05
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/249,487
 : FILING DATE: 01-DEC-1997
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Pubst, Patricia L.
 : REGISTRATION NUMBER: 31,284
 : REFERENCE/DOCKET NUMBER: 08RF145
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (404) 815-6558
 : TELEFAX: (404) 815-6555
 : INFORMATION FOR SEQ ID NO: 5:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 8 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 : RECOMBINANT: NO
 : ANTI-SENSE: NO
 : FRAGMENT TYPE: Internal
 : US-08-249-387-5

Query Match 27.3% Score 6.0 DB 1: Length 8:
 Best Local Similarity 100.0% Pred No. 2.5e+05
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Caps 0:

QY 2 SKK 4

11

100 2 SKK 4

RESULT 15

US-08-467-264-19
 : Sequence 19, Application US/08467264
 : Patent No. 5705156
 : GENERAL INFORMATION:
 : APPLICANT: Pastan, Ira
 : APPLICANT: Fitzgerald, David
 : APPLICANT: Chaudhary, Vijay K.
 : TITLE OF INVENTION: Pseudomonas ES Toxins and their Anticancer Activity
 : NUMBER OF SEQUENCES: 20
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Townsend and Towns
 : STREET: One Market Plaza, Steuart Street Tower
 : CITY: San Francisco
 : STATE: California

COUNTRY: USA
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,264
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/522,182
 FILING DATE: 11-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/130,422
 FILING DATE: 01-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 48,498
 REFERENCE/DOCKET NUMBER: 15280-125-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-467-264-19

Query Match 27.3% Score 3: DB 1: Length 8:
 Best Local Similarity 100.0% Pred No. 2.5e+05
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Caps 0:

QY 2 SKK 4

11

100 3 SKK 5

RESULT 16

US-08-416-035-3
 : Sequence 3, Application US/08416035
 : Patent No. 5739278
 : GENERAL INFORMATION:
 : APPLICANT: Baum, Gunter
 : APPLICANT: Cogl, Deborah E.
 : TITLE OF INVENTION: Methods and Compositions for Protein
 : TITLE OF INVENTION: Tyrosine Phosphatases
 : NUMBER OF SEQUENCES: 9
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Seed and Berry
 : STREET: 6400 Columbia Center, 701 Fifth Avenue
 : CITY: Seattle
 : STATE: Washington
 : COUNTRY: USA
 : ZIP: 98104
 : COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/416,035
 FILING DATE: 30-MAR-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/59,949
 FILING DATE: 10-MAY-1994
 ATTORNEY/AGENT INFORMATION:

1 NAME: Sharkey, Richard G.
2 REGISTRATION NUMBER: 42,624
3 REFERENCE/DOCKET NUMBER: 940610, 54,
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: (206) 622-4900
6 TELEFAX: (206) 682-6031
7 TELEFAX: 3723836
8 INFORMATION FOR SEQ ID NO: 1:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 8 amino acids
11 TYPE: amino acid
12 TOPOLOGY: linear
13 MOLECULE TYPE: peptide
14 FEATURE:
15 NAME/KEY: modified site
16 LOCATION: 3
17 OTHER INFORMATION: /note: "Wherein ty is
18 OTHER INFORMATION: phosphorylated."
19 US-08-416-035-3
20
21 Query Match 27.3%, Score 3, DB 1, Length 8,
22 Best Local Similarity 100.0%, Pred. No. 2, 5e+05,
23 Matches 3, Conservative 0, Mismatches 0, Indels 0,
24 Gaps 0:
25
26 QY 1 ASK 3
27 11
28 6 ASK 8
29
30 RESULT 47
31 US-08-416-035-4
32 Sequence 9, Application US/0841606,
33 Patent No. 5759278
34 GENERAL INFORMATION:
35 APPLICANT: Baum, Genter
36 APPLICANT: Baum, Genter
37 APPLICANT: Fischer, Edmund B
38 TITLE OF INVENTION: Methods and Compositions for Protein
39 TITLE OF INVENTION: Tyrosine Phosphatases
40 NUMBER OF SEQUENCES: 9
41 CORRESPONDENCE ADDRESS:
42 ADDRESSEE: Seed and Betty
43 STREET: 6100 Columbia Center, 711 Fifth Avenue
44 CITY: Seattle
45 STATE: Washington
46 COUNTRY: USA
47 ZIP: 98104
48 COMPUTER READABLE FORM:
49 MEDIUM TYPE: Floppy disk
50 COMPUTER: IBM PC compatible
51 OPERATING SYSTEM: PC DOS/MS-DOS
52 SOFTWARE: Patent In Release #1.0, Version #1.25
53 CURRENT APPLICATION DATA:
54 APPLICATION NUMBER: US/8/416,253
55 FILING DATE: 30-MAR-1995
56 CLASSIFICATION: 530
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER: US/8/416,035
59 FILING DATE: 10-MAY-1993
60 ATTORNEY/AGENT INFORMATION:
61 NAME: Sharkey, Richard G.
62 REGISTRATION NUMBER: 32,629
63 REFERENCE/DOCKET NUMBER: 940610, 54,
64 TELECOMMUNICATION INFORMATION:
65 TELEPHONE: (206) 622-4900
66 TELEFAX: (206) 682-6031
67 TELEFAX: 3723836
68 INFORMATION FOR SEQ ID NO: 9:
69 SEQUENCE CHARACTERISTICS:
70 LENGTH: 8 amino acids
71 TYPE: amino acid
72 TOPOLOGY: linear
73 MOLECULE TYPE: peptide

1 US-08-416-035-9
2 Query Match 27.3%, Score 3, DB 1, Length 8,
3 Best Local Similarity 100.0%, Pred. No. 2, 5e+05,
4 Matches 3, Conservative 0, Mismatches 0, Indels 0,
5 Gaps 0:
6
7 QY 1 ASK 4
8 11
9 6 ASK 8
10
11 RESULT 48
12 US-08-424-253-13
13 Sequence 13, Application US/80624253
14 Patent No. 5785968
15 GENERAL INFORMATION:
16 APPLICANT: KIMACHI, Kazuhiko
17 APPLICANT: MAEDA, Hiroaki
18 APPLICANT: NISHIYAMA, Kiyoto
19 APPLICANT: TOKIYOSHI, Sachio
20 APPLICANT: TOHYA, Yukinobu
21 APPLICANT: MIKAMI, Takeshi
22 TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT
23 TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
24 NUMBER OF SEQUENCES: 23
25 CORRESPONDENCE ADDRESS:
26 ADDRESSEE: WEDNER, GENTER, MUELLER & PLAYER
27 STREET: 233 20th Street, N.W., Suite 300
28 CITY: Washington
29 STATE: D.C.
30 COUNTRY: U.S.A.
31 ZIP: 20036-8218
32 COMPUTER READABLE FORM:
33 MEDIUM TYPE: Floppy disk
34 COMPUTER: IBM PC compatible
35 OPERATING SYSTEM: PC-DOS/MS DOS
36 SOFTWARE: Patent In Release #1.0, Version #1.25
37 CURRENT APPLICATION DATA:
38 APPLICATION NUMBER: US/8/024,253
39 FILING DATE: 1993-01
40 CLASSIFICATION: 424
41 PRIOR APPLICATION DATA:
42 APPLICATION NUMBER: JP 79189/1992
43 FILING DATE: 28 FEB-1992
44 ATTORNEY/AGENT INFORMATION:
45 NAME: GENTER, Herbert L.
46 REGISTRATION NUMBER: 24,392
47 REFERENCE/DOCKET NUMBER: P-500 23744
48 TELECOMMUNICATION INFORMATION:
49 TELEPHONE: (202) 687-0400
50 TELEFAX: (202) 695-0606
51 TELEFAX: 440736 WPCR
52 INFORMATION FOR SEQ ID NO: 13:
53 SEQUENCE CHARACTERISTICS:
54 LENGTH: 8 amino acids
55 TYPE: amino acid
56 TOPOLOGY: unknown
57 MOLECULE TYPE: protein
58 US-08-024-253-13
59
60 Query Match 27.3%, Score 3, DB 1, Length 8,
61 Best Local Similarity 100.0%, Pred. No. 2, 5e+05,
62 Matches 3, Conservative 0, Mismatches 0, Indels 0,
63 Gaps 0:
64
65 QY 8 NIK 10
66 11
67 1 NIK 4
68
69 RESULT 49
70 US-08-209-261B-1C
71 Sequence 10, Application US/08259261B
72 Patent No. 5759152

```

: GENERAL INFORMATION:
: APPLICANT: Black, Christopher
: APPLICANT: Tosi, Pierre-Francois
: APPLICANT: Atkin, Andrew
: APPLICANT: Lazarre, Jaime E.
: APPLICANT: Nicolau, Yves Claude
: TITLE OF INVENTION: Diagnostic Device and Method
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Jones & Askew
: STREET: 191 Peachtree Street, Ste. 4200
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30333-1769
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.10
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/209,261B
: FILING DATE: 16-MAR-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Stults, Larry W.
: REGISTRATION NUMBER: 34,025
: REFERENCE/DOCKET NUMBER: 05213-0061
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404) 818-3700
: TELEFAX: (404) 818-3799
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-209-261B-10

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Query Match 27.3% Score 3: DB 1: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 8 NIK 10
ID 6 NIK 8

```

```

RESULT 40
US-08-612-302A-19
: Sequence 39, Application US/08/213-0061
: Patent No. 5811297 5780297
: GENERAL INFORMATION:
: APPLICANT: GOPAL, T. Veerkat
: TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER
: NUMBER OF SEQUENCES: 56
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ratner & Pres'rid
: STREET: One Westlakes, Betwyn
: CITY: Valley Forge
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19482
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS DOS 5.0
: SOFTWARE: PatentIn Release #1.0, Version #1.10
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/612,302A
: FILING DATE: 7 March 1996
: CLASSIFICATION: 424

```

```

: ATTORNEY/AGENT INFORMATION:
: NAME: Amzel, Viviana
: REGISTRATION NUMBER: 30,930
: REFERENCE/DOCKET NUMBER: AMBA-020
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (610) 407-6700
: TELEFAX: (610) 407-3701
: TELEX: n.a.
: INFORMATION FOR SEQ ID NO: 39:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: n.a.
: TOPOLOGY: n.a.
: US-08-512-302A-19

Query Match 27.3% Score 3: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
DB 6 KPK 8

RESULT 41
US-08-373-190-48
: Sequence 48, Application US/08373190
: Patent No. 5851829
: GENERAL INFORMATION:
: APPLICANT: MARASCO, WAYNE
: APPLICANT: HASELLINE, WILLIAM
: TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS
: NUMBER OF SEQUENCES: 79
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
: STREET: 140 WAIVER STREET
: CITY: BOSTON
: STATE: MA
: COUNTRY: US
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/373,190
: FILING DATE: 17-JAN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/56735
: FILING DATE: 16-JUL-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: RESNICK, DAVID S.
: REGISTRATION NUMBER: 34,235
: REFERENCE/DOCKET NUMBER: 41956-PCT-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-523-3400
: TELEFAX: 617-523-6440
: TELEX: STRE UR 2002
: INFORMATION FOR SEQ ID NO: 48:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: ORIGINAL SOURCE:
: US-08-373-190-48

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Query Match 27.3%; Score 3; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
 DB 6 KPK 8

RESULT 42
 US-08-968-676-82
 Sequence 82; Application US/08-968676
 Patent No. 5919639
 GENERAL INFORMATION:
 APPLICANT: Humphreys, Robert E.
 APPLICANT: Adams, Sharon
 TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
 NUMBER OF SEQUENCES: 165
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kevin M. Farrell, P.C.
 STREET: P.O. Box 999
 CITY: York Harbor
 STATE: ME
 COUNTRY: USA
 ZIP: 03911
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08-968-676
 FILING DATE: 05-FEB-1997

CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Farrell, Kevin M.
 REGISTRATION NUMBER: 35,505
 REFERENCE/DOCKET NUMBER: REH-9601
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (207) 363-0558
 TELEFAX: (207) 363-0528
 INFORMATION FOR SEQ ID NO: 82:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-968-676-82

Query Match 27.3%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KRN 8
 DB 4 KRN 6

RESULT 43
 US-09-016-365A-47
 Sequence 47; Application US/0901636A
 Patent No. 5955431
 GENERAL INFORMATION:
 APPLICANT: Stevens, Richard L.
 APPLICANT: Huang, Chifu
 TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 NUMBER OF SEQUENCES: 165
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02210-2211
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016.366A
 FILING DATE: January 30, 1998
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/037,090
 FILING DATE: 05-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Plummer, Elizabeth R.
 REGISTRATION NUMBER: 36,647
 REFERENCE/DOCKET NUMBER: R0801/7093
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELEX:
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-016-366A-47

Query Match 27.3%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
 DB 4 PKR 6

RESULT 44
 US-08-438-190A-48
 Sequence 48; Application US/08438190A
 Patent No. 5965371
 GENERAL INFORMATION:
 APPLICANT: MARASCO, WAYNE
 APPLICANT: HASELTINE, WILLIAM
 TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
 TITLE OF INVENTION: PROTEINS
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ADDRESS: CUSHMAN
 STREET: 130 WATER STREET
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: US
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/438.190A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: EISENSTEIN, RONALD L.
 REGISTRATION NUMBER: 30628

REFERENCE/DOCKET NUMBER: 41956
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438 190A-48

Query Match 27.3% Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
DB 5 KPK 8

RESULT 45
US-08-318 856A-3
Sequence 3; Application US/08318856A
Patent No. 5972351
GENERAL INFORMATION:

APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,856A
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068 8
FILING DATE: April 3, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704 7
FILING DATE: August 20, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: April 5, 1993
ATTORNEY/AGENT INFORMATION:

NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 263-PP1R1577US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-8250
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
US-08-318-856A-3

Query Match 27.3% Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
DB 1 KPK 3

RESULT 46
US-08-318-856A-29
Sequence 29; Application US/08318856A
Patent No. 5972351
GENERAL INFORMATION:
APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STA
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,856A
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068 8
FILING DATE: April 3, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704 7
FILING DATE: August 20, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: April 5, 1993
ATTORNEY/AGENT INFORMATION:

NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 263-PP1R1577US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-8250
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-318-856A-29

Query Match 27.3% Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
DB 1 KPK 3

RESULT 47
US-08-318-856A-68
Sequence 68; Application US/08318856A
Patent No. 5972351
GENERAL INFORMATION:

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1  APPLICANT: Adrian V.S. Hill, et al.
2  TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
3  TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
4  TITLE OF INVENTION: ANTIGENS (AS AMENDED)
5  NUMBER OF SEQUENCES: 86
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Wenderoth, Lind & Ponsark, L.L.P.
8  STREET: 2033 K Street, N.W., Suite 800
9  CITY: Washington
10 STATE: D.C.
11 COUNTRY: U.S.A.
12 ZIP: 20006
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: WordPerfect 5.1+
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/418,856A
20 FILING DATE: October 3, 1994
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: GB 92 08 568.8
23 FILING DATE: April 3, 1992
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: GB 92 17 704.7
26 FILING DATE: August 23, 1992
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: WO PCT/GB94/011
29 FILING DATE: April 5, 1995
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Lee Cheng
32 REGISTRATION NUMBER: 40,949
33 REFERENCE/DOCKET NUMBER: 463-PP1R15770S
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (202) 721-8250
36 TELEFAX: (202) 721-8250
37 INFORMATION FOR SEQ ID NO: 68:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 8 amino acid residues
40 TYPE: amino acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: peptide
44 US 08-418 856A-68
45
46 Query Match 27.4% Score 3: DB 2: Length 8:
47 Best Local Similarity 100.0% Pred No 2.5e+05;
48 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
49
50 QY 4 KPK 6
51 ILI
52 DB 1 KPR 3
53
54 RESULT 49
55 US-08-619 013-11
56 Sequence 11, Application US/0819013
57 Patent No. 5,945,522
58 GENERAL INFORMATION:
59 APPLICANT: Chan, Andrew C.
60 TITLE OF INVENTION: B-LINK PROTEINS
61 NUMBER OF SEQUENCES: 13
62 CORRESPONDENCE ADDRESS:
63 ADDRESSEE: Fehr, Wolfgang, Test, Albritton & Herbert
64 STREET: Four Embarcadero Center, Suite 3400
65 CITY: San Francisco
66 STATE: California
67 COUNTRY: United States
68 ZIP: 94111-4187
69 COMPUTER READABLE FORM:
70 MEDIUM TYPE: Floppy disk
71 COMPUTER: IBM PC compatible
72 OPERATING SYSTEM: PC-DOS/MS-DOS
73 SOFTWARE: Patent In Release #1.0, Version #1.30
74 CURRENT APPLICATION DATA:
75 APPLICATION NUMBER: US/08/619,013
76 FILING DATE: 17-MAR-1997
77 CLASSIFICATION: 435
78 PRIOR APPLICATION DATA:
79 APPLICATION NUMBER: US 08/788,322
80 FILING DATE: 24-JAN-1997
81 ATTORNEY/AGENT INFORMATION:
82 NAME: Silva, Robin M.
83 REGISTRATION NUMBER: 38,304
84 REFERENCE/DOCKET NUMBER: A-64383-1/RFT/RMS
85 TELECOMMUNICATION INFORMATION:
86 TELEPHONE: (415) 781-1989

```

```

1  APPLICANT: Adrian V.S. Hill, et al.
2  TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
3  TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
4  TITLE OF INVENTION: ANTIGENS (AS AMENDED)
5  NUMBER OF SEQUENCES: 86
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Wenderoth, Lind & Ponsark, L.L.P.
8  STREET: 2033 K Street, N.W., Suite 800
9  CITY: Washington
10 STATE: D.C.
11 COUNTRY: U.S.A.
12 ZIP: 20006
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: WordPerfect 5.1+
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/418,856A
20 FILING DATE: October 3, 1994
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: GB 92 08 568.8
23 FILING DATE: April 3, 1992
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: GB 92 17 704.7
26 FILING DATE: August 23, 1992
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: WO PCT/GB94/011
29 FILING DATE: April 5, 1995
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Lee Cheng
32 REGISTRATION NUMBER: 40,949
33 REFERENCE/DOCKET NUMBER: 463-PP1R15770S
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (202) 721-8250
36 TELEFAX: (202) 721-8250
37 INFORMATION FOR SEQ ID NO: 68:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 8 amino acid residues
40 TYPE: amino acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: peptide
44 US 08-418 856A-68
45
46 Query Match 27.4% Score 3: DB 2: Length 8:
47 Best Local Similarity 100.0% Pred No 2.5e+05;
48 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
49
50 QY 4 KPK 6
51 ILI
52 DB 1 KPR 3
53
54 RESULT 49
55 US-08-418-856A-69
56 Sequence 69, Application US/0818856A
57 Patent No. 5,972,351
58 GENERAL INFORMATION:
59 APPLICANT: Adrian V.S. Hill, et al.
60 TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
61 TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
62 NUMBER OF SEQUENCES: 86
63 CORRESPONDENCE ADDRESS:
64 ADDRESSEE: Wenderoth, Lind & Ponsark, L.L.P.
65 STREET: 2033 K Street, N.W., Suite 800
66 CITY: Washington
67 STATE: D.C.
68 COUNTRY: U.S.A.
69 ZIP: 20006
70 COMPUTER READABLE FORM:
71 MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb

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Job time : 20.9167 secs

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1 TELEFAX: (415) 398-3249
2 TELEX: 910 277299
3 INFORMATION FOR SEQ ID NO: 11:
4 SEQUENCE CHARACTERISTICS:
5 LENGTH: 8 amino acids
6 TYPE: amino acid
7 STRANDEDNESS: unknown
8 TOPOLOGY: unknown
9 MOLECULE TYPE: protein
10 US-08-819-913-11

Query Match: 27.3% Score 11.00 E-10 Length 8
Best Local Similarity 100.0% Pref No. 2 (3-00)
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKP 5
DB 1 KKP 3

RESULT 50
US-08-482-627-2
1 Sequence 2, Application US/08482627
2 Patent No. 5998134
3 GENERAL INFORMATION:
4 APPLICANT: Lee, Wen-Hwa
5 APPLICANT: Lee, Eva Y-H, P
6 TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor
7 TITLE OF INVENTION: and Regulator
8 NUMBER OF SEQUENCES: 5
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Campbell and Flores
11 STREET: 4370 La Jolla Village Drive, Suite 700
12 CITY: San Diego
13 STATE: California
14 COUNTRY: United States
15 ZIP: 92122
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC Compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.0
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/482-627
23 FILING DATE: 07-JUN-1995
24 CLASSIFICATION: 435
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 07/951,947
27 FILING DATE: 28-SEP-1992
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Campbell, Cathryn A.
30 REGISTRATION NUMBER: 31,815
31 REFERENCE/DOCKET NUMBER: P-UC 1992
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (619) 535-9001
34 TELEFAX: (619) 535-8949
35 INFORMATION FOR SEQ ID NO: 2:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 8 amino acids
38 TYPE: amino acid
39 STRANDEDNESS:
40 TOPOLOGY: Linear
41 US-08-482-627-2

Query Match: 27.3% Score 11.00 E-10 Length 8
Best Local Similarity 100.0% Pref No. 2 (3-00)
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 9 IKA 11
DB 1 IKA 3
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 11.3333 Seconds
(without alignments)
93.340 Million cell updates/sec

Title: US-09-787-443-2

Perfect score: 11

Sequence: 1 AKKEHQKDTQ 1:

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2054

Minimum DB seq length: 8
Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	27.3	9	2 A42266	peptidylglycine mg
2	3	27.3	10	2 F00785	NADH2 dehydrogenas
3	3	27.3	11	2 P03217	T-cell receptor be
4	3	27.3	11	2 P00441	translacion elonga
5	3	27.3	12	2 F64573	hypothetical prote
6	3	27.3	13	2 T05533	hypothetical prote
7	3	27.3	13	2 S22995	hypothetical prote
8	3	27.3	13	2 S47356	T-cell antigen rec
9	3	27.3	13	2 S47357	T-cell antigen rec
10	3	27.3	13	2 S47376	T-cell antigen rec
11	3	27.3	13	2 S47377	T-cell antigen rec
12	3	27.3	13	2 S47378	T-cell antigen rec
13	3	27.3	13	2 S47382	T-cell antigen rec
14	3	27.3	13	2 S47385	T-cell antigen rec
15	3	27.3	13	2 S47392	hypothetical prote
16	3	27.3	13	2 A86126	hypothetical prote
17	3	27.3	14	1 QMVAVV	mastoparan - Yello
18	3	27.3	14	1 QMVAHM	mastoparan M - hor
19	3	27.3	14	1 QMVAHX	mastoparan X - hor
20	3	27.3	14	1 QMVAH2	mastoparan C - hor
21	3	27.3	14	2 S29632	xylan 1,4-beta-xy
22	3	27.3	14	2 B34135	DNA binding protei
23	3	27.3	14	2 PC1215	homeotic protein E
24	3	27.3	14	2 S14336	mastoparan B - hor
25	3	27.3	14	2 PH0135	T-cell receptor be
26	3	27.3	14	2 PH1471	T-cell receptor be
27	3	27.3	14	2 PC0765	T-cell receptor be
28	3	27.3	14	2 PC0779	unidentified 27-2K
29	3	27.3	14	2 F81754	hypothetical prote

30	3	27.3	15	2 S02381	probable membrane
31	3	27.3	15	2 A60156	cellulase (EC 3.2.
32	3	27.3	15	2 PS0450	23K protein 4307 -
33	3	27.3	15	2 PA0076	fructose-bisphosph
34	3	27.3	15	2 PA0061	protein QF200039 -
35	3	27.3	15	2 A49177	22K protein pl, m
36	3	27.3	15	2 S77987	cytochrome-c oxida
37	3	27.3	15	2 PH1788	T cell receptor al
38	3	27.3	15	2 G49655	T-cell receptor be
39	3	27.3	15	2 PH0764	T-cell receptor be
40	3	27.3	15	2 S29175	D-galactose-bindin
41	3	27.3	8	2 B24749	neuropeptide B - b
42	2	18.2	8	2 S37141	rpsA protein - Erw
43	2	18.2	8	2 A21440	variant surface gl
44	2	18.2	8	2 P-0323	Iq heavy chain CRD
45	2	18.2	8	2 I48934	apolipoprotein A-I
46	2	18.2	8	2 A54823	olfactory receptor
47	2	18.2	8	2 PT0653	T-cell receptor be
48	2	18.2	8	2 I48935	apolipoprotein A-I
49	2	18.2	8	2 B54823	olfactory receptor
50	2	18.2	8	2 A61597	cytochrome P450 AL
51	2	18.2	8	2 I57532	gene Tnslow prote
52	2	18.2	8	2 A47618	beta-galactosidase
53	2	18.2	8	2 I64832	Ca2+-transporting
54	2	18.2	8	2 PC1002	leucine-tRNA ligas
55	2	18.2	9	1 Y8PG	thymic factor - pi
56	2	18.2	9	2 A60957	thymocyte growth p
57	2	18.2	9	2 S35538	ribosomal protein
58	2	18.2	9	2 A44873	caldesmon - rabbit
59	2	18.2	9	2 S30494	cat gene leader pe
60	2	18.2	9	2 H24362	chloramphenicol O-
61	2	18.2	9	2 S02384	probable membrane
62	2	18.2	9	2 C36730	hutu protein - Kle
63	2	18.2	9	2 S19523	orf AB protein - S
64	2	18.2	9	2 D57444	neuropeptide Grb-A
65	2	18.2	9	2 A61620	locustamytotropin I
66	2	18.2	9	2 S77984	cytochrome-c oxida
67	2	18.2	9	2 I54379	gene NF2 protein -
68	2	18.2	9	2 PT0315	Ig heavy chain CRD
69	2	18.2	9	2 PC2197	zymogen granule me
70	2	18.2	9	2 C60070	gastrin - domestic
71	2	18.2	9	2 S66635	alpha-2-macroglobu
72	2	18.2	9	2 S66636	alpha-2-macroglobu
73	2	18.2	9	2 C56978	collagen alpha 1(I
74	2	18.2	9	2 S78762	ribosomal protein
75	2	18.2	9	2 PC7076	spectrin alpha cha
76	2	18.2	9	2 PC7078	unidentified 48.7K
77	2	18.2	9	2 PH0943	T-cell receptor be
78	2	18.2	9	2 PH0937	T-cell receptor be
79	2	18.2	9	2 S78426	52.5K protein - sp
80	2	18.2	10	2 S28055	cytochrome b559 co
81	2	18.2	10	2 S39392	calpain (bc 3.4.22
82	2	18.2	10	2 S33844	alpha-2-macroglobu
83	2	18.2	10	2 A60410	beta-neoendorphin
84	2	18.2	10	2 B49581	stathokinin II - ye
85	2	18.2	10	2 A24867	scyllorhinin I - s
86	2	18.2	10	2 D37397	hypothetical prote
87	2	18.2	10	2 JQ0943	hypothetical i.3K
88	2	18.2	10	2 S18396	probable glucose-6
89	2	18.2	10	2 S48182	bacterioferritin -
90	2	18.2	10	2 S70251	nitrogenase (EC 1.
91	2	18.2	10	2 I40032	trpE protein - Bac
92	2	18.2	10	2 F44644	neurotoxin-associa
93	2	18.2	10	2 A44646	neurotoxin-associa
94	2	18.2	10	2 I44644	neurotoxin-associa
95	2	18.2	10	2 JP0072	ribosomal protein
96	2	18.2	10	2 S62880	polygalacturonase
97	2	18.2	10	2 PH0165	triose-phosphate 1
98	2	18.2	10	2 H61308	hemocyanin subunit
99	2	18.2	10	2 A42089	transcription fact
100	2	18.2	10	2 B56899	serum heterodimer,
101	2	18.2	10	2 S43625	cytochrome-c oxida
102	2	18.2	10	2 PT0251	Ig heavy chain CRD

103	2	18.2	10	2	PTC284	Ig heavy chain CRD	176	2	18.2	12	2	SL15815	translation elonga
104	2	18.2	10	2	S23370	T-cell receptor al	177	2	18.2	12	2	SL1298	hemagglutinin prec
105	2	18.2	10	2	F49033	T-cell receptor ga	178	2	18.2	12	2	A44874	proboospectin - fr
106	2	18.2	10	2	S71948	matrix metalloprot	179	2	18.2	12	2	S29859	gene p10 protein -
107	2	18.2	10	2	C54823	factory receptor	180	2	18.2	12	2	A58501	24K p10 protein and bla
108	2	18.2	10	2	PTC664	T-cell receptor be	181	2	18.2	12	2	B58503	outer membrane por
109	2	18.2	10	2	C54823	factory receptor	182	2	18.2	12	2	C49215	urease (EC 3.5.1.5
110	2	18.2	10	2	S65367	cytochrome-c oxida	183	2	18.2	12	2	B44618	extracellular lipa
111	2	18.2	10	2	PH0894	T-cell receptor be	184	2	18.2	12	2	S56122	type 1 DNA methyl
112	2	18.2	10	2	PH0894	T-cell receptor be	185	2	18.2	12	2	S71034	potB protein - Sal
113	2	18.2	10	2	PA4374	telomeric and tetr	186	2	18.2	12	2	S69123	proton-translocat
114	2	18.2	10	2	PA0116	terredxin: NALP re	187	2	18.2	12	2	A40763	sucrose-6-phosphat
115	2	18.2	10	2	P50220	terredxin: NALP re	188	2	18.2	12	2	D28551	hypothetical prote
116	2	18.2	10	2	A44671	maxodehydrascorba	189	2	18.2	12	2	T44420	hypothetical prote
117	2	18.2	10	2	P207P8	NADH2 dehydrogenas	190	2	18.2	12	2	H61497	seed protein ws-17
118	2	18.2	10	2	P207P8	NADH2 dehydrogenas	191	2	18.2	12	2	J00356	cycloleonorin -
119	2	18.2	10	2	EC00C	eledoisin - curled	192	2	18.2	12	2	C34135	DNA-binding protei
120	2	18.2	11	2	EC00C	eledoisin - musky	193	2	18.2	12	2	A33099	163K exoantigen -
121	2	18.2	11	2	A38841	rhodopsin: tomoloq	194	2	18.2	12	2	A56878	light yellow cell
122	2	18.2	11	2	P20662	photosystem 2: 17.5	195	2	18.2	12	2	SI0624	lipovitellin - Afr
123	2	18.2	11	2	B26744	medaschicklin:in -	196	2	18.2	12	2	SI0626	lipovitellin - Afr
124	2	18.2	11	2	D61033	anti protein pha	197	2	18.2	12	2	A34858	proteinase E - bla
125	2	18.2	11	2	S42449	hypothetical prote	198	2	18.2	12	2	S29830	dimethylalanine mo
126	2	18.2	11	2	J60395	quinoline 2-oxid	199	2	18.2	12	2	I39390	acetylcholine rece
127	2	18.2	11	2	S66606	pyrroloquinoline q	200	2	18.2	12	2	S47360	T-cell antigen rec
128	2	18.2	11	2	S56244	hypothetical prote	201	2	18.2	12	2	PH1174	T-cell receptor al
129	2	18.2	11	2	H43669	59K heat shock pro	202	2	18.2	12	2	A49033	T-cell receptor de
130	2	18.2	11	2	PC2372	probable secreted	203	2	18.2	12	2	B49033	T-cell receptor de
131	2	18.2	11	2	S33519	protein: QA300523 -	204	2	18.2	12	2	S74196	3-hydroxy-3-methyl
132	2	18.2	11	2	PTC287	seed protein ws 23	205	2	18.2	12	2	I46922	gene Bata protein
133	2	18.2	11	2	G61497	wound-induced prot	206	2	18.2	12	2	S68402	NAD(+)-glycohydrol
134	2	18.2	11	2	S15775	chaperonin 12 homo	207	2	18.2	12	2	PH1611	Ig H chain V-D-J r
135	2	18.2	11	2	S41742	DNA binding protei	208	2	18.2	12	2	S68271	major urinary prot
136	2	18.2	11	2	A44135	variant surface al	209	2	18.2	12	2	PH0802	T-cell receptor al
137	2	18.2	11	2	A11512	6-phosphofructokin	210	2	18.2	12	2	PH0790	T-cell receptor al
138	2	18.2	11	2	A26120	galbladder stone	211	2	18.2	12	2	PH0931	T-cell receptor be
139	2	18.2	11	2	S57789	Ig heavy chain CRD	212	2	18.2	12	2	PC4377	telomeric and tetr
140	2	18.2	11	2	PTC287	collagen alpha 1(I	213	2	18.2	12	2	S71380	lebetin 1 isoform
141	2	18.2	11	2	D56979	collagen alpha 1(I	214	2	18.2	12	2	I41235	glutamine-tRNA lig
142	2	18.2	11	2	A34573	ribosomal: bov	215	2	18.2	12	2	S21163	NAD ADP-ribosyltra
143	2	18.2	11	2	S28765	6-phosphofructokin	216	2	18.2	12	2	PC0776	NADH2 dehydrogenas
144	2	18.2	11	2	S54457	pyridoxal kinase (217	2	18.2	12	4	JX0315	aminotransferase c
145	2	18.2	11	2	A14454	dystrophin-associa	218	2	18.2	12	4	PC2121	extracellular lipa
146	2	18.2	11	2	A61483	Ig H chain V-D-J r	219	2	18.2	13	2	A44818	ribosomal: protein
147	2	18.2	11	2	PC6664	protein kinase C i	220	2	18.2	13	2	S78519	tubulin beta chain
148	2	18.2	11	2	PH1581	antigen variant	221	2	18.2	13	2	S39413	calreticulin, hepa
149	2	18.2	11	2	PH0044	beta-D-galactosida	222	2	18.2	13	2	A33208	outer membrane pro
150	2	18.2	11	2	PH1376	cytochrome-c oxida	223	2	18.2	13	2	A60336	lactose phosphotra
151	2	18.2	11	2	S53456	T-cell receptor be	224	2	18.2	13	2	E39778	OLL protein - vacc
152	2	18.2	11	2	S65372	T-cell receptor be	225	2	18.2	13	2	PN0122	crabrolin - Europe
153	2	18.2	11	2	PH0934	T-cell receptor be	226	2	18.2	13	2	JZVHP1	VCAM-1 5'UTR bindi
154	2	18.2	11	2	PH0742	T-cell receptor be	227	2	18.2	13	2	A59387	protocatechuate 3,
155	2	18.2	11	2	PH0742	glucamylase Al (E	228	2	18.2	13	2	A60458	oxfx protein - Esc
156	2	18.2	11	2	A48373	hypothetical prote	229	2	18.2	13	2	B36342	argA protein - Sal
157	2	18.2	11	2	H84082	hypothetical prote	230	2	18.2	13	2	S12388	probable endopepti
158	2	18.2	11	2	SI15015	pyrE leader peptid	231	2	18.2	13	2	PC2371	unidentified 85K p
159	2	18.2	12	1	ARECPE	tyrosine 3-monooxy	232	2	18.2	13	2	PC2369	spore proteinase g
160	2	18.2	12	2	PH0577	tyrosine 3-monooxy	233	2	18.2	13	2	A61288	phloroglucinol red
161	2	18.2	12	2	PH0578	tyrosine 3-monooxy	234	2	18.2	13	2	A32453	ribosomal: protein
162	2	18.2	12	2	PH0579	tyrosine 3-monooxy	235	2	18.2	13	2	S36887	protein QA300045 -
163	2	18.2	12	2	PH0580	tyrosine 3-monooxy	236	2	18.2	13	2	PA0031	protein QA300052 -
164	2	18.2	12	2	PH0581	tyrosine 3-monooxy	237	2	18.2	13	2	PA0023	20K protein - rape
165	2	18.2	12	2	PH0576	proteasome chain i	238	2	18.2	13	2	S28425	2S albumin large c
166	2	18.2	12	2	S09384	urease (EC 3.5.1.5	239	2	18.2	13	2	S09716	photosystem I 13K
167	2	18.2	12	2	A49215	fructose-bisphosph	240	2	18.2	13	2	S00316	hypothetical 1.6K
168	2	18.2	12	2	A26856	1-aminocyclopropan	241	2	18.2	13	2	JQ2109	protein L7 - commo
169	2	18.2	12	2	C36201	T-cell receptor be	242	2	18.2	13	2	B44957	hypothetical 1.6K
170	2	18.2	12	2	S26555	T-cell receptor be	243	2	18.2	13	2	JQ2319	hypothetical prote
171	2	18.2	12	2	S26556	T-cell receptor be	244	2	18.2	13	2	JQ1350	GTP-binding protei
172	2	18.2	12	2	S26554	histone H2B - kuma	245	2	18.2	13	2	S29488	deoxynucleotidyltr
173	2	18.2	12	2	S65409	translation elonga	246	2	18.2	13	2	I84603	Ig heavy chain CRD
174	2	18.2	12	2	G49410		247	2	18.2	13	2	PT0305	Ig kappa chain V-I
175	2	18.2	12	2	S01222		248	2	18.2	13	2	B61458	

249	2	18.2	13	2	A61458	Ig kappa chain V-1	322	2	18.2	14	2	A23996	beta-granin - rat
250	2	18.2	13	2	PL0157	Ig kappa chain V-1	323	2	18.2	14	2	A37789	heat shock cognate
251	2	18.2	13	2	G61458	Ig lambda chain V-	324	2	18.2	14	2	PC4376	telomeric and tetr
252	2	18.2	13	2	S61798	T-cell-specific tr	325	2	18.2	14	2	S68095	calcium-binding pr
253	2	18.2	13	2	G56046	urinary tract ston	326	2	18.2	14	2	PC4382	dehydrin 4.5K poly
254	2	18.2	13	2	A39836	aggreccin - bovine	327	2	18.2	14	2	H83778	hypothetical prote
255	2	18.2	13	2	PH5595	Ig H chain V-D-J r	328	2	18.2	14	2	B83836	hypothetical prote
256	2	18.2	13	2	G32265	Ig heavy chain C r	329	2	18.2	14	2	S39931	S-allele-associate
257	2	18.2	13	2	D37267	Ig heavy chain C r	330	2	18.2	14	2	S39930	S-allele-associate
258	2	18.2	13	2	PH0788	T-cell receptor al	331	2	18.2	14	2	F81280	H-transferring tw
259	2	18.2	13	2	PN0348	unidentified QM02	332	2	18.2	14	2	F33160	probable proteolys
260	2	18.2	13	2	G61576	ribosomal protein	333	2	18.2	14	2	S21747	H-transferring tw
261	2	18.2	13	2	H85575	hypothetical prote	334	2	18.2	14	2	PA0044	glutamate dehydrog
262	2	18.2	13	2	S01304	H-transferring tw	335	2	18.2	14	2	S21241	NADH2 dehydrogenas
263	2	18.2	14	1	BSTG	lombesin - fire-be	336	2	18.2	15	2	S21240	oligo-1,6-glucosid
264	2	18.2	14	1	QMWAPP	polistes mas-opara	337	2	18.2	15	2	S21202	glucan 1,4-alpha-g
265	2	18.2	14	2	PC2373	probable IMP dehyd	338	2	18.2	15	2	A47146	topoisomerase I -
266	2	18.2	14	2	C40944	hypothetical prote	339	2	18.2	15	2	A49155	glucan 1,4-alpha-g
267	2	18.2	14	2	S39332	S-allele-associate	340	2	18.2	15	2	S26518	vasotocin-associat
268	2	18.2	14	2	JN0389	histamine releasin	341	2	18.2	15	2	S26531	T-cell receptor al
269	2	18.2	14	2	S14332	histone H4-1 prec	342	2	18.2	15	2	PN0118	T-cell receptor al
270	2	18.2	14	2	A44515	Irf EG leader pept	343	2	18.2	15	2	A38304	hemoglobin beta ch
271	2	18.2	14	2	A32654	fibrinopeptide A -	344	2	18.2	15	2	S16888	heterogeneous ribo
272	2	18.2	14	2	GH0328	probrusin tetradec	345	2	18.2	15	2	A28497	ribosomal protein
273	2	18.2	14	2	S54945	gene C protein - E	346	2	18.2	15	2	S158116	neurotensin-relate
274	2	18.2	14	2	S53388	Km(1) protein - ES	347	2	18.2	15	2	S146512	Dp116 - human
275	2	18.2	14	2	A41589	25K elastin bindin	348	2	18.2	15	2	S149407	troponin - rabbit
276	2	18.2	14	2	S63535	amy-opallulohase -	349	2	18.2	15	2	H33208	placental calcium-
277	2	18.2	14	2	T46634	acyl carrier prote	350	2	18.2	15	2	JP0101	calreticulin, uter
278	2	18.2	14	2	S58862	botulinum neurotox	351	2	18.2	15	2	S129501	fibrinogen alpha c
279	2	18.2	14	2	S58866	botulinum neurotox	352	2	18.2	15	2	S65717	fibrinopeptide A -
280	2	18.2	14	2	S36892	ribosomal protein	353	2	18.2	15	2	PG0681	prostaglandin D-sy
281	2	18.2	14	2	S48685	extension protein	354	2	18.2	15	2	PG0692	photosystem I 19.0
282	2	18.2	14	2	S13864	methyl coenzyme M	355	2	18.2	15	2	PM0004	photosystem I 18.5
283	2	18.2	14	2	S29783	hypothetical prote	356	2	18.2	15	2	PG0617	chlorophyll a/b-bi
284	2	18.2	14	2	PA0109	protein for 13 - Ara	357	2	18.2	15	2	S140665	terminal protein -
285	2	18.2	14	2	PA0045	protein for1 - Arabi	358	2	18.2	15	2	J16610	ilvBN leader pepti
286	2	18.2	14	2	PT0026	calotropis Di - mu	359	2	18.2	15	2	PN0629	leukocyte chemoatt
287	2	18.2	14	2	PN0147	omega-gliadin 1 d	360	2	18.2	15	2	S21411	integration host f
288	2	18.2	14	2	S31951	omega-gliadin 2	361	2	18.2	15	2	S71920	modulation protein
289	2	18.2	14	2	S31951	chaperone, Tcpl-re	362	2	18.2	15	2	A15389	proteinase ECP 32
290	2	18.2	14	2	S31902	chaperone, Tcpl-re	363	2	18.2	15	2	S33781	urease (EC 3.5.1.5
291	2	18.2	14	2	S33803	chaperone, Tcpl-re	364	2	18.2	15	2	E41383	acetylactate synth
292	2	18.2	14	2	S35267	acetyl CoA carboxy	365	2	18.2	15	2	C41383	23K variable histo
293	2	18.2	14	2	A39239	actin 5 - slime mo	366	2	18.2	15	2	A56863	32K variable histo
294	2	18.2	14	2	PA1001	protein QE203026	367	2	18.2	15	2	A17340	photosystem I reac
295	2	18.2	14	2	PA1004	protein QE203076	368	2	18.2	15	2	S36891	ribonucleoside-dip
296	2	18.2	14	2	A61308	benzoylanin chain 2	369	2	18.2	15	2	S36890	ribosomal protein
297	2	18.2	14	2	G61308	benzoylanin chain 3	370	2	18.2	15	2	S36889	ribosomal protein
298	2	18.2	14	2	B61306	benzoylanin chain 4	371	2	18.2	15	2	A48372	benzoyl-CoA liase
299	2	18.2	14	2	S03150	benzoylanin chain 5	372	2	18.2	15	2	T09463	ribosomal protein
300	2	18.2	14	2	S03150	benzoylanin chain 5	373	2	18.2	15	2	A28965	ribulose-bisphosph
301	2	18.2	14	2	S4284	glutathione - duck f	374	2	18.2	15	2	PA0040	malate dehydrogena
302	2	18.2	14	2	PT0252	Ig heavy chain CkO	375	2	18.2	15	2	PA0018	photosystem I 9K p
303	2	18.2	14	2	PT0254	Ig heavy chain CkO	376	2	18.2	15	2	PA0001	photosystem I iron
304	2	18.2	14	2	PT0294	Ig heavy chain CkO	377	2	18.2	15	2	PA0029	protein QA100012 -
305	2	18.2	14	2	S23639	Ig kappa chain J s	378	2	18.2	15	2	PA0020	protein QA100028 -
306	2	18.2	14	2	S57567	I cell receptor V-	379	2	18.2	15	2	PA0046	protein QA100044 -
307	2	18.2	14	2	A49039	T-cell receptor be	380	2	18.2	15	2	PA0034	protein QA300050 -
308	2	18.2	14	2	A28018	very late antigen-	381	2	18.2	15	2	PT0082	protein QA600023 -
309	2	18.2	14	2	B28018	very late antigen-	382	2	18.2	15	2	PA0009	seed storage prote
310	2	18.2	14	2	PT0040	glycogen phosphory	383	2	18.2	15	2	A56970	GLYMA1 - soybean (
311	2	18.2	14	2	A47421	leukotriene B-4 12	384	2	18.2	15	2	PA0006	lectin A3 - Psopho
312	2	18.2	14	2	F48354	glycoprotein compo	385	2	18.2	15	2	PA0008	lectin B2 - Psopho
313	2	18.2	14	2	C44824	synaptosomal-assoc	386	2	18.2	15	2	PN0148	omega-gliadin 3 -
314	2	18.2	14	2	A65032	troponin T, cardia	387	2	18.2	15	2	S50218	24K protein 4413 -
315	2	18.2	14	2	PH1617	Ig H chain V-D-J r	388	2	18.2	15	2	PC4268	alpha-globulin - r
316	2	18.2	14	2	PH1598	Ig H chain V-D-J r	389	2	18.2	15	2	PA0114	photosystem I, iro
317	2	18.2	14	2	PH0792	T cell receptor al	390	2	18.2	15	2	PA0057	adenylate isopente
318	2	18.2	14	2	PH0800	T-cell receptor al	391	2	18.2	15	2	PA0087	cytochrome c2 - fu
319	2	18.2	14	2	PH0795	T-cell receptor al	392	2	18.2	15	2	PA0093	enninatin synthetas
320	2	18.2	14	2	PT5210	T-cell receptor al	393	2	18.2	15	2	PA0102	fructose-bisphosph
321	2	18.2	14	2	PH0762	T-cell receptor be	394	2	18.2	15	2	PA0105	heat shock protein

395	2	18.2	15	2	PA0553	protein GF250C06 -
396	2	18.2	15	2	PA0552	protein GF250C05 -
397	2	18.2	15	2	PA0554	protein GF250C07 -
398	2	18.2	15	2	PA0556	protein GF250C02 -
399	2	18.2	15	2	PA0586	protein GF250C04 -
400	2	18.2	15	2	PA0544	serine proteinase
401	2	18.2	15	2	PA0544	serine proteinase
402	2	18.2	15	2	PA0573	serine proteinase
403	2	18.2	15	2	PA0573	serine proteinase
404	2	18.2	15	2	PA0573	serine proteinase
405	2	18.2	15	2	PA0573	serine proteinase
406	2	18.2	15	2	PA0573	serine proteinase
407	2	18.2	15	2	PA0573	serine proteinase
408	2	18.2	15	2	PA0573	serine proteinase
409	2	18.2	15	2	PA0573	serine proteinase
410	2	18.2	15	2	PA0573	serine proteinase
411	2	18.2	15	2	PA0573	serine proteinase
412	2	18.2	15	2	PA0573	serine proteinase
413	2	18.2	15	2	PA0573	serine proteinase
414	2	18.2	15	2	PA0573	serine proteinase
415	2	18.2	15	2	PA0573	serine proteinase
416	2	18.2	15	2	PA0573	serine proteinase
417	2	18.2	15	2	PA0573	serine proteinase
418	2	18.2	15	2	PA0573	serine proteinase
419	2	18.2	15	2	PA0573	serine proteinase
420	2	18.2	15	2	PA0573	serine proteinase
421	2	18.2	15	2	PA0573	serine proteinase
422	2	18.2	15	2	PA0573	serine proteinase
423	2	18.2	15	2	PA0573	serine proteinase
424	2	18.2	15	2	PA0573	serine proteinase
425	2	18.2	15	2	PA0573	serine proteinase
426	2	18.2	15	2	PA0573	serine proteinase
427	2	18.2	15	2	PA0573	serine proteinase
428	2	18.2	15	2	PA0573	serine proteinase
429	2	18.2	15	2	PA0573	serine proteinase
430	2	18.2	15	2	PA0573	serine proteinase
431	2	18.2	15	2	PA0573	serine proteinase
432	2	18.2	15	2	PA0573	serine proteinase
433	2	18.2	15	2	PA0573	serine proteinase
434	2	18.2	15	2	PA0573	serine proteinase
435	2	18.2	15	2	PA0573	serine proteinase
436	2	18.2	15	2	PA0573	serine proteinase
437	2	18.2	15	2	PA0573	serine proteinase
438	2	18.2	15	2	PA0573	serine proteinase
439	2	18.2	15	2	PA0573	serine proteinase
440	2	18.2	15	2	PA0573	serine proteinase
441	2	18.2	15	2	PA0573	serine proteinase
442	2	18.2	15	2	PA0573	serine proteinase
443	2	18.2	15	2	PA0573	serine proteinase
444	2	18.2	15	2	PA0573	serine proteinase
445	2	18.2	15	2	PA0573	serine proteinase
446	2	18.2	15	2	PA0573	serine proteinase
447	2	18.2	15	2	PA0573	serine proteinase
448	2	18.2	15	2	PA0573	serine proteinase
449	2	18.2	15	2	PA0573	serine proteinase
450	2	18.2	15	2	PA0573	serine proteinase
451	2	18.2	15	2	PA0573	serine proteinase
452	2	18.2	15	2	PA0573	serine proteinase
453	2	18.2	15	2	PA0573	serine proteinase
454	2	18.2	15	2	PA0573	serine proteinase
455	2	18.2	15	2	PA0573	serine proteinase
456	2	18.2	15	2	PA0573	serine proteinase
457	2	18.2	15	2	PA0573	serine proteinase
458	2	18.2	15	2	PA0573	serine proteinase
459	2	18.2	15	2	PA0573	serine proteinase
460	2	18.2	15	2	PA0573	serine proteinase
461	2	18.2	15	2	PA0573	serine proteinase
462	2	18.2	15	2	PA0573	serine proteinase
463	2	18.2	15	2	PA0573	serine proteinase
464	2	18.2	15	2	PA0573	serine proteinase
465	2	18.2	15	2	PA0573	serine proteinase
466	2	18.2	15	2	PA0573	serine proteinase
467	2	18.2	15	2	PA0573	serine proteinase

ALIGNMENTS

RESULT: 1
 A42266
 peptidylglycine monooxygenase (EC 1.14.17.3), rPAM-5 - rat (fragment)
 N:Altozate names: peptidylglycine alpha-amidating monooxygenase
 C:Species: Rattus norvegicus (Norway rat)
 G:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-1995
 G:Accession: A42266
 R:Ripper, B.A.; Green, C.B.; Campbell, T.A.; Stoffers, D.A.; Keutmann, H.T.; Mains, J.; Biol. Chem. 267, 4008-4015, 1992
 A:Title: Alternative splicing and endoproteolytic processing generate tissue-specific
 A:Reference: Rattus norvegicus (Norway rat)
 A:Accession: A42266
 A:Species: Rattus norvegicus (Norway rat)
 A:Molecule type: mRNA
 A:Accession: A42266
 A:Keywords: oxidoreductase

Query Match: 27.8% Score 3; DB 2; Length 9;
 Best Local Similarity: 100.0% Pred No 2.8e-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY R KD: 10
 ID 6 KD: 5

RESULT 2

P02785
 NAM2 glyoxylate reductase (EC 1.1.1.93) 27K chain - fava bean mitochondrion (fragment)
 N:Altozate names: complex 1 27K chain; NADH-ubiquinone reductase 27K chain
 C:Species: mitochondrion, Fava faba (fava bean)
 G:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 03-Jun-2002
 G:Accession: P02785

Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 6 AKK 8

RESULT 8

S47356
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47356
K:Lehner, P.J.

submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47356
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35680; NID:q527449; PIDN:CAA4749.1; PID:q527450
C:Keywords: T-cell receptor

Query Match 27.8%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 9

S47357
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47357
K:Lehner, P.J.

submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47357
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35681; NID:q527451; PIDN:CAA4750.1; PID:q527452
C:Keywords: T-cell receptor

Query Match 27.8%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 10

S47376
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47376
K:Lehner, P.J.

submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47376
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35702; NID:q527497; PIDN:CAA84771.1; PID:q527498
C:Keywords: T-cell receptor

Query Match 27.8%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 11

S47377
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47377
K:Lehner, P.J.

submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by
A:Reference number: S47355
A:Accession: S47377
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35703; NID:q527505; PIDN:CAA84775.1; PID:q527506
C:Keywords: T-cell receptor

Query Match 27.8%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 12

S47378
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47378
K:Lehner, P.J.

submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by
A:Reference number: S47355
A:Accession: S47378
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35707; NID:q527507; PIDN:CAA84776.1; PID:q527508
C:Keywords: T-cell receptor

Query Match 27.8%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 13

S47382
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47382; S47370
K:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by T
 A:Reference number: S47355
 A:Accession: S47382
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-13 <LEH>
 A:Cross-references: EMBL:235687; NID:q527463; FIDN:AA84756.1; PID:q527464; EMBL:235695;
 C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
 III
 Db 9 DTQ 11

RESULT 14
 S47385
 T cell antigen receptor VJ junction beta chain - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05 Nov 1999
 C:Accession: S47385
 A:Reference number: S47385
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-13 <LEH>
 A:Cross-references: EMBL:235705; NID:q527503; FIDN:AA84774.1; PID:q527504
 C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
 III
 Db 9 DTQ 11

RESULT 15
 S47392
 T-cell antigen receptor VJ junction beta chain - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05 Nov-1999
 C:Accession: S47392
 A:Reference number: S47392
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-13 <LEH>
 A:Cross-references: EMBL:235713; NID:q527561; FIDN:AA84782.1; PID:q527522
 C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
 III
 Db 9 DTQ 11

RESULT 16
 A86126
 hypothetical protein 25883 [imported], Escherichia coli (strain 0157:H7, substrain EDL9

A:Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by T
 A:Reference number: S47355
 A:Accession: S47392
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-13 <LEH>
 A:Cross-references: EMBL:235713; NID:q527561; FIDN:AA84782.1; PID:q527522
 C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
 III
 Db 9 DTQ 11

C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: A86126
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; M
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou, K.; Apo
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A55480; MUID:2107935; PMID:11206551
 A:Accession: A86126
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-13 <STH>
 A:Cross-references: GB:AF005174; NID:q12519285; PIDN:AAG59469.1; GSPDR:GN00145; UWG
 A:Experimental source: Strain 0157:H7, substrain EDL933
 C:Genetics:
 A:Gene: 25883

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
 III
 Db 8 AKK 10

RESULT 17
 QMVAV
 mastoparan yellowjacket (Vespula lewisii)
 C:Species: Vespula lewisii
 C:Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 08-Dec-1995
 C:Accession: A01776
 R:Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.; Fujino, M.; Kitada, C.
 Chem. Pharm. Bull. 27, 1942-1944, 1979
 A:Title: A new mast cell degranulating peptide mastoparan in the venom of Vespula-1
 A:Reference number: A01776; MUID:80155337; PMID:540362
 A:Accession: A01776
 A:Molecule type: protein
 A:Residues: 1-14 <HIR>
 A:Note: the active peptide was also synthesized
 C:Comment: This cytoactive peptide from wasp venom induces mast cell degranulation
 C:Superfamily: mastoparan
 C:Keywords: amidated carboxyl end
 F.14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 27.3% Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
 III
 Db 10 AKK 12

RESULT 18
 OMVHM
 mastoparan M - hornet (Vespa mandarinia)
 N:Alternate names: mast cell-degranulating peptide
 C:Species: Vespa mandarinia
 C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 08-Dec-1995
 C:Accession: A01777
 R:Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
 Biomed. Res. 2, 447-449, 1981
 A:Title: A new mast cell degranulating peptide, mastoparan-M, in the venom of the h
 A:Reference number: A01777
 A:Accession: A01777
 A:Molecule type: protein
 A:Residues: 1-14 <HIR>
 C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation
 C:Superfamily: mastoparan
 C:Keywords: amidated carboxyl end; venom
 F.14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 27.3% Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
 III
 Db 10 AKK 12

RESULT 19
 OMVHM
 mastoparan M - hornet (Vespa mandarinia)
 N:Alternate names: mast cell-degranulating peptide
 C:Species: Vespa mandarinia
 C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 08-Dec-1995
 C:Accession: A01777
 R:Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
 Biomed. Res. 2, 447-449, 1981
 A:Title: A new mast cell degranulating peptide, mastoparan-M, in the venom of the h
 A:Reference number: A01777
 A:Accession: A01777
 A:Molecule type: protein
 A:Residues: 1-14 <HIR>
 C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation
 C:Superfamily: mastoparan
 C:Keywords: amidated carboxyl end; venom
 F.14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 27.3% Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
 III
 Db 10 AKK 12

RESULT 20
 OMVHM
 mastoparan M - hornet (Vespa mandarinia)
 N:Alternate names: mast cell-degranulating peptide
 C:Species: Vespa mandarinia
 C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 08-Dec-1995
 C:Accession: A01777
 R:Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
 Biomed. Res. 2, 447-449, 1981
 A:Title: A new mast cell degranulating peptide, mastoparan-M, in the venom of the h
 A:Reference number: A01777
 A:Accession: A01777
 A:Molecule type: protein
 A:Residues: 1-14 <HIR>
 C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation
 C:Superfamily: mastoparan
 C:Keywords: amidated carboxyl end; venom
 F.14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 27.3% Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
 III
 Db 10 AKK 12

RESULT 21
 OMVHM
 mastoparan M - hornet (Vespa mandarinia)
 N:Alternate names: mast cell-degranulating peptide
 C:Species: Vespa mandarinia
 C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 08-Dec-1995
 C:Accession: A01777
 R:Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
 Biomed. Res. 2, 447-449, 1981
 A:Title: A new mast cell degranulating peptide, mastoparan-M, in the venom of the h
 A:Reference number: A01777
 A:Accession: A01777
 A:Molecule type: protein
 A:Residues: 1-14 <HIR>
 C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation
 C:Superfamily: mastoparan
 C:Keywords: amidated carboxyl end; venom
 F.14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 27.3% Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
 III
 Db 10 AKK 12

RESULT 22
 OMVHM
 mastoparan M - hornet (Vespa mandarinia)
 N:Alternate names: mast cell-degranulating peptide
 C:Species: Vespa mandarinia
 C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 08-Dec-1995
 C:Accession: A01777
 R:Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
 Biomed. Res. 2, 447-449, 1981
 A:Title: A new mast cell degranulating peptide, mastoparan-M, in the venom of the h
 A:Reference number: A01777
 A:Accession: A01777
 A:Molecule type: protein
 A:Residues: 1-14 <HIR>
 C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation
 C:Superfamily: mastoparan
 C:Keywords: amidated carboxyl end; venom
 F.14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 27.3% Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
 III
 Db 10 AKK 12


```

Query Match      27.3% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 3
DB      10 AKK 12

RESULT 19
QWVHX
mastoparan X hornet (Vespa xanthoptera)
C:Species: Vespa xanthoptera
C:Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 06-Dec-1995
C:Accession: A01778
Kikurai, Y.; Kawada, M.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 27, 1945-1946, 1979
A:Title: A new mast cell degranulating peptide homologous to mastoparan in the venom of
A:Reference number: A01778; MUI0:86155438; PMID:54367
A:Accession: A01778
A:Molecule type: protein
A:Residues: 1-14 <HR>
C:Comment: This cytotoxic peptide from hornet venom induces mast cell degranulation.
C:Superfamily: mastoparan
C:Keywords: amidated carboxyl end
F:14/Modified site: amidated carboxyl end (len) #status experimental

Query Match      27.3% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 3
DB      10 AKK 12

RESULT 20
QWVHX
mastoparan C European hornet
C:Species: Vespa crabro (European hornet)
C:Date: 28-Feb-1986 #sequence_revision 26-Feb-1999 #text_change 06-Dec-1995
C:Accession: A01779
R:Argiolas, A.; Pisano, J.J.
J. Biol. Chem. 259, 10106-10111, 1984
A:Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin.
A:Reference number: A32441; MUI0:84289493; PMID:6266393
A:Accession: A01779
A:Molecule type: protein
A:Residues: 1-14 <ARG>
C:Comment: This cytotoxic peptide from hornet venom induces mast cell degranulation.
C:Superfamily: mastoparan
C:Keywords: amidated carboxyl end; venom
F:14/Modified site: amidated carboxyl end (len) #status experimental

Query Match      27.3% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 3
DB      10 AKK 12

RESULT 21
S29632
xylan 1,4-beta xylosidase (EC 3.2.1.4) - Thermotoga sp. (strain FJSS-B.1) (fragment)
N:Alternate names: beta-xylosidase
C:Species: Thermotoga sp.
A:Variety: FJSS-B.1
C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 18-Jun-1999
C:Accession: S29632
R:Ruttersmith, L.B.; Daniel, R.M.
Biochim. Biophys. Acta 1156, 167-172, 1993

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A:Title: Thermostable beta-glucosidase and beta-xylosidase from Thermotoga sp. strain
A:Reference number: S29631; MUI0:93152594; PMID:8427876
A:Accession: S29632
A:Molecule type: protein
A:Residues: 1-14 <RUI>
C:Comment: Although the beta-xylosidase enzyme activity was apparently confirmed for
C:Function:
A:Description: hydrolyzes short chain oligosaccharides and xylobiose to produce D-xyl
A:Note: plays an important role in the relief of end-product inhibition of endoxylan
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match      27.3% Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 3
DB      1 AKK 3

RESULT 22
B34135
DNA-binding protein q Crithidia fasciculata mitochondrion (fragment)
C:Species: mitochondrion Crithidia fasciculata
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999
C:Accession: B34135
R:Tittawella, L.
FEBS Lett. 260, 57-63, 1990
A:Title: Kinetoplast DNA-acquiring proteins from the parasitic protozoan Crithidia
A:Reference number: A34135
A:Accession: B34135
A:Molecule type: protein
A:Residues: 1-14 <IIT>
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SCS6
C:Keywords: mitochondrion

Query Match      27.3% Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 3
DB      6 AKK 8

RESULT 23
PCL215
homeotic protein Egrbx5 - tapeworm (Echinococcus granulosus) (fragment)
C:Species: Echinococcus granulosus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C:Accession: PCL215
R:Oliver, G.; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Flietiz, W.; Et
Gene 121, 337-342, 1992
A:Title: Homeoboxes in flatworms.
A:Reference number: JCL386; MUI0:93077050; PMID:1359988
A:Accession: PCL215
A:Molecule type: DNA
A:Residues: 1-14 <CHI>
A:Cross-references: EMBL:X66821
C:Keywords: homeobox

Query Match      27.3% Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 KER 5
DB      9 KER 11

```

```

RESULT 24
SI4336
Masoparan, P. hornet (Vespa basalis)
C:Species: Vespa basalis
C:Date: 19 Mar 1997 #sequence_revision 19-Mar-1997 #text_change 09-Apr-1999
C:Accession: SI4336
R:Bio, C:Loc: Huang, J.-L.
Biochem. J. 274, 453-456, 1991
A:Title: Structure and biological activities of a new masoparan isolated from the venom
A:Reference number: SI4336; MUID:4174755; PMID:2006909
A:Accession: SI4336
A:Molecule type: protein
A:Residues: 1-14 <acc>
A:Experimental source: venom
C:Function:
A:Description: possesses a potent hemolytic activity which acts in synergy with the lethal
A:Keywords: amidated carboxyl end; mast cell; venom
F:14/Modified site: amidated carboxyl end (acc); stat is experimental

Query Match 27.3%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 10 AKK 12

RESULT 25
PH0135
T-cell receptor beta chain V-D J region: MS1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 10-May-1997
C:Accession: PH0135
R:Martin, K.; Howell, M.D.; Jaraquemada, D.; Flierlango, M.; Kiehlert, J.; Brostoff, S.; Lo
J. Exp. Med. 173, 19-24, 1991
A:Title: A myelin basic protein peptide is immunoreactivity cytotoxic T cells in the context
A:Reference number: PH0135; MUID:91086943; PMID:1702117
A:Accession: PH0135
A:Molecule type: mRNA
A:Residues: 1-14 <MAR>
C:Keywords: T-cell receptor

Query Match 27.3%; Score 4; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 11 DTQ 14

RESULT 26
PH1471
T-cell receptor beta chain (clone A24/0744) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1471
R:Casanova, J.L.; Martinon, F.; Goubetier, H.; Barthelemy, C.; Pannetier, C.; Kiehlert, A.; Kie
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of a two class I major histocompatib
A:Reference number: PH1430; MUID:9371742; PMID:1210111
A:Accession: PH1471
A:Molecule type: mRNA
A:Residues: 1-14 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Support family: immunoglobulin hemolysis
C:Keywords: receptor; T-cell

Query Match 27.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 27
PH0765
T-cell receptor beta chain (HL) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0765
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility comp
A:Allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0765
A:Molecule type: mRNA
A:Residues: 1-14 <CAS>
A:Cross-references: EXHL:X60859; NID:g51139; PIDN:CAA43249.1; PID:g51140
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 28
PC7079
unidentified 27.2K protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: PC7079
R:Tsuqita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe,
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles
A:Reference number: PC7072
A:Accession: PC7079
A:Molecule type: protein
A:Residues: 1-14 <ISU>
A:Experimental source: strain C57BL/6Cr Slc, male; brain; striatum
C:Keywords: brain

Query Match 27.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
DB 7 KKE 9

RESULT 29
FB3754
Hypothetical protein BB0848 (imported) - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: FB3754
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, K.; Masui, N.; Fujii, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A:Reference number: A94630; MUID:20512582; PMID:11058132
A:Accession: FB3754
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <SLH>
A:Cross references: GNAI001310; GNAI000004; NID:g10173440; PIDN:BA004557.1; GSPDB
A:Experimental source: strain C-125

```

C:Accession: B00548
 Query Match 27.4% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 KDT 10
 DB 2 KDT 4
 RESULT 40
 S02383
 Probable membrane antigen CUL - human herpesvirus 4 (fragment)
 C:Species: human herpesvirus 4; Epstein-Barr virus
 C:Date: 01-Dec-1989 #sequence_revision 6; text_change 06-Feb-1999
 C:Accession: S02381
 R:Wallis, D.; Cannon, F.
 EMBO J. 7, 1191-1196, 1988
 A:Title: The expression of novel antigens from the Epstein Barr virus large internal repeat
 A:Reference number: S02381; M010:88296424; PMID:284116
 A:Accession: S02381
 A:Molecule type: DNA
 A:Residues: 1-15 <SWAL>
 A:Cross references: EMBL:X07814; NID:059167; with CAA30731; P11039605;
 C:Keywords: membrane protein; surface antigen
 Query Match 27.4% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 KDT 7
 DB 1 KDT 13
 RESULT 41
 A60156
 Cellulase (EC 3.2.1.4) - Clostridium hist. (fragment)
 N:Alternate names: endo-1,4-beta-glucanase
 C:Species: Clostridium jesi
 C:Date: 22-Jan-1993 #sequence_revision 22 Jan 1993 #text_change 22-Nov-1995
 C:Accession: A60156
 R:Fujino, T.; Sasaki, T.; Ohmiva, K.; Shimizu, S.
 Appl. Environ. Microbiol. 56, 1175-1178, 1990
 A:Title: Purification and properties of an endo-1,4-beta-glucanase translocated from a Clo
 A:Reference number: A60156; M010:625056; PMID:216354
 A:Accession: A60156
 A:Molecule type: protein
 A:Residues: 1-15 <FUD>
 C:Function:
 A:Description: hydrolysis of 1,4-beta-D-glucan. It is an enzyme that breaks down polysaccharides such as ce
 A:Pathway: cellulose degradation
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 Query Match 27.4% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKK 3
 DB 1 AKK 15
 RESULT 42
 PS0450
 23K protein p1, mitochondrial - Crithidia fasciculata (fragment)
 C:Species: Crithidia fasciculata
 C:Date: 03-Feb-1994 #sequence_revision 6; Feb-1994 #text_change 11-Apr-1995
 C:Accession: PS0450
 R:Tsuigita, A.; Miyatake, N.
 submitted to JIPID, April 1995

A:Reference number: PS0208
 A:Accession: PS0450
 A:Molecule type: protein
 A:Residues: 1-15 <TSU>
 A:Experimental source: germ. strain Nihonbare
 C:Comment: molecular weight 23K, pI 5.3.
 Query Match 27.4% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KDT 9
 DB 8 KDT 10
 RESULT 43
 PA0076
 Fructose-bisphosphate aldolase (EC 4.1.2.13) - fungus (Fusarium sporotrichioides) (f
 C:Species: Fusarium sporotrichioides
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C:Accession: PA0076
 R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporot
 A:Reference number: PA0051
 A:Accession: PA0076
 A:Molecule type: protein
 A:Residues: 1-15 <CHO>
 C:Keywords: aldehyde-lyase; carbon-carbon lyase
 Query Match 27.4% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KDT 5
 DB 6 KDT 10
 RESULT 44
 PA0061
 Protein QF200639 - fungus (Fusarium sporotrichioides) (fragment)
 C:Species: Fusarium sporotrichioides
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C:Accession: PA0061
 R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporot
 A:Reference number: PA0061
 A:Accession: PA0061
 A:Molecule type: protein
 A:Residues: 1-15 <CHO>
 Query Match 27.4% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 KDT 10
 DB 11 KDT 13
 RESULT 45
 A49177
 22K protein p1, mitochondrial - Crithidia fasciculata (fragment)
 C:Species: Crithidia fasciculata
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 19-May-1994
 C:Accession: A49177; PH1826
 R:Tittawalla, L.
 Exp. Cell Res. 256, 143-151, 1993
 A:Title: Identification of DNA binding proteins in the parasitic protozoan Crithidia
 A:Reference number: A49177; M010:93245912; PMID:8482355

A:Accession: A49177
A:Molecule type: protein
A:Residues: 1-15 <RT>
C:Status: Sequence extracted from NCBI backbone (NCBI:148)
C:Comment: This protein binds with mitochondrial DNA.
C:Keywords: DNA binding; Mitochondrion

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 1 AKK 15

RESULT 36

S77987
Cytochrome oxidase (EC 1.9.3.1) chain VIc.2 - biopsy tumor (fragments)
C:Species: Thunus obesus (Bigeye tuna)
C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 04-Sep-1998
C:Accession: S77987
R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linde, L.; Lottspeich, F.; Kadenbach, B.
Submitted to the Protein Sequence Database, June 1997

A:Reference number: S77980
A:Accession: S77987
A:Molecule type: protein
A:Residues: 1-8; 9-15 <ARN>
A:Experimental source: heart

C:Genetics:

A:Genome: nuclear

C:Function:

A:Pathway: oxidative phosphorylation; respiratory chain

C:Keywords: electron transfer; membrane associated complex; mitochondrial inner membrane

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 7 AKK 9

RESULT 37

PH1788
T cell receptor alpha chain V region (clone 2B4.V alpha 24.4) human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1788
R:Portet, S.; Yockey, C.E.; Rieckert, M.; Park, S.
J. Exp. Med. 179, 1-16, 1994

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1750; MCID:9401569; PMID:849407

A:Accession: PH1788

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-15 <POR>

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERG 6
DB 5 ERG 7

RESULT 38

G49655
T cell receptor beta chain variable region (clone 1) human (fragment)
C:Species: Homo sapiens (man)

C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: G49655; F49655; A49655
R:Grom, A.A.; Thompson, S.D.; Laylink, L.; Passo, M.; Choi, E.; Glass, D.N.
Proc. Natl. Acad. Sci. U.S.A. 90, 11104-11108, 1993
A:Title: Dominant T-cell receptor beta chain variable region V beta 14- clones in j
A:Reference number: A49655; MCID:94068553; PMID:8248215
A:Accession: G49655
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-15 <GR>
A:Experimental source: hip joint, synovial tissues
A:Note: this was designated clone 1
A:Note: sequence extracted from NCBI backbone (NCBI:140453)
A:Accession: F49655
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-15 <GR2>
A:Experimental source: hip joint, synovial tissues
A:Note: sequence extracted from NCBI backbone (NCBI:140451)
A:Note: this was designated clone 2
A:Accession: A49655
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-15 <GR>
A:Experimental source: knee joint, synovial fluid lymphocytes
A:Note: this was designated clone SF-1
A:Note: sequence extracted from NCBI backbone (NCBI:140445)
C:Keywords: T cell receptor

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 12 DTQ 14

RESULT 39

PH0764
T cell receptor beta chain (PF2.10.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0764
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0740; MCID:92078846; PMID:1836010

A:Accession: PH0764

A:Molecule type: mRNA

A:Residues: 1-15 <CAS>

A:Cross-references: EMBL:X60858; NID:q53652; PIDN:CAA43248.1; PID:q53653

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 10 DTQ 12

RESULT 40

S29175
D-galactose-binding lectin V - Axinella polypoides (fragment)
C:Species: Axinella polypoides
C:Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 14-Nov-1997
C:Accession: S29175
R:Buck, F.; Luth, C.; Strupat, K.; Bretting, H.
Biochim. Biophys. Acta 1159, 1-9, 1992

A:Title: Comparative investigations on the amino-acid sequences of different isolectins
 A:Reference number: S29172; MUID:94003351; PMID:1390966
 A:Accession: S29175
 A:Molecule type: protein
 A:Residues: 1-15 <BUC>

Query Match 27.3%; Score 2; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EQ 6
 II
 DB 6 EQ 8

RESULT 41
 B24749
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2009
 C:Accession: B24749
 R:Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
 A:Title: Isolation, sequencing, synthesis, and pharmacological characterization of two
 A:Reference number: A94074; MUID:26067985; PMID:385519.
 A:Accession: B24749
 A:Molecule type: protein
 A:Residues: 1-8 <YAN>
 C:Superfamily: unadsorbed animal peptides
 C:Keywords: neuropeptide

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 6 QR 7
 II
 DB 6 QR 7

RESULT 42
 S37141
 C:Species: Erwinia chrysanthemi
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1995
 C:Accession: S37141
 R:Douillie, A.; Ioussaint, A.; Faelen, M.
 Submitted to the EMBL Data Library, August 1994
 A:Description: Identification of the integration host factor genes of E. chrysanthemi.
 A:Reference number: S37139
 A:Accession: S37141
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-8 <KQ>
 A:Cross-references: EMBL:X74750; NID:q199666; PIN:FAA2769.1; PID:4581168

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
 II
 DB 5 AK 6

RESULT 43
 A21440
 C:Species: Trypanosoma brucei
 C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Mar-1998
 C:Accession: A21440
 R:Parsons, M.; Nelson, R.G.; Watkins, K.P.; Arabian, N.
 Cell 38, 309-316, 1984

variant surface glycoprotein pSic1 - Trypanosoma brucei (fragment)

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
 II
 DB 5 AK 6

RESULT 44
 PT0323
 Iq heavy chain CRD3 region (clone J2-106B) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0323
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity a
 A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0323
 A:Molecule type: DNA
 A:Residues: 1-8 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QR 7
 II
 DB 5 QR 6

RESULT 45
 148934
 apolipoprotein A-II - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: 148934
 R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takehashi, N.; Maezaki, Y.; Nadeau,
 Mamm. Genome 5, 349-355, 1994
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A:Reference number: 148934; MUID:94319082; PMID:8043949
 A:Accession: 148934
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-8 <RES>
 A:Cross-references: EMBL:005691; NID:q497010; PID:9642826

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
 II
 DB 7 AK 8

RESULT 46
 A54823
 olfactory receptor 17 - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
 C:Accession: A54823

A:Title: Trypanosome mRNAs share a common 5' spliced leader sequence.
 A:Reference number: A90853; MUID:84282716; PMID:6088073
 A:Accession: A21440
 A:Molecule type: mRNA
 A:Residues: 1-8 <PAR>
 A:Cross-references: GB:K02195; NID:q162150; PID:q162151
 C:Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KE 4
 II
 DB 4 KE 5

R:Chess, A.; Simon, I.; Cedar, H.; Axel, R.

Cell 78, 823-834, 1994

A:Title: Allelic inactivation regulates olfactory receptor gene expression.

A:Reference number: A54823; MUID:94373818; PMID:8087849

A:Accession: A54823

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <CHE>

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ER 5

DB 2 ER 3

RESULT 47

PT0653

T-cell receptor beta chain V-D-J region (121-48); mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0653

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Functional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0653

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FEF>

A:Experimental source: day 4 postnatal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ER 5

DB 7 ER 8

RESULT 48

148935

apolipoprotein A-II - western wild mouse (fragment)

C:Species: Mus spretus (western wild mouse)

C>Date: 02-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 25-Nov-1999

C:Accession: 148935

R:Ko, M.S.; Ward, X.; Horton, J.H.; Haas, J.; Nakatani, N.; Marzaki, Y.; Nakatani, J.H.

Mamm. Genome 5, 349-355, 1994

A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A:Reference number: 148934; MUID:94319582; PMID:8087849

A:Accession: 148935

A:Status: preliminary; translated from cDNA/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-8 <RES>

A:Cross-references: EMBL:U05692; NID:9457011; PIR:AA004611; PDB:464287

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2

DB 7 AK 8

RESULT 49

B54823

olfactory receptor 17 - western wild mouse (fragment)

C:Species: Mus spretus (western wild mouse)

C>Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999

C:Accession: B54823

R:Chess, A.; Simon, I.; Cedar, H.; Axel, R.

Cell 78, 823-834, 1994

A:Title: Allelic inactivation regulates olfactory receptor gene expression.

A:Reference number: A54823; MUID:94373818; PMID:8087849

A:Accession: B54823

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <CHE>

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ER 5

DB 2 ER 3

RESULT 50

A61597

cytochrome P450 AL-1 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: A61597

R:Shimeno, H.; Toda, A.; Ogata, S.; Naganatsu, A.

Drug Metab. Dispos. 19, 291-297, 1991

A:Title: Purification and aminopyrine monooxygenase activity of liver microsomal cy.

A:Reference number: A61597; MUID:91292910; PMID:1676625

A:Accession: A61597

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <SHI>

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KE 4

DB 6 KE 7

Search completed: September 30, 2003, 10:09:41

Job time : 15.4167 secs

GenCore version 5.1.1.6
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EM protein protein search, using sw mode.

Run on: September 30, 2003, 10:07:04 : Search time: 6.25 Seconds
(with all arguments)
82,717 matches found: 1 positive/sec

Title: US-09-787-443-2

Perfect score: 11

Sequence: 1 AKRQRKKDTG 11

Scoring table: glg60

gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 707

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	27.3	10	1 XVRN_DICM1	P01177 dictyostell
2	3	27.3	12	1 PSL1_ELYEP	Q47406 clover yeli
3	3	27.3	13	1 LPA4_P0001	P04111 porphyramen
4	3	27.3	14	1 MAST_VESHA	P21654 vespa basid
5	3	27.3	14	1 MAST_VESPR	P01516 vespa crabr
6	3	27.3	14	1 MAST_VESLE	P01514 vespa lew
7	3	27.3	14	1 MAST_VESCA	Q04205 vespa manda
8	3	27.3	14	1 MAST_VESKA	P01515 vespa xanth
9	3	27.3	14	1 KRM_KAKKA	P03411 rata caprar
10	3	27.3	15	1 COX2_LAB1P	P04774 thaurus obe
11	3	27.3	15	1 COX2_LAB1P	P04774 thaurus obe
12	2	18.2	8	1 ACTA_VAFPA	P00709 carcinus ma
13	2	18.2	8	1 NRB_BOVIN	P05037 tes toures
14	2	18.2	8	1 NS1_MYCHI	P01152 mycobacteri
15	2	18.2	8	1 RSL_EWCHI	P07985 ewalia chr
16	2	18.2	8	1 RST_MYCHI	P03564 mycobacteri
17	2	18.2	8	1 GH09_SAT	P06575 rattus norv
18	2	18.2	9	1 COX2_THED-B	P00975 thaurus obe
19	2	18.2	9	1 HMTL_KLEAF	P12181 klebsiella
20	2	18.2	9	1 LMT3_LJUNE	P41455 acasta miq
21	2	18.2	9	1 LKCA_STEAT	P06884 staphylococ
22	2	18.2	9	1 RSLC_SERMA	P08946 seiralia ma
23	2	18.2	9	1 RTIC_BOVIN	P04926 bos taurus
24	2	18.2	9	1 THYF_FIG	P01255 sus scrofa
25	2	18.2	9	1 ULAD_HUMAN	P01929 homo sapien
26	2	18.2	9	1 ULAK_MOUSE	P09031 mus muscula
27	2	18.2	10	1 COXA_ONMY	P05128 oncorhynch
28	2	18.2	10	1 COXA_RAT	P04431 rattus norv
29	2	18.2	10	1 COXQ_SHEEP	P03337 ovis aries
30	2	18.2	10	1 MALE_KLEP	Q05564 klebsiella
31	2	18.2	10	1 MSL_MICAT	P01553 microplitis
32	2	18.2	10	1 NS1_MYCHI	P01155 mycobacteri
33	2	18.2	10	1 PSBP_CAVAN	Q03367 capsicum 48

P01084	pinus pinas	10	1	RCA_PINPS
P01545	dictyostelli	10	1	SP34_DICM0
Q10997	halocynthia	10	1	SPI_HAIRO
Q46464	campylobact	10	1	SYK_CAMUP
P08608	scyllorhinu	10	1	TKN1_SCYCA
P42635	aedes aegyp	10	1	TKS2_AEDAE
P40751	urechis uni	10	1	TKUL_UREUN
P38007	chlamydia t	10	1	UXA6_CHLTR
P83347	bacteroides	11	1	ASL2_BACSE
P12797	megascolia	11	1	HRK_MEGFL
P59072	pseudonaja	11	1	NXSN_PSETE
P82684	carausius m	11	1	PKC1_CARMO
P55173	pseudomonas	11	1	P002_PSEFL
P80464	comamonas t	11	1	Q20A_COMTE
P29207	rana ridibu	11	1	TKNA_RANRT
P22691	rana catesb	11	1	TKN1_RANCA
P01293	eleidone mos	11	1	TKN_ELEMO
P99013	saccharomyc	11	1	JXB2_YEAST
P83322	pacaeus mon	12	1	FAR7_PENMO
P83327	oncorhynch	12	1	H2AX_ONCHY
Q10584	megathura c	12	1	HCYB_MEGCR
P82995	rattus norv	12	1	HS9A_RAT
P80903	methanobact	12	1	PORD_METTM
P36207	ginkgo bilo	12	1	KR16_GINBI
Q47881	elm yellows	12	1	RS19_ELYEP
Q56251	tomato big	12	1	RS19_TOBBP
P80863	caecilius su	12	1	SO15_BACSU
P56572	rattus norv	12	1	UH03_RAT
P17776	escherichia	12	1	YZPY_ECOLI
P82386	litoria ran	13	1	AU11_LITRA
P82387	litoria ran	13	1	AU12_LITRA
P42717	parapolybia	13	1	BRK_PARID
P49818	canis fami	13	1	CH60_CANFA
P17233	vespa anali	13	1	CRBL_VESAN
P01518	vespa crabr	13	1	CRBL_VESCR
P17235	vespa lew	13	1	CRBL_VESLE
P17234	vespa xanth	13	1	CRBL_VESKA
P28489	bos taurus	13	1	CRIC_BOVIN
P80941	lymantria d	13	1	ESDE_LYMDI
P14445	cavia porce	13	1	FIBA_CAVPO
P56574	rattus norv	13	1	IDHP_RAT
P49823	canis fami	13	1	ODPA_CANFA
P57793	eubacterium	13	1	PHGR_EUBOX
P20118	pisum sativ	13	1	PSAE_PEA
Q47716	mycoplasma	13	1	RPOC_MYCGA
Q44592	ash yellows	13	1	RS19_ASHYP
P80867	caecilius su	13	1	VC16_BACSU
P08944	alytes obst	14	1	ALY1_ALYOB
P20728	calotropis	14	1	CALL_CALGI
P35586	limulus pol	14	1	COX2_LIMPO
Q10583	megathura c	14	1	HCYA_MEGCR
P18854	rhizobium m	14	1	LPW_RHIME
P42716	parapolybia	14	1	MAST_PARID
P01517	polistes ja	14	1	MAST_POLJA
P17238	vespa orien	14	1	MAST_VESOR
P58815	methanobact	14	1	MCRX_METTM
P58816	methanobact	14	1	MCR2_METTM
P46979	eisenia foe	14	1	MY14_EISFO
Q46228	clover prol	14	1	RS19_CLOPP
Q48878	loofah wic	14	1	RS19_LOWBP
O52093	pigeon pea	14	1	RS19_PPWBP
Q44160	prunus arme	14	1	RS19_PRUPP
P12509	human immu	14	1	TAT_HVIW2
P12511	human immu	14	1	TAT_HVI18
P82470	schistocerc	14	1	TKN1_SCHGR
P81352	clostridium	14	1	UN07_CLOPA
P80173	caecilius ce	15	1	48KD_BACCE
P83137	malva parvi	15	1	APP3_MALPA
P29260	prunus sero	15	1	AH2_PRUSE
P42559	manduca sex	15	1	ALLS_MANSE
P82648	lactobacilli	15	1	ASPI_LACSN
P31720	rattus norv	15	1	CLQA_RAT
P81266	microplitis	15	1	EFLA_MICCR

107	1	18.2	2	18.2	15	1	FIBA_ANADOL	P22501 anas platyr	180	9.1	8	1	URMV_ORCLI	P82455 orconectes
108	2	18.2	2	18.2	15	1	FIRB_ALBUJO	P24927 abizzia ju	181	9.1	8	1	P1P_BRANA	P81707 brassica na
109	2	18.2	2	18.2	15	1	LEC2_PSRSC	P24985 psophocarpa	182	9.1	8	1	PPK2_PERAM	P82692 periplaneta
110	2	18.2	2	18.2	15	1	LEC3_PSDOS	P24985 psophocarpa	183	9.1	8	1	PPK3_PERAM	P82692 periplaneta
111	2	18.2	2	18.2	15	1	LMA2_LOCM1	P84937 locusta mig	184	9.1	8	1	PPCH_PANBO	P80939 pandalus bo
112	2	18.2	2	18.2	15	1	MCA1_BAC70	P80972 bacillus th	185	9.1	8	1	RI34_BOVIN	P82929 bos taurus
113	2	18.2	2	18.2	15	1	MCA2_BAC70	P80972 bacillus th	186	9.1	8	1	UC26_MAIZE	P80632 zea mays (m
114	2	18.2	2	18.2	15	1	MRAA_MET16	P22949 melanosare	187	9.1	8	1	UF06_MOUSE	P38644 mus musculus
115	2	18.2	2	18.2	15	1	MM01_PAT	P81593 ratius norv	188	9.1	8	1	UPA1_HUMAN	P30087 homo sapien
116	2	18.2	2	18.2	15	1	NU23_SQU10	P80263 solanum tub	189	9.1	8	1	UPAA_HUMAN	P30096 homo sapien
117	2	18.2	2	18.2	15	1	NX57_PSE15	P50973 pseudonaja	190	9.1	8	1	WP1_PERAT	P83195 perkinsus a
118	2	18.2	2	18.2	15	1	ONC1_CNEMY	P84287 anorthyncha	191	9.1	8	1	AL10_CARMA	P81813 carcinus ma
119	2	18.2	2	18.2	15	1	PG15_PELAC	P80564 pelobates	192	9.1	8	1	AL31_CARMA	P81814 carcinus ma
120	2	18.2	2	18.2	15	1	R13A_SPLC1	P84554 sphincter ol	193	9.1	8	1	ALC1_CHDRE	P82678 chlamydomon
121	2	18.2	2	18.2	15	1	RS10_BAST	P59653 bacillus st	194	9.1	8	1	BS43_SERPL	P83375 seriatia pl
122	2	18.2	2	18.2	15	1	RS40_BACST	P59662 bacillus st	195	9.1	8	1	BOK_CLOPA	P81337 clostridium
123	2	18.2	2	18.2	15	1	RS9_BACST	P59662 bacillus st	196	9.1	8	1	CCAP_CARMA	P38556 carcinus ma
124	2	18.2	2	18.2	15	1	TERM_BPM2	P19647 bacterioph	197	9.1	8	1	CUNU_CONGE	P05486 conus geogr
125	2	18.2	2	18.2	15	1	THC_CLOPA	P83447 clostridium	198	9.1	8	1	CONU_CONVE	P05487 conus stri
126	2	18.2	2	18.2	15	1	UT17_MAIZE	P83624 zea mays (m	199	9.1	8	1	DI1_NEPNO	P24916 nephrops no
127	2	18.2	2	18.2	15	1	UT20_MAIZE	P80626 zea mays (m	200	9.1	8	1	DSIP_RABIT	P01158 oryctolagus
128	2	18.2	2	18.2	15	1	UT27_MAIZE	P80633 zea mays (m	201	9.1	8	1	FAR1_CALVO	P41857 calliphora
129	2	18.2	2	18.2	15	1	UNCL_PINES	P81106 pinus plac	202	9.1	8	1	FAR2_CALVO	P41873 panagrellus
130	2	18.2	2	18.2	15	1	UNCL_PINES	P81106 pinus plac	203	9.1	8	1	FAR3_CALVO	P41858 calliphora
131	2	18.2	2	18.2	15	1	UNCL_PINES	P81106 pinus plac	204	9.1	8	1	FAR4_CALVO	P83276 macrobrachi
132	2	18.2	2	18.2	15	1	UP12_METAN	P84439 metathizium	205	9.1	8	1	FAR5_PENMO	P41859 calliphora
133	2	18.2	2	18.2	15	1	UP12_METAN	P84439 metathizium	206	9.1	8	1	FAR6_CALVO	P83319 penaeus mon
134	2	18.2	2	18.2	15	1	VORA_PETIM	P72437 marquellia	207	9.1	8	1	FAR7_CALVO	P43170 ascaris suu
135	2	18.2	2	18.2	15	1	ACT1_HOVAL	P80907 me-hanabact	208	9.1	8	1	FAR8_CALVO	P41860 calliphora
136	2	18.2	2	18.2	15	1	ACT1_HOVAL	P80907 me-hanabact	209	9.1	8	1	FAR9_CALVO	P82661 panagrellus
137	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	210	9.1	8	1	FAR5_PENMO	P83320 penaeus mon
138	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	211	9.1	8	1	FAR6_CALVO	P41861 calliphora
139	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	212	9.1	8	1	FAR6_CALVO	P83279 macrobrachi
140	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	213	9.1	8	1	FAR7_CALVO	P41862 calliphora
141	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	214	9.1	8	1	FAR8_CALVO	P83281 macrobrachi
142	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	215	9.1	8	1	FAR9_CALVO	P43172 ascaris suu
143	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	216	9.1	8	1	FAR9_CALVO	P41865 calliphora
144	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	217	9.1	8	1	FAR9_CALVO	P41868 calliphora
145	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	218	9.1	8	1	FAR9_CALVO	P38495 calinectes
146	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	219	9.1	8	1	FAR9_CALVO	P19346 erythrocebu
147	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	220	9.1	8	1	FAR9_CALVO	P19345 macaca fusc
148	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	221	9.1	8	1	FAR9_CALVO	P19344 papio anubi
149	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	222	9.1	8	1	FAR9_CALVO	P19343 papio hamad
150	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	223	9.1	8	1	FAR9_CALVO	P19342 theropithec
151	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	224	9.1	8	1	FAR9_CALVO	P80159 treponema h
152	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	225	9.1	8	1	FAR9_CALVO	P83350 sarcophaga
153	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	226	9.1	8	1	FAR9_CALVO	P82992 rhodopseudo
154	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	227	9.1	8	1	FAR9_CALVO	P83058 bombina var
155	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	228	9.1	8	1	FAR9_CALVO	P08945 litorea aur
156	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	229	9.1	8	1	FAR9_CALVO	P08946 phyllomedusa
157	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	230	9.1	8	1	FAR9_CALVO	P31799 locusta mig
158	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	231	9.1	8	1	FAR9_CALVO	P29177 bos taurus
159	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	232	9.1	8	1	FAR9_CALVO	P19853 clypeaster
160	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	233	9.1	8	1	FAR9_CALVO	P19852 clypeaster
161	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	234	9.1	8	1	FAR9_CALVO	P12481 human immu
162	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	235	9.1	8	1	FAR9_CALVO	P34966 cavia porce
163	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	236	9.1	8	1	FAR9_CALVO	P04277 homo sapien
164	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	237	9.1	8	1	FAR9_CALVO	P41492 sarcophaga
165	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	238	9.1	8	1	FAR9_CALVO	P42995 bufo regula
166	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	239	9.1	8	1	FAR9_CALVO	P23879 cyprinus ca
167	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	240	9.1	8	1	FAR9_CALVO	P42998 eisenia foe
168	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	241	9.1	8	1	FAR9_CALVO	P80027 octopus vul
169	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	242	9.1	8	1	FAR9_CALVO	P80028 oryctolagus
170	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	243	9.1	8	1	FAR9_CALVO	P42994 rala clavat
171	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	244	9.1	8	1	FAR9_CALVO	P43000 squalus aca
172	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	245	9.1	8	1	FAR9_CALVO	P81179 diatrepes a
173	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	246	9.1	8	1	FAR9_CALVO	P83360 lycopersico
174	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	247	9.1	8	1	FAR9_CALVO	P82691 periplaneta
175	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	248	9.1	8	1	FAR9_CALVO	P82003 bombyx mori
176	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	249	9.1	8	1	FAR9_CALVO	
177	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	250	9.1	8	1	FAR9_CALVO	
178	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	251	9.1	8	1	FAR9_CALVO	
179	2	18.2	2	18.2	15	1	AKB1_CIRAB	P44926 styllus alb	252	9.1	8	1	FAR9_CALVO	

253	1	9.1	9	1	RE42_LITRC	P82075	litoria rub	326	1	9.1	10	1	MOSQ_CLYVA	P19962	clypeaster
254	1	9.1	9	1	SAMP_MUSCA	P19095	mustelus ca	327	1	9.1	10	1	NO40_TOBAC	P55962	nicotiana t
255	1	9.1	9	1	SAP_STOXA	P24047	stomopneute	328	1	9.1	10	1	OPP2_BOVIN	P11180	bos taurus
256	1	9.1	9	1	TALI_PICJA	P17440	pichia jadi	329	1	9.1	10	1	PAP1_PARMA	P81863	pardachirus
257	1	9.1	9	1	TALI_PICJA	P17440	pichia jadi	330	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
258	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	331	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
259	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	332	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
260	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	333	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
261	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	334	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
262	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	335	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
263	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	336	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
264	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	337	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
265	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	338	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
266	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	339	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
267	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	340	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
268	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	341	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
269	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	342	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
270	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	343	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
271	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	344	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
272	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	345	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
273	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	346	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
274	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	347	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
275	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	348	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
276	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	349	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
277	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	350	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
278	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	351	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
279	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	352	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
280	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	353	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
281	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	354	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
282	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	355	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
283	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	356	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
284	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	357	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
285	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	358	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
286	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	359	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
287	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	360	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
288	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	361	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
289	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	362	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
290	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	363	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
291	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	364	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
292	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	365	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
293	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	366	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
294	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	367	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
295	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	368	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
296	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	369	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
297	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	370	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
298	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	371	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
299	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	372	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
300	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	373	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
301	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	374	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
302	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	375	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
303	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	376	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
304	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	377	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
305	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	378	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
306	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	379	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
307	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	380	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
308	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	381	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
309	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	382	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
310	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	383	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
311	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	384	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
312	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	385	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
313	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	386	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
314	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	387	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
315	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	388	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
316	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	389	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
317	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	390	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
318	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	391	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
319	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	392	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
320	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	393	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
321	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	394	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
322	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	395	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
323	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	396	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
324	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	397	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
325	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	398	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien

P19962 clypeaster
P55962 nicotiana t
P11180 bos taurus
P81863 pardachirus
P22103 homo sapien
P22103 homo sapien
P80901 melhanobact
P80525 fasciola he
P83382 locusta mig
P80465 comamonas t
P80466 comamonas t
P29221 acholeptasm
P35946 phocine dis
P82923 bos laurus
P49325 bacillus th
P56923 rana tempor
P16224 locusta mig
P30249 locusta mig
P30250 locusta mig
P19851 gallus gall
P28500 oncorhynch
P22689 rana catesb
P29135 rana ridibu
P22690 rana catesb
P10292 sus scrofa
P08610 phyllomedus
P42634 aedes aegypt
P40752 urechis uni
P19425 aedes aegypt
P19118 nicotiana p
P81737 leucophaea
P81738 leucophaea
P81739 leucophaea
P81740 leucophaea
P81741 leucophaea
P36573 rattus norv
P40930 homo sapien
P30088 homo sapien
P30090 homo sapien
P30091 homo sapien
P30094 homo sapien
P30095 homo sapien
P32118 homo sapien
P32080 homo sapien
P34990 homo sapien
P17339 morganella
P38003 chlamydia t
P99012 saccharomyc
P80699 bacillus su
P09037 crinia geor
P83146 bacteroides
P30423 bothrops in
P30424 bothrops in
P1021 aekistodon
P40562 aekistodon
P82087 litoria cit
P82088 litoria cit
P82089 litoria cit
P82090 litoria cit
P82091 litoria cit
P82092 litoria cit
P22790 achatina fu
P11496 periplaneta
P99501 canis famli
P81095 bacillus su
P58848 conus aulic
P58849 conus aulic
P58807 conus marmo
P81350 clostridium
P56571 rattus norv
P83321 penaeus mon
P81864 calliphora
P81672 pinus pinas

AC Q46490:
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 40S ribosomal protein S19 (Fragment)
 GN RPSS OR RPS19
 OS Clover yellow edge phytoplasm
 OC Bacteria; Firmicutes; Mollicutes; Actinobacteriales
 OC Actinobacteriales; Mollicutes; Actinobacteriales
 OC NCBI_TaxID=35775;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:94350802; PubMed:8071196;
 RA Gundersen C.E., Lee I.M., Reiner S.A., Davis R.P., Kinoshita T.
 RT "Phylogeny of mycoplasma-like organisms (Mycoplasmas): a basis for
 their classification."
 RI J. Bacteriol. 176:5244-5254(1994)
 CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S10 THAT BINDS STRONGLY
 CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 CC
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 DR FMH1: L27019; AAA83940.1;
 DR HAMAP: MF_03531; 1;
 DR InterPro: IPR002222; Ribosomal_S19
 DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL
 KW Ribosomal protein; rRNA-binding;
 FT N-TER
 FT N-TER
 SQ SEQUENCE 12 AA; 1409 MW; 40C478EF833AA3 CR=64;
 Query Match 27.3%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.2e-03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKK 3
 DB 3 AKK 5
 RESULT 4
 LPAA_PUFGI STANDARD; PRI: 14 AA;
 ID LPAA_PUFGI
 AC P81411;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Lipid A-associated protein (Fragment)
 GN Porphyromonas gingivalis (Bacteroides class)
 OS Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonadaceae
 OC NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE
 RX STRAIN-W56; PubMed:9846747;
 RA Sharp L., Poole S., Reddi K., Fletcher J., Nair S., Wilson M.,
 RA Curtis M., Henderson B., Tabona P.
 RT "A lipid A-associated protein of Porphyromonas gingivalis, derived
 RT from the haemagglutinating domain of the Rf protease gene family, is
 RT a potent stimulator of interleukin 6 synthesis."
 RL Microbiology 144:3019-3025(1998)
 CC -!- FUNCTION: IS ASSOCIATED WITH LIPID A, A THE SUBSTRATE FOR GLYCOPHILIPID
 CC THAT ANCHORS THE LIPIDOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE
 CC CELL.
 CC VARIANT 12 12 G -> F
 FT VARIANT 13 13
 FT N-TER

SQ SEQUENCE 13 AA; 1346 MW; 38EA796EAF63AB7 CRC64;
 Query Match 27.3%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e-03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 KDT 10
 DB 8 KDT 10
 RESULT 4
 MAST_VESPA STANDARD; PRI: 14 AA;
 ID MAST_VESPA
 AC P21654;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mastoparan B.
 OS Vespa basalis (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7444;
 RN [1]
 RP SEQUENCE
 RC TISSUE-Venom;
 RX MEDLINE-91174755; PubMed-206909;
 RA Lo C.-L., Hwang L.-L.;
 RT "Structure and biological activities of a new mastoparan isolated
 RT from the venom of the hornet Vespa basalis."
 RL Biochem. J. 274:453-456(1991).
 CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
 CC that couple to phospholipase C.
 DR PIR: S14336; S14336.
 KW Mast cell degranulation; Amidation
 FT MOD_RES 14 14
 FT MOD_RES 14 14
 SQ SEQUENCE 14 AA; 1613 MW; D35944CA193A19A2 CRC64;
 Query Match 27.3%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.2e-03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKK 5
 DB 10 AKK 12
 RESULT 5
 MAST_VESCR STANDARD; PRI: 14 AA;
 ID MAST_VESCR
 AC P01516;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mastoparan C.
 OS Vespa crabro (European hornet).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7445;
 RN [1]
 RP SEQUENCE
 RC TISSUE-Venom;
 RX MEDLINE-84289340; PubMed-6206053;
 RA Argolas A., Pisano J.J.;
 RT "Isolation and characterization of two new peptides, mastoparan C and
 RT crabrolin, from the venom of the European hornet, Vespa crabro."
 RL J. Biol. Chem. 259:10106-10111(1984).
 CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
 CC that couple to phospholipase C.
 DR PIR: A01774; QMVPF2.
 KW Mast cell degranulation; Amidation.

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FT MDL_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA: 1508 MW: 5500676.056A19779664.

Query Match: 27.4% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 10 AKK 12

RESULT 6
MAST_VESPA
ID MAST_VESPA STANDARD: PRI: 14 AA.
AC P01514.
DT 21-JUL-1986 (Rel. 01, Created)
DI 21-JUL-1986 (Rel. 01, Last sequence update)
DE Mastoparan M (Mast cell degranulating peptide)
OS Vespa manducaria (Hornet)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Vespoidea;
OC Vespidae; Vespinae; Vespa.
CX NCBI_TaxID=7446;
RN 1;
RP SEQUENCE AND SYNTHESIS.
SC TISSUE: Venom.
RX MEDLINE=80155337; PubMed=540463;
RA Hirai Y., Yasuhara T., Yoshida H., Nakajima T.,
RT "A new mast cell degranulating peptide homologous to mastoparan in
RT Vespa lewisii."
RL Chem. Pharm. Bull. 27:1942-1943(1979).
CC 1- FUNCTION: Mast cell degranulating peptide. Activates 3 proteins
CC that couple to phospholipase C.
DR PIR: AC1776; QMVAVV.
DR PDB: 107N; 20-JUN-01.
KW Mast cell degranulation; Amidation; 3D-structure.
FT MDL_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA: 1480 MW: 4760634.026A1040404.

Query Match: 27.4% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 10 AKK 12

RESULT 7
MAST_VESMA
ID MAST_VESMA STANDARD: PRI: 14 AA.
AC P04205.
DT 20-MAR-1987 (Rel. 04, Created)
DI 20-MAR-1987 (Rel. 04, Last sequence update)
DE Mastoparan M (Mast cell degranulating peptide)
OS Vespa manducaria (Hornet)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Vespoidea;
OC Vespidae; Vespinae; Vespa.
CX NCBI_TaxID=7446;
RN 1;
RP SEQUENCE.
SC TISSUE: Venom.
RA Hirai Y., Yasuhara T., Yoshida H., Nakajima T.,
RT "A new mast cell degranulating peptide homologous to mastoparan in
RT the hornet Vespa manducaria."
RL Biomed. Res. 2:447-449(1981).
CC 1- FUNCTION: Mast cell degranulating peptide. Activates 3 proteins
CC that couple to phospholipase C.
DR PIR: A01777; QMVHMM.

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KW Mast cell degranulation; Amidation.
FT MDL_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA: 1480 MW: 4760634.026A1040404.

Query Match: 27.4% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 10 AKK 12

RESULT 8
MAST_VESXA
ID MAST_VESXA STANDARD: PRI: 14 AA.
AC P01515.
DT 21-JUL-1986 (Rel. 01, Created)
DI 21-JUL-1986 (Rel. 01, Last sequence update)
DE Mastoparan X (MP-X)
OS Vespa xanthoptera (Japanese hornet)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Vespoidea;
OC Vespidae; Vespinae; Vespa.
CX NCBI_TaxID=7448;
RN 1;
RP SEQUENCE.
SC TISSUE: Venom.
RX MEDLINE=80155338; PubMed=540463;
RA Hirai Y., Kuwada M., Yasuhara T., Yoshida H., Nakajima T.,
RT "A new mast cell degranulating peptide homologous to mastoparan in
RT the venom of Japanese hornet (Vespa xanthoptera)."
RL Chem. Pharm. Bull. 27:1945-1946(1979).
CC 1- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR: A01778; QMVHXX.
DR PDB: 1A13; 16-FEB-99.
KW Mast cell degranulation; Amidation; 3D-structure.
FT MDL_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA: 1509 MW: 5785000.777A7AB0DD CRC64;

Query Match: 27.4% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 10 AKK 12

RESULT 9
KNN_RANMA
ID KNN_RANMA STANDARD: PRI: 14 AA.
AC P43053.
DT 01-FEB-1995 (Rel. 01, Created)
DI 01-FEB-1995 (Rel. 01, Last sequence update)
CC 1- FUNCTION: Mast cell degranulating peptide. Activates 3 proteins
CC that couple to phospholipase C.
DR PIR: A01779; QMVHXX.

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DE Panamargarin.
OS Panamargarin (Chinese frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=121156;
KN [1]
RP SEQUENCE.
RC TISSUE: SKIN SECRETION;
RX MEDLINE=90026452; PubMed=280554;
RA Tang Y.Q., Tian S.H., Wu S.X., Hua J., Wu D.F., Zhao E.M., Lu Y.A.,
KA Zhu Y.Q., Zou G., Tsou K.;
RT *Isolation and structure of panamargarin, a new tachykinin from the
RT skin of Chinese frog *Rana maculata*.*
RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 42:574-579(1999).
RN [2]
RP SYNTHESIS.
RX MEDLINE=92253600; PubMed=2140987;
RA Lu Y.A., Peng J.L., Zhu Y.Q., Wu S.X., Tang Y.Q., Tian S.H., Zou G.,
RT *Synthesis and biological activity of a new frog skin peptide,
RT panamargarin.*
RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 43:720-727(1996).
CC *FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC *SUBCELLULAR LOCATION: Secreted.
CC *TISSUE SPECIFICITY: SKIN.
CC *SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DE INTERPRO: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ; 1
KW Amphibia; defense peptide; Tachykinin; Neuropeptide; Acylation.
FT MOD_RES 14 16 AMIDATION
SQ SEQUENCE 14 AA; 1617 MW; D459AE46804674D CR64;
Query Match 27.4%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKK 3
DB 7 AKK 9
RESULT 19
CXI_THD08 STANDARD; PRI; 15 AA.
AC PR0978;
DT 01-NOV-1997 (Rel. 35, Created)
UT 01-NOV-1997 (Rel. 35, Last sequence update)
PT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cytochrome c oxidase polypeptide γ -2 (human) (2)
OS Thomas Giesus (Bigeys tuna)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Eupercaria; Neocentropomidae;
OC Acanthomorphi; Acanthopterygii; Perciformes; Scombridae; Scombridae;
OC Scombridae; Tunnus.
OX NCBI_TaxID=8241;
KN [1]
RP SEQUENCE.
RC TISSUE: Heart;
RX MEDLINE=97454291; PubMed=943095;
RA Arnold S., Lee I., Kim M., Song E., Finkbeiner D.;
KA Kadenbach B.;
RT *The subunit structure of cytochrome oxidase from tuna heart and
RT liver.*
RL Eur. J. Biochem. 248:99-103(1997).
CC *FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT
CC *CATALYTIC ACTIVITY: 4 ferredoxinase
CC *C * 2 H(2)O;
CC *SUBCELLULAR LOCATION: Mitochondrion inner membrane
DR E.C.: S77987; S77987.

KW Oxidoreductase; inner membrane; Mitochondrion.
FT NON_TER 1
FT NON_CONS 8 9
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1696 MW; 424C966C73A40294 CR64;
Query Match 27.4%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKK 3
DB 7 AKK 9
RESULT 11
GR78_HORSE STANDARD; PRI; 15 AA.
AC P16392;
DT 01-AUG-1990 (Rel. 15, Created)
DI 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 78 kDa glucose-regulated protein (GRP 78) (Immunoglobulin heavy chain
DE binding protein) (Bip) (Fragment).
GN HSPAS OR GRP78
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RX MEDLINE=90147817; PubMed=1689156;
KA Oblas B., Hoyd N.D., Luben-Narod J., Reyes V.E., Leeman S.E.;
RT *Isolation and identification of a polypeptide in the Hsp 70 family
RT that binds substance P.*
RL Biochem. Biophys. Res. Commun. 166:978-983(1990).
CC *FUNCTION: Probably plays a role in facilitating the assembly of
CC multimeric protein complexes inside the ER.
CC *SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC *SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
DE INTERPRO: IPR01023; HSP70.
DR PROSITE: PS00247; HSP70_1; PARTIAL.
DR PROSITE: PS00329; HSP70_2; PARTIAL.
DR PROSITE: PS00366; HSP70_3; PARTIAL.
KW ATP-binding; Endoplasmic reticulum.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1647 MW; B119D2D0EC26DB CR64;
Query Match 27.4%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 KKE 4
DB 5 KKE 7
RESULT 12
ACT_CAPMA STANDARD; PRI; 8 AA.
AC P80709;
DT 01-OCT-1996 (Rel. 34, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Actin (Fragment).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchiata; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6757;
RN [1]
RP SEQUENCE.
RA Lachaise F., Sureau G., Carpentier G., Granjeon E., Webster S.,

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RA  Baglioniassarian D.;
PT  "A transaldolase. An enzyme implicated in crab steroidogenesis."
RL  Eukaryote 5-23-32(1996).
CC  -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
CC  IN VARIOUS TYPES OF CELL MOTILITY AND ARE UNUSUALLY OVERLY EXPRESSED
CC  IN ALL EUKARYOTIC CELLS.
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PT OF THIS PROTEIN IS:
CC  6.8. ACTS MW IS: 46 kDa.
CC  -1- SIMILARITY: Belongs to the actin family.
DR  InterPro: IPR004001; Actin.
DR  InterPro: IPR004000; Actin 1 kDa.
DR  PROSITE: PS00406; ACTINS_1; PARTIAL.
DR  PROSITE: PS00432; ACTINS_2; PARTIAL.
DR  PROSITE: PS01132; ACTINS_ACT LIKE; PARTIAL.
KW  Structural protein.
FT  NON_TER 1
FT  NON_TER 8
SQ  SEQUENCE 8 AA: 976 MW; 1424035AB2FAABX CR 04;
Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RK 8
DB 1
7 RK 8

RESULT 14
NS1_MYCTD
ID NS1_MYCTD STANDARD; PRT; 8 AA.
AC P15507
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae;
CC Bovidae; Bovinae; Bos.
CC NCBI_TaxID:9913;
RN 1;
RP SEQUENCE.
RX MEDLINE:86067985; PubMed:3865135.
KA Yang H, Yip J, Pratta W, Majumder A, Gupta P,
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine."
KL Proc Natl Acad Sci U S A 92:1003-1007, 1995.
CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR: R24749; R24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8
FT MOD_RES 8
SQ SEQUENCE 8 AA: 1082 MW; R7D416372606729 CR 04.
Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QR 7
DB 1
6 QR 7

RESULT 14
NS1_MYCTD
ID NS1_MYCTD STANDARD; PRT; 8 AA.
AC P81152;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE 30 kDa non secretory protein 3 (Fragment).
OS Mycobacterium tuberculosis.
CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
CC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
CC NCBI_TaxID:1773;
RN 1;
RP SEQUENCE.
RC STRAIN:H37Rv;
RA Prasad H.K. Annals of the N.Y. Acad. Sci.
RC Submitted (09-1997) to the SWISS-PROT data bank.
CC -1- CAUTION: We are unable to find this protein in the translation of
CC the genome of strain H37Rv.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA: 819 MW; 8B3D340B19C0C2D2 CR 64;
Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
DB 1
7 AK 8

RESULT 15
RS1_ERWCH
ID RS1_ERWCH STANDARD; PRT; 8 AA.
AC P37985;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 42, Last annotation update)
DE 30S ribosomal protein S1 (Fragment).
CC RPSA.
OS Erwinia chrysanthemi.
CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Pectobacterium.
CC NCBI_TaxID:556;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN:3937;
RA Dossillie A., Toussaint A., Faclen M.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BINDS MRNA; THUS FACILITATING RECOGNITION OF THE
CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT
CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X74750; CAA52769.1;
DR PIR: S37141; S37141.
KW Ribosomal protein; Repeat; RNA-binding.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA: 837 MW; 9E18733DC5B339CD CR 64;
Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
DB 1
5 AK 6

RESULT 16
RS7_MYC11

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ID RS7_MYCIT STANDARD: PRT: 8 AA.
 AC P33564;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S7 (Fragment).
 GN RPS3.
 OS Mycobacterium intracellulare.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
 CX NCBI_TaxID=1767;
 FN [1]
 SEQUENCE FROM N.A.
 MEDLINE=94197130; PubMed=8451117;
 KA Nair J., Kouse D.A., Morris S.L.;
 RI "Nucleotide sequence analysis of the ribosomal S12 gene of
 RI Mycobacterium intracellulare."
 RL Nucleic Acids Res. 21:1039-1049(1993).
 CC -!- FUNCTION: One of the primary rRNA binding proteins. It binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center, probably blocks exit of the E-site
 CC tRNA (by similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
 CC and S11 (by similarity).
 CC -!- SIMILARITY: BELONGS TO THE S/P FAMILY OF RIBOSOMAL PROTEINS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation;
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 CC or send an email to license@isb.sib.ch).
 CC
 DR EMBL: D08171; AAA25376.1;
 DR PIR: S35538; S35538.
 DR HAMAP: MF_00480; 1;
 DR InterPro: IPR000235; Ribosomal_S7.
 DR PROSITE: PS00052; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; rRNA-binding; rRNA binding.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 850 MW; 6327616768732417 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 7 SK 8
 II
 DB 2 RK 3

 RESULT 17
 CHOU9_RAT
 ID CHOU9_RAT STANDARD: PRT: 8 AA.
 AC P56575;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Unknown protein from 2D-page of heart tissue (Spot 49) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10116;
 FN [1]
 SEQUENCE.
 RC STRAIN=Histar; TISSUE=Heart;
 RA Li X.-P., Pleissner K.-P., Scheller C., Knitz-Zachrasek V., Salikov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN

CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 ER 5
 II
 DB 2 ER 3

 RESULT 18
 COXE_IHUCR
 ID COXE_IHUCR STANDARD: PRT: 9 AA.
 AC P80575;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome c oxidase polypeptide via (EC 1.9.3.1) (Fragment).
 OS Thunnus obesus (Bigeye tuna).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 CC Scombridae; Thunnus.
 CX NCBI_TaxID=8241;
 FN [1]
 SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=97454291; PubMed=9310466;
 RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
 RA Kadenbach B.;
 RI "The subunit structure of cytochrome-c oxidase from tuna heart and
 RI liver."
 RL Eur. J. Biochem. 248:99-103(1997).
 CC -!- CHAINS: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
 DR PIR: S77984; S77984.
 DR InterPro: IPR001349; COX6A.
 DR PROSITE: PS01329; COX6A; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1136 MW; 62E072C9CB0776DB CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 KE 4
 II
 DB 1 KE 2

 RESULT 19
 HUTU_KLEAE
 ID HUTU_KLEAE STANDARD: PRT: 9 AA.
 AC P12381;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolonepropionate
 DE hydrolase) (Fragment).
 GN HUTU.
 OS Klebsiella aerogenes.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.


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ER EMBL: X58516; AA16528.1; 1; 1;
DR EMBL: X02872; CAA26630.1; 1; 1;
DR EMBL: X60827; CAA43217.1; 1; 1;
DR EMBL: X65462; CAA46454.1; 1; 1;
DR F01: B24362; B24362;
DR PIR: S10494; S30494;
KW Leader peptide; Antibiotic resistance; Peptide;
SQ SEQUENCE 9 AA: 1074 MW: 569CA5AA95B555166044;

Query Match: 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3
DE 1
DE 2 KK 3

RESULT 24
RS10_SERMA
ID RS10_SERMA STANDARD; PRT; 9 AA
AC 066936;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S10 (Fragment)
GN RPS1;
OS Serratia marcescens;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia;
OX NCBI_TaxID: 615;
RN 11;
RP SEQUENCE FROM N.A.
RA Nadrani S.M., Lindahl L., Zengel J.M.;
RL Submitted (APR-1998) to the EMBL/Genbank/DDBJ databases;
CC 1 FUNCTION: Involved in the binding of tRNA to the ribosomes (by similarity);
CC 1 SIMILARITY: BELONGS TO THE S10 FAMILY OF RIBOSOMAL PROTEINS;
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CC
DR EMBL: AF058451; AAC14294.1;
DR HAMAP: MF00598; 1;
DR BLOCK: PR021848; Ribosomal_S10;
DR PROSITE: PS00361; RIBOSOMAL_S10; 1; 1;
KW Ribosomal protein;
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA: 1214 MW: DE0943 0410430030601;

Query Match: 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QK 7
DE 1
DE 4 QK 5

RESULT 25
RT13_BOVIN
ID RT13_BOVIN STANDARD; PRT; 9 AA
AC PR2926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S10 (S10c2) (EMBL-854) (Fragment);
GN MRPS13;

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OS Bos taurus (Bovine);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos;
OX NCBI_TaxID: 9913;
RN 11;
RP SEQUENCE;
RC TISSUE=Liver;
RX MEDLINE:212764; PubMed 11279123;
RA Koe E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
PT *The small subunit of the mammalian mitochondrial ribosome; identification of the full complement of ribosomal proteins present.*;
RL J. Biol. Chem. 276:19363-19374 (2001);
CC 1 SUBUNIT: Component of the mitochondrial ribosome small subunit (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC 1 SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion;
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA: 1032 MW: D44ID73776DB0589 CRC64;

Query Match: 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
DE 1
DE 8 AK 9

RESULT 24
THYF_PIG
ID THYF_PIG STANDARD; PRT; 9 AA
AC P01255;
DT 21-JUL-1996 (Rel. 61, Created)
DT 21-JUL-1996 (Rel. 61, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Thymic factor;
OS Sus scrofa (Pig);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus;
OX NCBI_TaxID: 9823;
RN 11;
RP SEQUENCE;
RX MEDLINE:74024571; PubMed 914862;
RA Pless J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
RT *Structural study of circulating thymic factor: a peptide isolated from pig serum. II. Amino acid sequence.*;
RL J. Biol. Chem. 272:8045-8047 (1977);
CC 1 MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
DR PIR: A01521; YEPG;
KW Pyrrolidone carboxylic acid
FT MISC_RES 3
FT MISC_RES 3
SQ SEQUENCE 9 AA: 876 MW: D5U0B87866C5B33D CRC64;

Query Match: 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
DE 1
DE 2 AK 3

RESULT 25
CLAD_HUMAN
ID CLAD_HUMAN STANDARD; PRT; 9 AA
AC P33297;
DT 31-JUL-1993 (Rel. 26, Created)
DT 31-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 45, Last annotation update)
DE Unknown protein from 20-page of liver tissue (Spot 106) (Fragment);
GN

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CCOXS_SHEEP
 ID CCOXS_SHEEP STANDARD: PRT: 10 AA.
 AC P80337;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIII liver/heart (6019331)
 DE (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae;
 NC Bovidae; Caprinae; Ovis;
 NC NCBI_TaxID: 9940;
 RN [1]
 RP SEQUENCE.
 RC Tissue: Heart, and Liver;
 RA Freund R., Kadenbach B.;
 RL Submitted (MAR-1994) to the SWISS-PROT data bank.
 CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR CODED POLYPEPTIDE
 CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + 2 H⁺ → 4 ferrioxochrome
 c + 2 H₂O.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.
 KW Oxidoreductase; Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1027 MW: 34595CA340C76340CR64;
 Query Match 18.2% Score 2; DB 1; Length 10;
 Best local Similarity 100.0%; Pred. No. 9.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AK 2
 QD 3 AK 4
 RESULT 40
 MALE_KLEPN STANDARD: PRT: 10 AA.
 ID MALE_KLEPN
 AC Q05554;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 10-MAY-2000 (Rel. 39, Last annotation update)
 DE Maltose-binding periplasmic protein (Maltobioson binding protein)
 DE (MBBP) (Fragment).
 GN MALE.
 OS Klebsiella pneumoniae.
 NC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 NC Enterobacteriaceae; Klebsiella;
 NC NCBI_TaxID 5737;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1033-5P24 / KAY2026;
 RA MEDLINE-93211295; PubMed-8456774;
 RA Bacheller S., Perrin D., Rotnau M., Gilson F.;
 RT "Bacterial interspersed mosaic elements (BIMSEs) are present in the
 genome of Klebsiella".
 RL Mol. Microbiol. 7:537-544(1993)
 CC -!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE
 TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AM.
 CC CHEMOTAXIS TOWARD MALTOLOGICARBAHIDES.
 CC SUBCELLULAR LOCATION: Periplasmic.
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRA-CELLULAR SOLUTE-BINDING
 PROTEIN FAMILY 1.
 CC
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 or send an email to license@sib-sb.ch).

CC EMBL: X68329; CAA44006.1;
 DR InterPro: IPR006061; SBP_dom1;
 DR PROSITE: PS01037; SBP_BACTERIAL_1; PARTIAL.
 KW Transport; Sugar transport; Periplasmic.
 FT NON_TER 1
 SQ SEQUENCE 10 AA: 1159 MW: 8FD8DC4415A6UDDA CRC64;
 Query Match 18.2% Score 2; DB 1; Length 10;
 Best local Similarity 100.0%; Pred. No. 9.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 KD 9
 QD 2 KD 3
 RESULT 31
 MP2_MICOC STANDARD: PRT: 10 AA.
 ID MP2_MICOC
 AC P81533;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MP2 protein (fragment).
 OS Microplitis ocellatae (Braconid wasp).
 NC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 NC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
 NC Braconidae; Microgasterinae; Microplitis.
 NC NCBI_TaxID=99573;
 RN [1]
 RP SEQUENCE.
 RC Tissue: Larva;
 RA Takahashi M., Quicke D.L.J.;
 RL Submitted (OCT-1998) to the SWISS-PROT data bank.
 CC -!- TISSUE SPECIFICITY: SALIVARY GLANDS.
 CC -!- DEVELOPMENTAL STAGE: LARVAL.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1255 MW: FE4FD93366C41AFA CRC64;
 Query Match 18.2% Score 2; DB 1; Length 10;
 Best local Similarity 100.0%; Pred. No. 9.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 RQ 6
 QD 5 RQ 6
 RESULT 32
 NS1_MYCTU STANDARD: PRT: 10 AA.
 ID NS1_MYCTU
 AC P81135;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 30 kDa non-secretory protein 1 (fragment).
 OS Mycobacterium tuberculosis.
 NC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 NC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 NC NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE.
 RC STRAIN-H37RV;
 RA Prasad H.K., Anandhara P.S.;
 RL Submitted (DEC-1997) to the SWISS-PROT data bank.
 CC -!- CAUTION: We are unable to find this protein in the translation of
 the genome of strain H37RV.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1042 MW: 8767FE6AB2C73771 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 10;

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Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
DB 9 AK 10

RESULT 34
PSRF_CAPAN STANDARD; PRI: 1; AA:
AC Q03367;
DI 01-JUN-1994 (Rel. 29, Created)
DI 01-JUN-1994 (Rel. 29, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI)
DE (Fragment).
GN PSBF.
OS Capsicum annuum (bell pepper).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID:4072;
KN [1]
RP SEQUENCE FROM N.A.
SC STRAIN:cv. Camayo; TISSUE: Fruit, and Leaf;
RX MEDLINE:94099270; PubMed:1463853;
RA Kunitz M., Camara R., Weil J.-H., Schmitz R.;
RT "The psbL gene from bell pepper (Capsicum annuum): plastid KNA
editing also occurs in non-photosynthetic chlamyoplasts.";
RL Plant Mol. Biol. 20:1185-1198(1992).
CC -1- FUNCTION: This b-type cytochrome is tightly associated with the
CC reaction center of photosystem II and possibly is part of the
CC water oxidation complex.
CC -1- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC -1- SIMILARITY: Belongs to the psbL / psbF family.
CC
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CC or send an email to license@isb-sb.ch).
CC
DB EMBL: X65570; CAA46549.1;
DB PIR: S28055; S28055.
DB HAMAP: MF_00643; 1;
DB InterPro: IPR006216; IYF_0759.
DB PROSITE: PS00537; CYTOCHROME b559, LAMINAR.
KW Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane;
FT NON-TER 1
FT TRANSMEM 4 5 BY SIMILARITY.
FT DOMAIN 6 10 LUMENAL (P-TERMINAL);
SQ SEQUENCE 10 AA: 1180 MW: 817005.666kDa; CRK4.

Query Match 38.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QR 7
DB 9 QR 10

RESULT 34
RCA_PIPNS STANDARD; PRI: 1; AA:
AC P81084;
DI 15-JUL-1998 (Rel. 36, Created)
DI 15-JUL-1998 (Rel. 36, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE
DE (Fragment).
GN PIPNS.
OS
OS (Fragment).
OX NCBI_TaxID:31287;
KN [1]
RP SEQUENCE
SC STRAIN:DM 7;
RX Schreiner S.J.;
RT "Characterization of a surface protein in macrocysts of Dictyostelium
RL macrocysts."
CC -1- FUNCTION: THIS PROTEIN IS PRESENT IN THE MACROCYST PRIMARY WALL
CC WHICH IS PRODUCED BY AMOEBAE DURING THE ONSET OF SEXUAL
CC REPRODUCTION.
CC -1- SUBCELLULAR LOCATION: MACROCYST PRIMARY WALL.
CC Cell wall.
FT NON-TER 10
SQ SEQUENCE 10 AA: 1190 MW: 186707AA3345B50 CRG64;

Query Match 38.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DE Probable ribulose biphosphate carboxylase/oxygenase activase (Rubisco
DE activase) (RA) (Water stress responsive protein 4) (fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID:71647;
KN [1]
RP SEQUENCE.
RX TISSUE: Needle;
RX MEDLINE:98418576; PubMed:9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RX TISSUE: Needle;
RX MEDLINE:99274088; PubMed:10344291;
RA Costa P., Pionneau C., Baw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- FUNCTION: ACTIVATION OF RUBISCO (RUBULOSE-1,5-BISPHOSPHATE
CC CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT
CC CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A
CC CARBAMATE STRUCTURE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
CC -1- INDUCTION: By water stress.
CC -1- SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
KW Chloroplast; ATP-binding.
FT NON-TER 1
FT NON-TER 10
SQ SEQUENCE 10 AA: 1171 MW: C0A506D2C72B1EA6 CRG64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
DB 9 AK 10

RESULT 35
SP34_DICMU STANDARD; PRI: 10 AA:
AC P81545;
DI 15-JUL-1999 (Rel. 48, Created)
DI 15-JUL-1999 (Rel. 48, Last sequence update)
DI 15-JUL-1999 (Rel. 48, Last annotation update)
DE Surface protein P34 (fragment).
GN P34.
OS Dictyostelium mucoroides (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID:31287;
KN [1]
RP SEQUENCE.
SC STRAIN:DM 7;
RX Schreiner S.J.;
RT "Characterization of a surface protein in macrocysts of Dictyostelium
RL mucoroides."
CC -1- FUNCTION: THIS PROTEIN IS PRESENT IN THE MACROCYST PRIMARY WALL
CC WHICH IS PRODUCED BY AMOEBAE DURING THE ONSET OF SEXUAL
CC REPRODUCTION.
CC -1- SUBCELLULAR LOCATION: MACROCYST PRIMARY WALL.
CC Cell wall.
FT NON-TER 10
SQ SEQUENCE 10 AA: 1190 MW: 1B6A707AA3345B50 CRG64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CC 1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC
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CC or send an email to license@sib-sib.ch).
CC
DR EMBL: L77076; AAB41342.1;
DR HAMAP: MF_00252; 1;
DR InterPro: IPR006395; tRNA_Ligase-II;
DR PROSITE: PS50862; AA_IRNA_LIGASE-II; PARTIAL.
KW Aminoacyl-tRNA Synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Metal-binding; Magnesium;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1218 MW: 9CEA46AB13372B05 CRC64;

Query Match 18.2% Score 2: DB 1: Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KE 4
DB 11
6 KE 7

RESULT 38
TKNL_SCYCA STANDARD: PRT: 10 AA.
AC P08508;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Scyllorhinin I.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN 11
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=86192829; PubMed=2422058;
RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;
RT "Scyllorhinin I and II: two novel tachykinins from dogfish gut.";
RI FEBS Lett. 200:111-116(1986).
RN 12;
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazen N., Halment R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, Scyllorhinus canicula.";
RI Eur. J. Biochem. 214:469-474(1993).
CC 1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: A24867; A24867.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA: 1219 MW: D0602D6B59C33AA9 CRC64;

Query Match 18.2% Score 2: DB 1: Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 3
DB 11
2 KK 3

RESULT 37
SYK_CAMPUP STANDARD: PRT: 10 AA.
AC Q46464;
DT 15-DEC-1992 (Rel. 37, Created)
DT 15-DEC-1992 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine tRNA Ligase) (LYSKS)
DE (Fragment).
DE LYSS.
OS Campylobacter upsaliensis.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=28080;
RN 11
RP SEQUENCE FROM N.A.
RC SPRAIN=ATCC 43954;
RX MEDLINE=97149302; PubMed=8996110;
RA Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;
RT "Characterization of Campylobacter upsaliensis for and its
RT localization in a highly conserved region of the Campylobacter
RT genome.";
RI Gene 183:219-224(1996).
CC 1- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) -> AMP + diphosphate
CC + L-lysyl-tRNA(Lys).
CC 1- COFACTOR: Binds 3 magnesium ions per subunit (by similarity).
CC 1- SUBUNIT: Homodimer (by similarity).
CC 1- SUBCELLULAR LOCATION: Cytoplasmic.

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Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KQ 5
II
DB 2 KQ 5

RESULT 41
UAA6_CHELTH STANDARD: PRI: 10 AA.
AC UAA6_CHELTH PRI: 10 AA.
DT 01-OCT-1994 (Rel. 40, Last sequence update)
DT 01-OCT-1994 (Rel. 40, Last sequence update)
DT 30-MAY-2000 (Rel. 59, Last annotation update)
DE Unknown protein from 20-page from elementary body (Fragment).
DE Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OC NCBI_TaxID:813;
RN [1]
RP SEQUENCE:
RC STRAIN-LZ/434/B-1
RA Bini L., Santucci A., Maqui B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Viretton E., Ratti G.,
RA Pallini V.,
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.44; ITS MW IS: 38.6 KDa.
DR SIOGA 2DPAGE: P38307;
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1243 MW: DAD39A33304H5339 CRC64:

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 1
II
DB 7 KK 8

RESULT 42
ASL2_HACSE STANDARD: PRI: 11 AA.
AC P81147; HACSE PRI: 11 AA.
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Acharan sulfate lyase 2 (EC 4.2.2.1) (Fragment).
CS Bacteroides stercoris.
OC Bacteriata; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OC NCBI_TaxID:46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN-HJ-15;
RX MESLINE-2123019; PubMed:11422884;
RA Kim B.T., Hong S.W., Kim W.S., Kim Y.S., Kim D.-H.;
RI "Purification and characterization of acharan sulfate lyases, two
RI novel heparinases, from Bacteroides stercoris HJ-15.";
RA Eur. J. Biochem. 268:2635-2641(2001).
CC -1- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparan and heparan sulfate.
CC -1- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -1- SUBUNIT: Monomer.
CC -1- PTM: The N-terminus is blocked.
CC -1- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding;
FT NON_TER 1 1
SQ SEQUENCE 11 AA: 11

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DI 10
II
DB 1 DI 2

RESULT 40
TKU1_UREN STANDARD: PRI: 10 AA.
AC P40751; UREN PRI: 10 AA.
DT 01-FEB-1995 (Rel. 41, Created)
DT 01-FEB-1995 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Greckistachykinin 1.
OC Urechis uncinatus.
OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinodermata; Echinodermata; Echinodermata;
OC NCBI_TaxID:6442;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Ventral nerve cord;
RX MESLINE-98236558; PubMed:8476412;
RA Ikeda T., Minakata H., Nomoto K., Kikuchi T., Ruzsaska Y.,
RI "Two novel tachykinin-related neuropeptides in the echinoid worm,
RI Urechis uncinatus.";
RA Biochem. Biophys. Res. Commun. 1993; (1993);
CC -1- FUNCTION: CONTRACTILE ACTION ON THE INNER TROPHIC BODY WALL.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation;
FT MID_RES 10 10
SQ SEQUENCE 10 AA: 1177 MW: C631C462F3965A6 16047

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
II
DB 1 AK 2

RESULT 39
TKS2_AEDAE STANDARD: PRI: 10 AA.
AC P42635; AEDAE PRI: 10 AA.
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sialokinin II.
OC Aedes aegypti (Yellowfever Mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Neotera; Diptera; Aedes.
OC NCBI_TaxID:7159;
RN [1]
RP SEQUENCE:
RC STRAIN-Rockefeller; TISSUE:Salivary gland;
RX MESLINE-54195119; PubMed:6278454;
RA Champagne L.E., Ribeiro J.M.C.;
RI "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
RI mosquito Aedes aegypti.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:148 142(1994).
CC -1- FUNCTION: VASODILATORY PEPTIDE MAY ACTIVATE MACROPHAGES AT THE
CC SITE OF FEEDING.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: B49581; B49581;
DR InterPro: IPR002040; Tachykinin;
DR PROSITE: PS0267; TACHYKININ; 1;
KW Tachykinin; Neuropeptide; Amidation;
FT MID_RES 10 10
SQ SEQUENCE 10 AA: 1146 MW: 527726535A6A 16047

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SQ SEQUENCE 11 AA: 1195 MW: 179089707AA451AL CW64;
Query Match 18.2% Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QK 7
DB 10 QK 11

RESULT 43
BRK_MSCFL
ID BRK_MSCFL STANDARD: PRT; 11 AA;
AC P12757;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DE Meqascoliaflavins ((Trb6)bradykinin-Lys-Ala) (Contains: Bradykinin like
peptide ((Trb6)bradykinin)).
OS Megascolia flavitrons (Garden dagger wasp) (Socially wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
NC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Scolioidea;
OX Scolidae; Megascolia.
NX NCBI_TaxID:7437;
RN 1;
RP SEQUENCE;
RC TISSUE-Venom;
RX MEDLINE 87253024; PubMed-3617088;
RA Yasuhara T, Mantel P, Nakajima T, Toki T;
RT "Two kinins isolated from an extract of the venom reservoirs of the
solitary wasp Megascolia flavitrons";
RE Toxicon 25:527-535(1987);
RN 12;
RP SEQUENCE;
RC TISSUE-Venom;
RA Nakajima T, Plek T, Yashara T, Mantel P;
RT "Two kinins isolated from the venom of Megascolia flavitrons";
RE Toxicon 26:34-34(1988);
OC FUNCTION: Both proteins have bradykinin like although lower
activities (e.g. smooth muscle contraction);
NC SUBCELLULAR LOCATION: Secreted, wasp venom reservoirs
CX 1. SIMILARITY: BELONGS TO THE BRADYKININ FAMILY;
DE PIR: B26744; B26744;
KW Bradykinin; Vasodilator;
FT PEPTIDE 1 11
FT PEPTIDE 1 5
SQ SEQUENCE 11 AA: 1273 MW: 148674.671AA1A7 CW64;

Query Match 18.2% Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QK 8
DB 9 QK 10

NXSN_PSEFE
ID NXSN_PSEFE STANDARD: PRT; 11 AA;
AC P59072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Short neurotoxin Ni (Alpha neurotoxin) (Pipera)
OS Pseudonaja textilis (Eastern Brown Snake)
OC Eukaryota; Metazoa; Chordata; Chelonia; Vertebrata; Euteleostomi;
NC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OX Elapidae; Acanthophiinae; Pseudonaja;
NX NCBI_TaxID:8674;
RN 1;
RP SEQUENCE, AND MASS SPECTROMETRY;

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TISSUE-Venom;
RX MEDLINE-99449692; PubMed-19518793;
RA Gong N.L., Arumugam A., Jayaseelan K.;
RT "Postsynaptic short chain neurotoxins from Pseudonaja textilis: cDNA
cloning, expression and protein characterization.";
RE Eur. J. Biochem. 265:982-989(1999);
OC FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
acetylcholine receptors (nAChR);
NC SUBCELLULAR LOCATION: Secreted;
CX 1. TISSUE SPECIFICITY: Expressed by the venom gland.
CX 1. MASS SPECTROMETRY: MW-6236; METHOD-Electrospray.
CX 1. MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
CX 1. SIMILARITY: Belongs to the snake toxin family.
DE InterPro: IPR003571; Snake toxin;
PR ProSite: PS00272; SNAKE_TOXIN; PARTIAL;
KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
KW Acetylcholine receptor inhibitor; Multigene family;
FT UNSURE 3
FT NCN_IER 11 11
SQ SEQUENCE 11 AA: 1315 MW: 101EF0C81B58732B CRC64;

Query Match 18.2% Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DI 10
DB 9 DI 10

RESULT 45
PKCL_CARMO
ID PKCL_CARMO STANDARD: PRT; 11 AA;
AC PB2584;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinnin-1 (3am-PK-1) (FXPRL-Amide);
OS Carastus morosus (Indian stick insect);
NC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatoidea; Euphasmida; Phasmatoidea;
OX Heteronemidae; Carastus;
NX NCBI_TaxID:7622;
RN 11;
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY;
RC TISSUE-Corpora cardiaca;
RA Predel R, Kellner R, Garde G;
RT "Myotropic neuropeptides from the retrocerebral complex of the stick
insect, Carastus morosus (Phasmatoidea: Lonchodidae).";
RE Eur. J. Entomol. 96:275-278(1999);
OC FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CX 1. (MYOTROPIC ACTIVITY);
CX 1. MASS SPECTROMETRY: MW-1235; METHOD-MALDI;
CX 1. SIMILARITY: BELONGS TO THE PYROKININ FAMILY;
DE InterPro: IPR01484; Pyrokinnin;
PR ProSite: PS00539; PYROKININ; FALSE_NEG;
KW Neuropeptide; Amidation; Pyrokinnin;
FT MOD_RES 11 11
FT AMIDATION;
SQ SEQUENCE 11 AA: 1236 MW: 2BFA5225BB46C1A8 CRC64;

Query Match 18.2% Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IQ 11
DB 5 IQ 6

RESULT 46
PQOC_PSEFL
ID PQOC_PSEFL STANDARD: PRT; 11 AA;
AC P55173;

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RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Intestine;
 RX MEDLINE:91254337; PubMed-2043143;
 RA Kozawa H., Hino J., Minamino N., Kandawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (*Rana catesbeiana*)
 RI brain and intestine."
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991)
 RN [2]
 RP SEQUENCE.
 RC TISSUE-Intestine;
 RX MEDLINE:94023216; PubMed-8210506;
 RA Kandawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RI "Four novel tachykinins in frog (*Rana catesbeiana*) brain and
 RL intestine."
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SURCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: D61031; D61033.
 DR InterPro: IPR002040; Tachykinin.
 DR PROSITE: PS00267; TACHYKININ; FALSE NEG.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MGI_RES 11 11
 SQ SEQUENCE 11 AA: 1350 MW: 3A34256C09143807 CRC64;

Query Match 18.2% Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.le-04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ER 5
 DB 5 ER 6

RESULT 50
 TRN_ELEM
 ID TRN_ELEM STANDARD; PRI; 11 AA.
 AC P01293;
 GI 21-JUN-1986 (Rel. 01, Created)
 RI 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Eledoisin.
 OS Eledone moschata (Musk octopus) (*Loligo pfeifferi*) and
 OS Eledone cirrosa (Curled octopus) (*Eledone cirrosa*).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Nautilus; Nautilus.
 OC Octopodiformes; Octopoda; Incirrata; Oct. 4 subcl. Pledone.
 OX NCBI_TaxID=6641, 102876;
 RN [1]
 RP SEQUENCE.
 RA Anastasi A., Erspamer V.;
 RI "The isolation and amino acid sequence of eledoisin, the active
 RT endocapside of the posterior salivary glands of *Eledone*."
 RL Arch. Biochem. Biophys. 101:56-65(1964)
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- SURCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: SKIN.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY
 DR PIR: A01561; EOCG.
 DR PIR: B01561; EOCG.
 DR PDB: 1MXQ; 18-FEB-03.
 DR InterPro: IPR002040; Tachykinin
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; L-tyrosine carboxylic acid;
 3D-structure.
 FT MGI_RES 11 11
 SQ SEQUENCE 11 AA: 1206 MW: 5700702559CIRAA; CRC64;

Query Match 18.2% Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.le-04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KD 9
 DB 4 KD 5

Search completed: September 10, 2003, 10:25:58
 Job time : 8.25 secs

Genome version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2003, 10:02:04 - Search time: 41.653.7 seconds
(without adjustments)
89.649 Million comp. updates/sec

Title: US-09-787-443-2

Perfect score: 11

Sequence: AKKERQKDTQ 11

Scoring table: OLIGO

Gapop 60.0 - Gapext 60.0

Searched: 830525 seqs, 258052504 residues

Word size: 9

Total number of hits satisfying chosen parameters: 3459

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database:

- 1: SP-archaea:
- 2: SP-bacteria:
- 3: SP-fungi:
- 4: SP-human:
- 5: SP-invertebrate:
- 6: SP-mammal:
- 7: SP-mhc:
- 8: SP-ordanelle:
- 9: SP-phage:
- 10: SP-plant:
- 11: SP-rodent:
- 12: SP-virus:
- 13: SP-vertebrate:
- 14: SP-unclassified:
- 15: SP-services:
- 16: SP-bacteriophage:
- 17: SP-archaea:

Prod. No. is the number of results produced by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	11	4	Q914G2
2	4	36.4	11	15	Q909W4
3	4	36.4	15	2	Q549J1
4	4	27.3	8	4	Q15895
5	3	27.3	10	2	P8316C
6	3	27.3	11	4	Q9H4H5
7	3	27.3	11	6	Q91RW5
8	3	27.3	12	2	Q8V1X8
9	3	27.3	12	16	Q25174
10	3	27.3	13	2	Q55044
11	3	27.3	13	4	Q9H4C1
12	3	27.3	13	6	Q914K5
13	3	27.3	13	8	Q914H5
14	3	27.3	13	8	Q914K4
15	3	27.3	13	8	Q914H6
16	3	27.3	13	8	Q914H2

17	3	27.3	13	8	Q914K6
18	3	27.3	13	8	Q914K3
19	3	27.3	13	12	Q81761
20	3	27.3	13	12	Q81794
21	3	27.3	13	12	Q81784
22	3	27.3	13	12	Q81778
23	3	27.3	13	12	Q81787
24	3	27.3	13	12	Q81775
25	3	27.3	13	12	Q81767
26	3	27.3	13	12	Q81798
27	3	27.3	13	12	Q81774
28	3	27.3	13	12	Q81766
29	3	27.3	13	12	Q81793
30	3	27.3	13	12	Q81768
31	3	27.3	13	12	Q81785
32	3	27.3	13	12	Q81800
33	3	27.3	13	12	Q81765
34	3	27.3	13	12	Q81781
35	3	27.3	13	12	Q81769
36	3	27.3	13	12	Q81773
37	3	27.3	13	12	Q81799
38	3	27.3	13	12	Q81786
39	3	27.3	13	12	Q81788
40	3	27.3	13	12	Q81763
41	3	27.3	13	12	Q81764
42	3	27.3	13	12	Q81796
43	3	27.3	13	12	Q81791
44	3	27.3	13	12	Q81790
45	3	27.3	13	12	Q81783
46	3	27.3	13	12	Q81789
47	3	27.3	13	12	Q81797
48	3	27.3	13	12	Q81795
49	3	27.3	13	12	Q81782
50	3	27.3	13	12	Q81780
51	3	27.3	13	12	Q81771
52	3	27.3	13	12	Q81779
53	3	27.3	13	12	Q81772
54	3	27.3	13	12	Q81792
55	3	27.3	13	12	Q81777
56	3	27.3	13	16	Q8X4F5
57	3	27.3	14	2	Q56750
58	3	27.3	14	2	Q46291
59	3	27.3	14	2	Q811Y9
60	3	27.3	14	4	Q15948
61	3	27.3	14	5	Q91WX8
62	3	27.3	14	11	Q9CS5H
63	3	27.3	14	13	P82831
64	3	27.3	14	16	Q9KEL4
65	3	27.3	15	2	Q9H4M8
66	3	27.3	15	2	Q47612
67	3	27.3	15	3	Q9URR0
68	3	27.3	15	4	Q9UCCT
69	3	27.3	15	4	Q9UCN2
70	3	27.3	15	4	Q81Z00
71	3	27.3	15	5	Q91TW4
72	3	27.3	15	5	Q91TW3
73	3	27.3	15	10	Q9SQ16
74	3	27.3	15	11	Q9QW72
75	3	27.3	15	12	Q66543
76	2	18.2	8	2	Q9H7T2
77	2	18.2	8	2	Q9AGP4
78	2	18.2	8	2	Q9R3X0
79	2	18.2	8	2	Q68485
80	2	18.2	8	2	Q93SR0
81	2	18.2	8	2	Q93SR0
82	2	18.2	8	2	Q92558
83	2	18.2	8	2	Q8RSR3
84	2	18.2	8	2	Q56429
85	2	18.2	8	2	Q9R9E0
86	2	18.2	8	2	Q45889
87	2	18.2	8	2	Q9R5R0
88	2	18.2	8	2	Q51594
89	2	18.2	8	2	Q53790

Q914K6	bryopsis sp
Q914K3	bryopsis sp
Q81761	hepatitis c
Q81794	hepatitis c
Q81784	hepatitis c
Q81778	hepatitis c
Q81787	hepatitis c
Q81775	hepatitis c
Q81767	hepatitis c
Q81798	hepatitis c
Q81774	hepatitis c
Q81766	hepatitis c
Q81793	hepatitis c
Q81768	hepatitis c
Q81785	hepatitis c
Q81800	hepatitis c
Q81765	hepatitis c
Q81781	hepatitis c
Q81769	hepatitis c
Q81773	hepatitis c
Q81799	hepatitis c
Q81786	hepatitis c
Q81788	hepatitis c
Q81763	hepatitis c
Q81764	hepatitis c
Q81796	hepatitis c
Q81791	hepatitis c
Q81790	hepatitis c
Q81783	hepatitis c
Q81789	hepatitis c
Q81797	hepatitis c
Q81795	hepatitis c
Q81782	hepatitis c
Q81780	hepatitis c
Q81771	hepatitis c
Q81779	hepatitis c
Q81772	hepatitis c
Q81792	hepatitis c
Q81777	hepatitis c
Q81777	hepatitis c
Q8X4F5	escherichia
Q56750	western x p
Q46291	canadian pe
Q811Y9	chroococcid
Q15948	homo sapien
Q91WX8	manduca sex
Q9CS5H	mus musculus
P82831	rana luteiv
Q9KEL4	bacillus ha
Q9H4M8	bacillus fi
Q47612	escherichia
Q9URR0	saccharomyc
Q9UCCT	homo sapien
Q9UCN2	homo sapien
Q81Z00	homo sapien
Q91TW4	crithidia f
Q91TW3	axinella po
Q9SQ16	oryza sativ
Q9QW72	rattus norv
Q66543	human herpe
Q9H7T2	escherichia
Q9AGP4	arthrobacte
Q9R3X0	planktothri
Q68485	klebsiella
Q93SR0	staphylococ
Q92558	synecococc
Q8RSR3	lactobacill
Q56429	thermus the
Q9R9E0	bacillus su
Q45889	clostridium
Q9R5R0	shigella dy
Q51594	escherichia
Q53790	streptococc

95	2	18.2	8	2	Q86MM5	Q86MM5	zebra mays (m
96	2	18.2	8	3	Q86MM6	Q86MM6	zebra mays (m
97	2	18.2	8	4	Q86MM7	Q86MM7	zebra mays (m
98	2	18.2	8	5	Q86MM8	Q86MM8	zebra mays (m
99	2	18.2	8	6	Q86MM9	Q86MM9	zebra mays (m
100	2	18.2	8	7	Q86MM10	Q86MM10	zebra mays (m
101	2	18.2	8	8	Q86MM11	Q86MM11	zebra mays (m
102	2	18.2	8	9	Q86MM12	Q86MM12	zebra mays (m
103	2	18.2	8	10	Q86MM13	Q86MM13	zebra mays (m
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105	2	18.2	8	12	Q86MM15	Q86MM15	zebra mays (m
106	2	18.2	8	13	Q86MM16	Q86MM16	zebra mays (m
107	2	18.2	8	14	Q86MM17	Q86MM17	zebra mays (m
108	2	18.2	8	15	Q86MM18	Q86MM18	zebra mays (m
109	2	18.2	8	16	Q86MM19	Q86MM19	zebra mays (m
110	2	18.2	8	17	Q86MM20	Q86MM20	zebra mays (m
111	2	18.2	8	18	Q86MM21	Q86MM21	zebra mays (m
112	2	18.2	8	19	Q86MM22	Q86MM22	zebra mays (m
113	2	18.2	8	20	Q86MM23	Q86MM23	zebra mays (m
114	2	18.2	8	21	Q86MM24	Q86MM24	zebra mays (m
115	2	18.2	8	22	Q86MM25	Q86MM25	zebra mays (m
116	2	18.2	8	23	Q86MM26	Q86MM26	zebra mays (m
117	2	18.2	8	24	Q86MM27	Q86MM27	zebra mays (m
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124	2	18.2	8	31	Q86MM34	Q86MM34	zebra mays (m
125	2	18.2	8	32	Q86MM35	Q86MM35	zebra mays (m
126	2	18.2	8	33	Q86MM36	Q86MM36	zebra mays (m
127	2	18.2	8	34	Q86MM37	Q86MM37	zebra mays (m
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135	2	18.2	8	42	Q86MM45	Q86MM45	zebra mays (m
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137	2	18.2	8	44	Q86MM47	Q86MM47	zebra mays (m
138	2	18.2	8	45	Q86MM48	Q86MM48	zebra mays (m
139	2	18.2	8	46	Q86MM49	Q86MM49	zebra mays (m
140	2	18.2	8	47	Q86MM50	Q86MM50	zebra mays (m
141	2	18.2	8	48	Q86MM51	Q86MM51	zebra mays (m
142	2	18.2	8	49	Q86MM52	Q86MM52	zebra mays (m
143	2	18.2	8	50	Q86MM53	Q86MM53	zebra mays (m
144	2	18.2	8	51	Q86MM54	Q86MM54	zebra mays (m
145	2	18.2	8	52	Q86MM55	Q86MM55	zebra mays (m
146	2	18.2	8	53	Q86MM56	Q86MM56	zebra mays (m
147	2	18.2	8	54	Q86MM57	Q86MM57	zebra mays (m
148	2	18.2	8	55	Q86MM58	Q86MM58	zebra mays (m
149	2	18.2	8	56	Q86MM59	Q86MM59	zebra mays (m
150	2	18.2	8	57	Q86		

245	2	18.2	10	10	Q9S926	Q9S926 glycolic max	309	2	18.2	11	7	Q77911	O77911 oreochromis
246	2	18.2	10	10	Q8LP17	Q8LP17 zea mays (m	310	2	18.2	11	8	Q8MEL7	Q8MEL7 sida hooker
247	2	18.2	10	10	Q9S936	Q9S936 beta vulgar	311	2	18.2	11	8	Q8MAZ1	Q8MAZ1 maripa pani
248	2	18.2	10	10	P82937	P82937 hordeum vul	312	2	18.2	11	8	Q8MB19	Q8MB19 wilsonia hu
249	2	18.2	10	10	P82938	P82938 hordeum vul	313	2	18.2	11	8	Q8MBM2	Q8MBM2 lajunaria p
240	2	18.2	10	10	P82434	P82434 nicotiana gl	314	2	18.2	11	8	Q8MB58	Q8MB58 seddera nlr
241	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	315	2	18.2	11	8	Q8MAZ3	Q8MAZ3 maripa repe
242	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	316	2	18.2	11	8	Q8MES5	Q8MES5 abelmoschus
243	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	317	2	18.2	11	8	Q8MEP0	Q8MEP0 hibiscus pe
244	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	318	2	18.2	11	8	Q8MES1	Q8MES1 alyogyne pl
245	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	319	2	18.2	11	8	Q8MBP3	Q8MBP3 hibiscus no
246	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	320	2	18.2	11	8	Q8MBE1	Q8MBE1 ipomoea alb
247	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	321	2	18.2	11	8	Q8MEP7	Q8MEP7 hibiscus dr
248	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	322	2	18.2	11	8	Q35374	Q35374 paramectum
249	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	323	2	18.2	11	8	Q8MEL9	Q8MEL9 pavonia has
250	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	324	2	18.2	11	8	Q8MB77	Q8MB77 odonellia h
251	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	325	2	18.2	11	8	Q8MER0	Q8MER0 hibiscus co
252	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	326	2	18.2	11	8	Q8MES3	Q8MES3 alyogyne cr
253	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	327	2	18.2	11	8	Q8MB79	Q8MB79 aniseia arg
254	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	328	2	18.2	11	8	Q8MBP5	Q8MBP5 merremia pe
255	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	329	2	18.2	11	8	Q8MBP5	Q8MBP5 hibiscus mi
256	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	330	2	18.2	11	8	Q8MER1	Q8MER1 hibiscus ca
257	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	331	2	18.2	11	8	Q8MER7	Q8MER7 bacteria viti
258	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	332	2	18.2	11	8	Q8A115	Q8A115 bacteria viti
259	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	333	2	18.2	11	8	Q37925	Q37925 bacterioph
260	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	334	2	18.2	11	8	Q9S8X4	Q9S8X4 glycine max
261	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	335	2	18.2	11	8	Q37784	Q37784 gossypium h
262	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	336	2	18.2	11	8	Q82070	Q82070 triticum ae
263	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	337	2	18.2	11	8	Q04131	Q04131 lycopersico
264	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	338	2	18.2	11	8	P83092	P83092 spinacia ol
265	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	339	2	18.2	11	8	P97755	P97755 rattus norv
266	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	340	2	18.2	11	8	Q99N81	Q99N81 mus musculu
267	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	341	2	18.2	11	8	Q9JIE6	Q9JIE6 rattus norv
268	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	342	2	18.2	11	8	Q8R2J7	Q8R2J7 mesocricetu
269	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	343	2	18.2	11	8	P89269	P89269 xestia c-ni
270	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	344	2	18.2	11	8	Q99269	Q99269 equine herp
271	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	345	2	18.2	11	8	Q84073	Q84073 influenza vi
272	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	346	2	18.2	11	8	Q9D232	Q9D232 human immun
273	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	347	2	18.2	11	8	Q9K7A4	Q9K7A4 bacillus ha
274	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	348	2	18.2	12	2	Q56442	Q56442 escherichia
275	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	349	2	18.2	12	2	Q9R5F7	Q9R5F7 helicobacte
276	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	350	2	18.2	12	2	Q9A08	Q9A08 thiobacillu
277	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	351	2	18.2	12	2	Q9R5F5	Q9R5F5 helicobacte
278	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	352	2	18.2	12	2	Q50303	Q50303 bacillus st
279	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	353	2	18.2	12	2	Q46747	Q46747 escherichia
280	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	354	2	18.2	12	2	Q9L4M9	Q9L4M9 streptococ
281	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	355	2	18.2	12	2	Q9R3B3	Q9R3B3 helicobacte
282	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	356	2	18.2	12	2	Q9ZAM7	Q9ZAM7 pseudomonas
283	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	357	2	18.2	12	2	Q8C0A7	Q8C0A7 saccharomyc
284	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	358	2	18.2	12	2	Q90MH0	Q90MH0 homo sapien
285	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	359	2	18.2	12	2	Q9H4F4	Q9H4F4 homo sapien
286	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	360	2	18.2	12	2	Q9H126	Q9H126 homo sapien
287	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	361	2	18.2	12	2	Q9UC37	Q9UC37 homo sapien
288	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	362	2	18.2	12	2	Q13695	Q13695 homo sapien
289	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	363	2	18.2	12	2	Q96PK0	Q96PK0 homo sapien
290	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	364	2	18.2	12	2	Q9UM28	Q9UM28 homo sapien
291	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	365	2	18.2	12	2	Q9H4X3	Q9H4X3 homo sapien
292	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	366	2	18.2	12	2	Q9BR06	Q9BR06 homo sapien
293	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	367	2	18.2	12	2	Q9UNV5	Q9UNV5 homo sapien
294	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	368	2	18.2	12	2	Q8N6B2	Q8N6B2 homo sapien
295	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	369	2	18.2	12	2	Q81VH0	Q81VH0 homo sapien
296	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	370	2	18.2	12	2	Q8MUN4	Q8MUN4 helicobact
297	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	371	2	18.2	12	2	Q9TWV4	Q9TWV4 lymnaea sta
298	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	372	2	18.2	12	2	Q26429	Q26429 drosophila
299	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	373	2	18.2	12	2	Q8MUN9	Q8MUN9 helicobact
300	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	374	2	18.2	12	2	Q61574	Q61574 ostertagia
301	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	375	2	18.2	12	2	Q9TVU2	Q9TVU2 halocynthia
302	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	376	2	18.2	12	2	Q9BFT9	Q9BFT9 tupaia mino
303	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	377	2	18.2	12	2	Q9TQW3	Q9TQW3 bos taurus
304	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	378	2	18.2	12	2	Q9XS31	Q9XS31 sus scrofa
305	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	379	2	18.2	12	2	Q9TRU2	Q9TRU2 bos taurus
306	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	380	2	18.2	12	2	Q9TRT8	Q9TRT8 bos taurus
307	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	381	2	18.2	12	2	Q9TRT7	Q9TRT7 bos taurus
308	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	382	2	18.2	12	2		


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FT  NON_TER      1
ET  NON_TER      11
SQ  SEQUENCE 11 AA: 1342 MW: 6805507A8772944 CRC64;

Query Match      36.4% Score 4: DB 4: Length 11;
Best Local Similarity 100.0%; Pred. No. 6,2e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 ROKK 8
DB  1111
DE  2 ROKK 5

RESULT 4
Q5486:
ID  Q5486 PRELIMINARY: PRI: 11 AA.
AC  Q5486
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DI  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE  (Cloning XP6A15A) (Fragment)
OS  Homo sapiens (Human)
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN  11
RP  SEQUENCE FROM N.A.
RC  TISSUE=Placenta;
RA  Lee C.-C., Yazdani A., Weinert M., Bailey J., Couch L., Xiong M.,
RT  Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RT  *Isolation of chromosome-specific genes by reciprocal probing of
RT  arrayed cDNAs and cosmid libraries.*;
RL  Hum. Mol. Genet. 0:0-0(1995).
DR  EMBL: L32075; AAA73865.1;
FI  NON_TER      1
FT  NON_TER      8
SQ  SEQUENCE 8 AA: 921 MW: C6C735B33686C1AA CRC64;

Query Match      27.3% Score 3: DB 4: Length 8;
Best Local Similarity 100.0%; Pred. No. 8,3e+05;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  9 DTQ 11
DB  1111
DE  1 DTQ 3

RESULT 5
P83160:
ID  P83160 PRELIMINARY: PRI: 10 AA.
AC  P83160
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DI  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE  Ribulose biphosphate carboxylase small chain (EC 4.1.1.39) (RuBisCO
DE  small subunit) (Fragment).
OS  Anabaena sp. (strain L31).
OC  Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
CX  NCBI_TaxID=29412;
RN  11
RP  SEQUENCE.
RA  Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL  Submitted (OCT-2001) to the SWISS-PROT data bank.
CC  -!- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-
CC  RIBULOSE 1,5-BISPHOSPHATE, THE PRIMARY EVENT IN PHOTOSYNTHETIC
CC  CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
CC  THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
CC  REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
CC  ACTIVE SITE.
CC  -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) -> 2 3-
CC  PHOSPHO-D-GLYCERATE.
CC  -!- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) -> 3-
CC  PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
CC  -!- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
CC  -!- SUBCELLULAR LOCATION: CYTOPLASMIC.

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00 11 SIMILARITY: BELONGS TO THE RUBISCO SMALL SUBUNIT FAMILY.
 KW Photosynthesis; Carbon dioxide fixation; Photosynthesis; lysate;
 KW Oxidoreductase; Monooxygenase; Calvin cycle;
 FT NON_TER 10
 SQ SEQUENCE 10 AA: 1322 MW: 88462D0H132767.1 (36764)

Query Match 27.3% Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KER 5
 DB 6 KER 8
 ID 11
 AC Q9H4H5 PRELIMINARY; PRI: 11 AA.
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE 5361120.2 (Novel Helicase C-terminal domain and SNF2 N-terminal
 DE domains containing protein) (Fragment).
 GN h626B11.1
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID 9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RA SOURCE 1
 BL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A051659; CAC17164.2;
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA: 1420 MW: 565232A1426155.4 (36764)

Query Match 27.3% Score 3; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
 DB 2 KKE 5
 ID 1
 AC Q9H4W5 PRELIMINARY; PRI: 11 AA.
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 25 kDa protein P25, peptide P4 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa;
 OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Ruminantia; Bovinae; Bos.
 OX NCBI_TaxID-9913;
 RN 11
 RP SEQUENCE.
 RA MEDLINE: 91372400; PubMed:1909472;
 RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Umeki A., Sato S.,
 RA Shiratsuchi A., Uchida K., Imahori K.
 XT *A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
 RT Ser/Thr-pro kinase (TPK II) from tau protein kinase fractions.*;
 RL FEBS Lett. 289:37-43(1991).
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA: 1276 MW: CAP72LAF55A76AA3 (36764)

Query Match 27.3% Score 3; DB 6; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KER 5
 DB 1 KER 4
 ID 1
 AC Q8VLX8 PRELIMINARY; PRI: 12 AA.
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Lysyl-tRNA synthetase (Fragment)
 GN LYSS.
 OS Thermus thermophilus.
 OC Bacteria; Deihnococcus Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID-274;
 RN 11
 RP SEQUENCE FROM N.A.
 RA STRAIN-K18;
 RA Spada S., Pembroke J., Wall J.C.;
 RT "Cloning and characterisation of the *czrB* metal cation efflux protein
 RT from *T. thermophilus*."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ307316; CAC83721.1;
 KW Aminoacyl tRNA synthetase.
 FT NON_TER 1
 SQ SEQUENCE 12 AA: 1327 MW: 5D2A33E27ECDB13 CRC64;

Query Match 27.3% Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
 DB 4 KKE 6
 ID 1
 AC Q25179 PRELIMINARY; PRI: 12 AA.
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein HP0429.
 GN HP0429.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 OX NCBI_TaxID=210;
 RN 11
 RP SEQUENCE FROM N.A.
 RA STRAIN-26695 / ATCC 700392;
 RA MEDLINE: 97394467; PubMed:9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.G., Glodek A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen *Helicobacter*
 RT *pylori*."
 RL Nature 388:539-547(1997).
 DR EMBL: AF005559; AAP07512.1;
 DR TIGR: HP0429.

KB Bysthelical proteins: Complete proteome.
SQ SEQUENCE 12 AA: 1375 MW: 20959AB482135338 CRC64:

Query Match 27.3% Score 3; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4

DL 6 KKE 8

RESULT 10

Q55094 PRELIMINARY: PRT: 13 AA.

AC Q55094.

DT 01-NOV-1996 (TRENBLREL: 01, Created)

DT 01-NOV-1996 (TRENBLREL: 01, Last sequence update)

DT 01-NOV-1998 (TRENBLREL: 08, Last annotation update)

DE Allophycocyanin (Fragment).

GN APCB.

OS Synechocystis sp.

OC Bacteria; Cyanobacteria; Charococcales; Synechocystis.

OX NCBI_TaxID:1143;

RN 11

RE SEQUENCE FROM N.A.

RX MEDLINE:96235188; PubMed:978795;

RA Brass S.; Ernst A.; Bger P.;

RT *An insertion element prevents physiological synthesis in NZ fixing

RI Synechocystis sp. strain B-8422.

RL Appl. Environ. Microbiol. 62:1464-1468 (1996).

DR EMBL:176084; AAC41532.1;

ET NON-TER

SQ SEQUENCE 13 AA: 1451 MW: 61191791D627776 CRC64:

Query Match 27.3% Score 3; DB 13; Length 13;

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKE 5

DL 9 KKE 11

RESULT 11

Q56401 PRELIMINARY: PRT: 13 AA.

AC Q56401.

DT 01-MAR-2001 (TRENBLREL: 16, Created)

DT 01-MAR-2001 (TRENBLREL: 16, Last sequence update)

DT 01-DEC-2001 (TRENBLREL: 19, Last annotation update)

DE Anotopolon-2B (Fragment).

GN ANOTOPOLON-2B.

OS Homo Sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Echinodermata; Echinodermata; Echinodermata.

OX NCBI_TaxID:9606;

RN 11

RE SEQUENCE FROM N.A.

RX MEDLINE:2042411; PubMed:1964717;

RA Mezquita J.; Mezquita P.; Monserat J.; Mezquita P.; Mezquita V.;

SA Villaresa X.; Mezquita C.;

RT *Genomic structure and alternative splicing of a novel and divergent

RI 2.1.

RE Biochem. Biophys. Res. Commun. 270:454-458 (2000).

DR EMBL:AJ289780; CAC08179.1;

ET NON-TER

SQ SEQUENCE 13 AA: 1548 MW: 35435454E48427464.

Query Match

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
DL 6 KKE 8

RESULT 12

Q574K5 PRELIMINARY: PRT: 13 AA.

AC Q574K5.

DT 01-MAY-2000 (TRENBLREL: 13, Created)

DT 01-MAY-2000 (TRENBLREL: 13, Last sequence update)

DT 01-MAY-2000 (TRENBLREL: 13, Last annotation update)

DE PSH (Fragment).

GN PSH.

OS Bryopsis sp. C.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;

OC Bryopsidaceae; Bryopsis.

OX NCBI_TaxID:104780;

RN 11

RE SEQUENCE FROM N.A.

RP STRAIN VARIOUS STRAINS;

RA Krellwitz E.C.; Kowalik K.V.; Manos P.S.;

RT *Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North

RI Atlantic and Caribbean based on coding and Non-coding sequences of the

RI Chloroplast psbB operon.;

RI Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL:AF170407; AAC56846.1;

DR EMBL:AF170383; AAC56798.1;

DR EMBL:AF170384; AAC56800.1;

DR EMBL:AF170385; AAC56802.1;

DR EMBL:AF170386; AAC56804.1;

DR EMBL:AF170387; AAC56806.1;

DR EMBL:AF170388; AAC56808.1;

DR EMBL:AF170389; AAC56810.1;

DR EMBL:AF170392; AAC56812.1;

DR EMBL:AF170391; AAC56814.1;

DR EMBL:AF170392; AAC56816.1;

DR EMBL:AF170393; AAC56818.1;

DR EMBL:AF170394; AAC56820.1;

KW Chloroplast.

ET NON-TER

SQ SEQUENCE 13 AA: 1366 MW: 2031687A2E93A338 CRC64:

Query Match

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKE 10

DL 7 KKE 9

RESULT 13

Q57HSC PRELIMINARY: PRT: 13 AA.

AC Q57HSC.

DT 01-MAY-2000 (TRENBLREL: 13, Created)

DT 01-MAY-2000 (TRENBLREL: 13, Last sequence update)

DE PSH (Fragment).

GN PSH.

OS Bryopsis sp. B.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;

OC Bryopsidaceae; Bryopsis.

OX NCBI_TaxID:104780;

RN 11

RE SEQUENCE FROM N.A.

RP STRAIN VARIOUS STRAINS;

RA Krellwitz E.C.; Kowalik K.V.; Manos P.S.;

RT *Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North

RI Atlantic and Caribbean based on coding and Non-coding sequences of the

RI Chloroplast psbB operon.;

RI Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL:AF170407; AAC56846.1;

DR EMBL:AF170383; AAC56798.1;

DR EMBL:AF170384; AAC56800.1;

DR EMBL:AF170385; AAC56802.1;

DR EMBL:AF170386; AAC56804.1;

DR EMBL:AF170387; AAC56806.1;

DR EMBL:AF170388; AAC56808.1;

DR EMBL:AF170389; AAC56810.1;

DR EMBL:AF170392; AAC56812.1;

DR EMBL:AF170391; AAC56814.1;

DR EMBL:AF170392; AAC56816.1;

DR EMBL:AF170393; AAC56818.1;

DR EMBL:AF170394; AAC56820.1;

KW Chloroplast.

ET NON-TER

SQ SEQUENCE 13 AA: 1366 MW: 2031687A2E93A338 CRC64:

Query Match

Best Local Similarity 100.0%; Pred. No. 8.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKE 10

DL 7 KKE 9


```

RT Chloroplast psbB Operon.
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RR EMBL: AF170406; AAD56844.1;
RW Chloroplast.
RT NON-TER 13 13
SQ SEQUENCE 13 AA: 1351 MW: 20416A202E3A338 CRC64:
Query Match 27.3% Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 KDT 10
LD 7 KDT 9
RESULT 14
Q9THS6 PRELIMINARY; PRT: 13 AA.
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DE PSB (Fragment).
GN PSB.
OS Bryopsis sp. B.
OC Chloroplast.
EC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;
CC Bryopsidaceae; Bryopsis.
CX NCB: TaxID=103785;
RN 111
RP SEQUENCE FROM N.A.
RA Kreilwitz E.C., Kowalik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
Atlantic and Caribbean based on Coding and Non-coding sequences of the
Chloroplast psbB Operon."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RR EMBL: AF170405; AAD56842.1;
RW EMBL: AF170395; AAD56822.1;
RR EMBL: AF170396; AAD56824.1;
RR EMBL: AF170397; AAD56826.1;
RR EMBL: AF170398; AAD56828.1;
RR EMBL: AF170399; AAD56830.1;
RR EMBL: AF170400; AAD56832.1;
RR EMBL: AF170401; AAD56834.1;
RR EMBL: AF170402; AAD56836.1;
RR EMBL: AF170403; AAD56838.1;
RR EMBL: AF170404; AAD56840.1;
RW Chloroplast.
RT NON-TER 13 13
SQ SEQUENCE 13 AA: 1366 MW: 20416A202E3A338 CRC64:
Query Match 27.3% Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 KDT 10
LD 7 KDT 9
RESULT 15
Q9THS6 PRELIMINARY; PRT: 13 AA.
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DE PSB (Fragment).
GN PSB.
OS Bryopsis sp. B.
OC Chloroplast.
EC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;

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CC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;
CC Bryopsidaceae; Bryopsis.
CX NCB: TaxID=103788;
RN 111
RP SEQUENCE FROM N.A.
RA Kreilwitz E.C., Kowalik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
Atlantic and Caribbean based on Coding and Non-coding sequences of the
Chloroplast psbB Operon."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RR EMBL: AF170407; AAD56780.1;
RW Chloroplast.
RT NON-TER 13 13
SQ SEQUENCE 13 AA: 1362 MW: 20426A7A2E93A338 CRC64:
Query Match 27.3% Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 KDT 10
LD 7 KDT 9
RESULT 16
Q9THS2 PRELIMINARY; PRT: 13 AA.
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DE PSB (Fragment).
GN PSB.
OS Bryopsis sp. B.
OC Chloroplast.
EC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;
CC Bryopsidaceae; Bryopsis.
CX NCB: TaxID=103787;
RN 111
RP SEQUENCE FROM N.A.
RA Kreilwitz E.C., Kowalik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
Atlantic and Caribbean based on Coding and Non-coding sequences of the
Chloroplast psbB Operon."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RR EMBL: AF170402; AAD56795.1;
RW Chloroplast.
RT NON-TER 13 13
SQ SEQUENCE 13 AA: 1366 MW: 20416A7A2E93A338 CRC64:
Query Match 27.3% Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 KDT 10
LD 7 KDT 9
RESULT 17
Q9THS2 PRELIMINARY; PRT: 13 AA.
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DE PSB (Fragment).
GN PSB.
OS Bryopsis sp. B.
OC Chloroplast.
EC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;

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QY 6 QKX 8
DB 8 QKX 10

RESULT 21
Q81784
ID Q81784 PRELIMINARY: PRT: 13 AA.
AC Q81784
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RC STRAIN-21;
RP SEQUENCE FROM N.A.
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84850; AAA45701.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 4649761442FC763 CRC64:

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QKX 8
DB 8 QKX 10

RESULT 22
Q81778
ID Q81778 PRELIMINARY: PRT: 13 AA.
AC Q81778
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RC STRAIN-SW3;
RP SEQUENCE FROM N.A.
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84850; AAA45695.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.

QY 6 QKX 8
DB 8 QKX 10

RESULT 23
Q81787
ID Q81787 PRELIMINARY: PRT: 13 AA.
AC Q81787
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RC STRAIN-Z6;
RP SEQUENCE FROM N.A.
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84862; AAA45704.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 4649761442FC763 CRC64:

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QKX 8
DB 8 QKX 10

RESULT 24
Q81775
ID Q81775 PRELIMINARY: PRT: 13 AA.
AC Q81775
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RC STRAIN-SA7;
RP SEQUENCE FROM N.A.
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992)
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A

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CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84852; AAA45693.1; -.
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 8 QRK 10

RESULT 25
Q81767 PRELIMINARY; PRT; 13 AA.
AC Q81767;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN HK5;
RX MEDLINE-92279243; PubMed-1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84849; AAA45685.1; -.
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 8 QRK 10

RESULT 26
Q81798 PRELIMINARY; PRT; 13 AA.
AC Q81798;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-SAL1;
RX MEDLINE-92279243; PubMed-1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84858; AAA45715.1; -.
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 8 QRK 10

RESULT 27
Q81774 PRELIMINARY; PRT; 13 AA.
AC Q81774;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SAL1;
RX MEDLINE-92279243; PubMed-1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84860; AAA45692.1; -.
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 8 QRK 10

RESULT 28
Q81766 PRELIMINARY; PRT; 13 AA.
AC Q81766;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

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DE Genome polyprotein (Fragment)
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive strand viruses, no DNA stage: Flaviviridae.
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:HK2;
RX MEDLINE=92279243; PubMed=1417578;
RA Rukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84861; AAA45710.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 111
8 QRK 10

RESULT 29
Q81793
ID Q81793 PRELIMINARY: PRI: 13 AA.
AC Q81793;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive strand viruses, no DNA stage: Flaviviridae.
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:IND3;
RX MEDLINE=92279243; PubMed=1417578;
RA Rukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84861; AAA45710.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 111
8 QRK 10

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RESULT 30
Q81768
ID Q81768 PRELIMINARY: PRI: 13 AA.
AC Q81768;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive strand viruses, no DNA stage: Flaviviridae.
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:PI0;
RX MEDLINE=92279243; PubMed=1417578;
RA Rukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84855; AAA45686.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 111
8 QRK 10

RESULT 31
Q81785
ID Q81785 PRELIMINARY: PRI: 13 AA.
AC Q81785;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive strand viruses, no DNA stage: Flaviviridae.
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:Z4;
RX MEDLINE=92279243; PubMed=1417578;
RA Rukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84848; AAA45702.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;

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Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 6 QPK 8
DB 11
8 QPK 10

RESULT 32
Q81760 ID Q81760 PRELIMINARY: PRT; 13 AA.
AC Q81760:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=111103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-US11;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M44853; AAA45717; 1.
DR InterPro: IPR002522; HCV_capsid; 1.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
PT 13
SQ SEQUENCE 13 AA: 1572 MW: 464797E1A42FC763 CRC64;

Query Match: 27.3% Score 3; DB 12; Length 13;
Best local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 6 QPK 8
DB 11
8 QPK 10

RESULT 33
Q81765 ID Q81765 PRELIMINARY: PRT; 13 AA.
AC Q81765:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=111103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-US4;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M44853; AAA45683; 1.
DR InterPro: IPR002522; HCV_capsid; 1.

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DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 464797E1A42FC763 CRC64;

Query Match: 27.3% Score 3; DB 12; Length 13;
Best local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 6 QPK 8
DB 11
8 QPK 10

RESULT 34
Q81781 ID Q81781 PRELIMINARY: PRT; 13 AA.
AC Q81781:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=111103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T9;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M44846; AAA45698; 1.
DR InterPro: IPR002522; HCV_capsid; 1.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
PT 13
SQ SEQUENCE 13 AA: 1557 MW: 46407E1A42FC763 CRC64;

Query Match: 27.3% Score 3; DB 12; Length 13;
Best local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 6 QPK 8
DB 11
8 QPK 10

RESULT 35
Q81769 ID Q81769 PRELIMINARY: PRT; 13 AA.
AC Q81769:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=111103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P8;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;

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BL      Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC      1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC      LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS.
CC      PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC      PROTEIN C AND MRNA (BY SIMILARITY).
DR      EMBL: M84856; AAA45687.1;
DR      InterPro: IPR002522; HCV_capsid;
DR      Pfam: PF01543; HCV_capsid; 1;
FT      NON_TER
SQ      SEQUENCE 13 AA: 1559 MW: 465463.642770; 8304;

      Query Match      27.3%; Score 3; DB 12; Length 13;
      Best Local Similarity 100.0%; Pred. No. 8.5e-03;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QKK 8
DB      8 QKK 10

      RESULT 46
      Q81773      PRELIMINARY; PRI: 13 AA.
AC      Q81773;
DT      01-NOV-1996 (TrEMBLrel. 01; Created)
DI      01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DE      01-NOV-2002 (TrEMBLrel. 22; Last annotation update)
DE      Genome polyprotein (Fragment).
GN      POLYPROTEIN.
OS      Hepatitis C virus.
OC      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
CC      Hepacivirus.
CX      NCBI_TaxID:11103;
KW      NON_TER
SQ      SEQUENCE FROM N.A.
RX      MEDLINE:92279243; PubMed:1317578;
RA      Bukh J., Purcell R.H., Miller R.H.;
RT      *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
PI      Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC      1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC      LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS.
CC      PROTEIN C AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC      PROTEIN C AND MRNA (BY SIMILARITY).
DR      EMBL: M84856; AAA45691.1;
DR      InterPro: IPR002522; HCV_capsid;
DR      Pfam: PF01543; HCV_capsid; 1;
FT      NON_TER
SQ      SEQUENCE 13 AA: 1572 MW: 464976.642770; 8304;

      Query Match      27.3%; Score 3; DB 12; Length 13;
      Best Local Similarity 100.0%; Pred. No. 8.5e-03;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QKK 8
DB      8 QKK 10

      RESULT 47
      Q81799      PRELIMINARY; PRI: 13 AA.
AC      Q81799;
DT      01-NOV-1996 (TrEMBLrel. 01; Created)
DI      01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DE      01-OCT-2002 (TrEMBLrel. 22; Last annotation update)
DE      Genome polyprotein (Fragment).
GN      POLYPROTEIN.
OS      Hepatitis C virus.
OC      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
CC      Hepacivirus.

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CX      NCBI_TaxID:11103;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-T10;
RX      MEDLINE-92279243; PubMed:1317578;
RA      Bukh J., Purcell R.H., Miller R.H.;
RT      *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RI      Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC      1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC      LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS.
CC      PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC      PROTEIN C AND MRNA (BY SIMILARITY).
DR      EMBL: M84843; AAA45716.1;
DR      InterPro: IPR002522; HCV_capsid;
DR      Pfam: PF01543; HCV_capsid; 1;
KW      Polyprotein.
FT      NON_TER
SQ      SEQUENCE 13 AA: 1572 MW: 454976.642770; 8304;

      Query Match      27.3%; Score 3; DB 12; Length 13;
      Best Local Similarity 100.0%; Pred. No. 8.5e-03;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QKK 8
DB      8 QKK 10

      RESULT 48
      Q81786      PRELIMINARY; PRI: 13 AA.
AC      Q81786;
DT      01-NOV-1996 (TrEMBLrel. 01; Created)
DI      01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DE      01-OCT-2002 (TrEMBLrel. 22; Last annotation update)
DE      Genome polyprotein (Fragment).
GN      POLYPROTEIN.
OS      Hepatitis C virus.
OC      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
CC      Hepacivirus.
CX      NCBI_TaxID:11103;
KW      NON_TER
SQ      SEQUENCE FROM N.A.
RX      MEDLINE-92279243; PubMed:1317578;
RA      Bukh J., Purcell R.H., Miller R.H.;
RT      *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RI      Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC      1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC      LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS.
CC      PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC      PROTEIN C AND MRNA (BY SIMILARITY).
DR      EMBL: M84828; AAA45703.1;
DR      InterPro: IPR002522; HCV_capsid;
DR      Pfam: PF01543; HCV_capsid; 1;
KW      Polyprotein.
FT      NON_TER
SQ      SEQUENCE 13 AA: 1572 MW: 454976.642770; 8304;

      Query Match      27.3%; Score 3; DB 12; Length 13;
      Best Local Similarity 100.0%; Pred. No. 8.5e-03;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QKK 8
DB      8 QKK 10

      RESULT 49
      Q81788      PRELIMINARY; PRI: 13 AA.
AC      Q81788;
DT      01-NOV-1996 (TrEMBLrel. 01; Created)

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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae
OC Hepacivirus
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN 28;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RC Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84839; AAA45705.1; -
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1.
KW POLYPROTEIN
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPK 8
DB 8 QPK 10

RESULT 40
Q81763 PRELIMINARY; PRT; 13 AA.
AC Q81763;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae
OC Hepacivirus
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DK9;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RC Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84851; AAA45682.1; -
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1.
KW POLYPROTEIN
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPK 8
DB 8 QPK 10

RESULT 41
Q81764 PRELIMINARY; PRT; 13 AA.
AC Q81764;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae
OC Hepacivirus
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DK9;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RC Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84837; AAA45713.1; -
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1.
KW POLYPROTEIN
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1571 MW: 464D1DE1A42FC763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPK 8
DB 8 QPK 10

RESULT 42
Q81796 PRELIMINARY; PRT; 13 AA.
AC Q81796;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae
OC Hepacivirus
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S52;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RC Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84837; AAA45713.1; -
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1.
KW POLYPROTEIN
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1571 MW: 464D1DE1A42FC763 CRC64;

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Query Match: 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GRK 8
DB 8 GRK 10

RESULT 44
Q81762
ID Q81762 PRELIMINARY; PRT: 13 AA.
AC Q81762;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN-DK12;
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC 1. SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
LPPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MRNA (BY SIMILARITY).
CC
DR EMBL: M84864; AAA45708.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
FT NON_TER 13
SEQUENCE 13 AA: 1572 MW: 464597E1A42FC763 CRC64;

Query Match: 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GRK 8
DB 8 GRK 10

RESULT 44
Q81762
ID Q81762 PRELIMINARY; PRT: 13 AA.
AC Q81762;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN-DK12;
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC 1. SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
LPPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MRNA (BY SIMILARITY).
CC

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DR EMBL: M84841; AAA45680.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
KW POLYPROTEIN.
FT NON_TER 13
SEQUENCE 13 AA: 1572 MW: 464597E1A42FC763 CRC64;

Query Match: 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GRK 8
DB 8 GRK 10

RESULT 45
Q81790
ID Q81790 PRELIMINARY; PRT: 13 AA.
AC Q81790;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN-DK12;
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC 1. SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
LPPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MRNA (BY SIMILARITY).
CC
DR EMBL: M84864; AAA45707.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
KW POLYPROTEIN.
FT NON_TER 13
SEQUENCE 13 AA: 1571 MW: 4640D1E1A42FC763 CRC64;

Query Match: 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GRK 8
DB 8 GRK 10

RESULT 46
Q81783
ID Q81783 PRELIMINARY; PRT: 13 AA.
AC Q81783;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN-DK12;
RX MEDLINE:92279243; PubMed:1317578;

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RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
CC EMBL: M84830; AAA45700.1; .
DR InterPro: IPR002522; HCV_capsid; 1.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64:
      27.3%; Score 3; DB 12; Length 13;
Query Match Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPK 8
DB 8 QPK 10

RESULT 47
Q81789 PRELIMINARY: PRT: 13 AA.
AC Q81789
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
CC Hepacivirus.
CC NCBI_taxid-11103;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN DK11;
RX MEDLINE 92279243; PubMed-1117578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
CC EMBL: M84831; AAA45706.1; .
DR InterPro: IPR002522; HCV_capsid; 1.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64:
      27.3%; Score 3; DB 12; Length 13;
Query Match Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPK 8
DB 8 QPK 10

RESULT 48
Q81797 PRELIMINARY: PRT: 13 AA.
AC Q81797
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.

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OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OC NCBI_taxid-11103;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN SA10;
RX MEDLINE 92279244; PubMed-1117578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
CC EMBL: M84844; AAA45714.1; .
DR InterPro: IPR002522; HCV_capsid; 1.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64:
      27.3%; Score 3; DB 12; Length 13;
Query Match Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPK 8
DB 8 QPK 10

RESULT 49
Q81795 PRELIMINARY: PRT: 13 AA.
AC Q81795
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
CC Hepacivirus.
CC NCBI_taxid-11103;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-IN08;
RX MEDLINE 92279244; PubMed-1117578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
CC EMBL: M84853; AAA45712.1; .
DR InterPro: IPR002522; HCV_capsid; 1.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
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      27.3%; Score 3; DB 12; Length 13;
Query Match Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPK 8
DB 8 QPK 10

RESULT 50
Q81782 PRELIMINARY: PRT: 13 AA.
AC Q81782

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GenCore version 5.1.5
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CM protein - protein search, using SW-2000

Run on: September 30, 2003, 10:07:53, Search type: 11 rows, 5 seconds
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99,341 Million ref., updates/sec

Title: US-09-787-443-2

Perfect score: 11

Sequence: 1 AKKERQKKUQ 11

Scoring table: OLIGO

Gapop 50.0, Gapext 60.0

Searched: 1287.7 seqs, 4231058 residues

Word size: 0

Total number of hits satisfying chosen parameters: 74359

Minimum hit seq length: 8

Maximum hit seq length: 15

Post-processing: Listing first 500 summaries

Database: Issued Patents AA.*

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- 4: /cgn2_6/ptodata/1/iss/6B_CGMS.pat*
- 5: /cgn2_6/ptodata/1/iss/70US_CGMS.pat*
- 6: /cgn2_6/ptodata/1/iss/Backlist.pat*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4	36.4	11	1	US-08-376-405A-11
4	4	36.4	11	1	US-08-376-405A-11
5	4	36.4	11	2	US-08-743-183-11
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8	4	36.4	12	1	US-08-548-943-12
9	4	36.4	12	3	US-08-461-4843-12
10	4	36.4	12	3	US-08-472-282A-12
11	4	36.4	12	3	US-09-045-249A-12
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165	3	27.3	8	5	PCT-US95-00644A-13	Sequence 13, Appl	238	3	27.3	9	2	US-08-894-339-1	Sequence 1, Appl
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RESULT 1

US-08-159-339A-989
Sequence 989, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kuber, Ralph J.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
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TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
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FILING DATE: 05-MAR-1993

ALIGNMENTS

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1  APPLICATION NUMBER: US 08/185,448
2  FILING DATE: 08-AUG-1993
3  ATTORNEY/AGENT INFORMATION:
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5  REGISTRATION NUMBER: 34,762
6  REFERENCE/DOCKET NUMBER: 0185,443-20030005
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10 TELE:
11 INFORMATION FOR SEQ ID NO: 989:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 10 amino acids
14 TYPE: amino acid
15 STRANDEDNESS: single
16 TOPOLOGY: linear
17 MOLECULE TYPE: peptide
18 US-08 159-339A-989
19
20 Query Match 36.4% Score 4; DB 4; Length 10;
21 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
22 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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24 QY 5 KSRQ 6
25 DB 4 KSRQ 7
26
27 RESULT 2
28 US 08-185-448-5
29 : Sequence 5; Application: US/05185448
30 : Patent No. 5580747
31 : GENERAL INFORMATION:
32 : APPLICANT: SULTZ, JOHN W.
33 : APPLICANT: WHITE, DOUGLAS H.
34 : TITLE OF INVENTION: NON-RADIOLACTIVE KINASE
35 : TITLE OF INVENTION: PHOSPHATASE AND PHOSPHATASE ASSAY
36 : NUMBER OF SEQUENCES: 11
37 : CORRESPONDENCE ADDRESS:
38 : ADDRESSEE: ANDRUS, SCOTLAND, STARK & SAWAL
39 : STREET: 100 E. WISCONSIN AVENUE, SUITE 115
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41 : STATE: WISCONSIN
42 : COUNTRY: USA
43 : ZIP: 53202
44 : COMPUTER READABLE FORM:
45 : MEDIUM TYPE: Floppy disk
46 : COMPUTER: IBM PC compatible
47 : OPERATING SYSTEM: PC-DOS/MS-DOS
48 : SOFTWARE: BALUOLIO Release #1.0, V01.00
49 : SOFTWARE: #1125
50 : CURRENT APPLICATION DATA:
51 : APPLICATION NUMBER: US 07/794,428
52 : FILING DATE: 12-NOV-1991
53 : ATTORNEY/AGENT INFORMATION:
54 : NAME: SARA, CHARLES S.
55 : REGISTRATION NUMBER: 30492
56 : REFERENCE/DOCKET NUMBER: 5,444,711
57 : TELECOMMUNICATION INFORMATION:
58 : TELEPHONE: (608) 255-2022
59 : TELEFAX: (608) 255-2182
60 : TELEX: 25832 ANDSTARK
61 : INFORMATION FOR SEQ ID NO: 5:
62 SEQUENCE CHARACTERISTICS:
63 LENGTH: 11 amino acids
64 TYPE: amino acid
65 TOPOLOGY: linear
66 MOLECULE TYPE: peptide
67 FEATURE:

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1  NAME/KEY: Binding-site
2  LOCATION: 1
3  OTHER INFORMATION: /label= LABEL
4  OTHER INFORMATION: /note= "LOCATION OF LISSAMINE RHODAMINE
5  OTHER INFORMATION: DETECTION TAG"
6  US-08-185-448-5
7
8  Query Match 36.4% Score 4; DB 1; Length 11;
9  Best Local Similarity 100.0%; Pred. No. 1.7e+02;
10 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
11
12 QY 5 KSRK 8
13 DB 3 KSRK 6
14
15 RESULT 3
16 US 08-476-405A-10
17 : Sequence 10; Application US/08476405A
18 : Patent No. 5776459
19 : GENERAL INFORMATION:
20 : APPLICANT: Vandenberg, Arthur A.
21 : TITLE OF INVENTION: Method of Treatment Using TCR VBeta5 Peptides
22 : NUMBER OF SEQUENCES: 27
23 : CORRESPONDENCE ADDRESS:
24 : ADDRESSEE: Connective Therapeutics, Inc.
25 : STREET: 3400 West Bayshore Road
26 : CITY: Palo Alto
27 : STATE: California
28 : COUNTRY: USA
29 : ZIP: 94403
30 : COMPUTER READABLE FORM:
31 : MEDIUM TYPE: Floppy disk
32 : COMPUTER: IBM PC compatible
33 : OPERATING SYSTEM: PC-DOS/MS-DOS
34 : SOFTWARE: Patent: Release #1.0, Version #1.25
35 : CURRENT APPLICATION DATA:
36 : APPLICATION NUMBER: US/08/476,405A
37 : FILING DATE:
38 : CLASSIFICATION: 424
39 : PRIOR APPLICATION DATA:
40 : APPLICATION NUMBER: US 09/059,020
41 : FILING DATE: 16-MAR-1993
42 : PRIOR APPLICATION DATA:
43 : APPLICATION NUMBER: US 07/755,512
44 : FILING DATE: 16-JUL-1991
45 : PRIOR APPLICATION DATA:
46 : APPLICATION NUMBER: US 07/708,022
47 : FILING DATE: 31-MAY-1991
48 : PRIOR APPLICATION DATA:
49 : APPLICATION NUMBER: US 07/554,529
50 : FILING DATE: 19-JUL-1990
51 : PRIOR APPLICATION DATA:
52 : APPLICATION NUMBER: US 07/467,577
53 : FILING DATE: 19-JAN-1990
54 : PRIOR APPLICATION DATA:
55 : APPLICATION NUMBER: US 07/352,804
56 : FILING DATE: 19-JUL-1989
57 : ATTORNEY/AGENT INFORMATION:
58 : NAME: Lowin, David A.
59 : REGISTRATION NUMBER: 29,326
60 : REFERENCE/DOCKET NUMBER: #86-P15
61 : TELECOMMUNICATION INFORMATION:
62 : TELEPHONE: 415-843-2899
63 : TELEFAX: 415-843-2899
64 : INFORMATION FOR SEQ ID NO: 10:
65 SEQUENCE CHARACTERISTICS:
66 LENGTH: 11 amino acids
67 TYPE: amino acid
68 STRANDEDNESS: single
69 TOPOLOGY: linear
70 MOLECULE TYPE: peptide
71 FEATURE:
72 US-08 476-405A-10

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Query Match 36.4%, Score 4; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred No. 1; 2e-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 BRQR 7
 DB 7 BRQR 10

RESULT 4
 US-08 476-405A-11
 : Sequence 11; Application US/847443A
 : Patent No. 5776459
 : GENERAL INFORMATION:
 : APPLICANT: Vandenberg, Arthur A.
 : TITLE OF INVENTION: Method of Treatment Using ErbB Virotoxic Peptides
 : NUMBER OF SEQUENCES: 27
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Connective Therapeutics, Inc.
 : STREET: 1400 West Bayshore Road
 : CITY: Palo Alto
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/476,405A
 FILING DATE:
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/069,120
 FILING DATE: 16-MAR-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/716,612
 FILING DATE: 16-JUL-1991

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/708,022
 FILING DATE: 31-MAY-1991

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/554,129
 FILING DATE: 19-JUL-1991

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/422,110
 FILING DATE: 19-JAN-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 02/042,062
 FILING DATE: 19-JUL-1999

ATTORNEY/AGENT INFORMATION:
 NAME: LEWIS, DAVID A.
 REGISTRATION NUMBER: 29,126

REFERENCE/DOCKET NUMBER: REF 016
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-2800

TELEFAX: 415-843-2899
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: peptide
 US-08 476-405A-11

Query Match 36.4%, Score 4; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred No. 1; 2e-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 BRQR 7

DB 111
 / BRQR 10

RESULT 5
 US-08 747-137-63
 : Sequence 63; Application US/08747117
 : Patent No. 5945014
 : GENERAL INFORMATION:
 : APPLICANT: VEN, RICHARD C.K.
 : TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
 : TREATMENT OF INHERITED IMMUNOLOGICAL AND DIAGNOSTIC USE
 : NUMBER OF SEQUENCES: 184
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Townsend and Townsend and Crew LLP
 : STREET: Two Embarcadero Center, 8th Floor
 : CITY: San Francisco
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747,137
 FILING DATE: 12-NOV-1996
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/212,546
 FILING DATE: 14-MAR-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/069,851
 FILING DATE: 01-JUN-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/959,560
 FILING DATE: 13-OCT-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/641,720
 FILING DATE: 15-JAN-1991

ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 46,429

REFERENCE/DOCKET NUMBER: 016197 00084005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-576-0200

INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amide acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant

US-08-747-137-63

Query Match 36.4%, Score 4; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred No. 1; 7e-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 BRQR 6
 DB 3 BRQR 6

RESULT 6
 US-09-100-930A-10
 : Sequence 10; Application US/29100930A
 : Patent No. 6248549
 : GENERAL INFORMATION:
 : APPLICANT: Van Eyk, Jennifer E.
 : APPLICANT: Mak, Alan S.
 : APPLICANT: Cole, Graham P.
 : TITLE OF INVENTION: Methods of Modulating Muscle Contraction

```
FILE REFERENCE: 1997-021-03US
CURRENT APPLICATION NUMBER: US/09/100,940A
CURRENT FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/950,478
PRIOR FILING DATE: 1997-06-24
PRIOR APPLICATION NUMBER: 60/959,595
PRIOR FILING DATE: 1998-06-16
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 10
LENGTH: 11
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)...(11)
OTHER INFORMATION: Residues 424 to 433 of chicken quizzard caldesmon
NAME/KEY: PEPTIDE
LOCATION: (11)
OTHER INFORMATION: Targeted Ser phosphorylating acid
US-09-100 930A 10

Query Match 36.4% Score 4: DB 1: Length 11:
Best Local Similarity 100.0% Pred. No. 1.7e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKE 4
DB 7 AKKE 10

RESULT 7
US-08-156-552A 18
Sequence 18: Application US/58-5652A
Patent No. 5726155
GENERAL INFORMATION:
APPLICANT: Bokoch, Gary M
TITLE OF INVENTION: REGULATION OF OXIDATIVE PEROXIDE USING
TITLE OF INVENTION: LMWG-DERIVED PEPTIDES AND ANALOGS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, 10550 N.
ADDRESS: Patent Counsel
STREET: 13566 No. 5726155th battery (U.S. Pat. 13566
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/156,552A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,944
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Logan, Adell C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: SCRF 491.1
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-100 930A 10

Query Match 36.4% Score 4: DB 1: Length 11:
Best Local Similarity 100.0% Pred. No. 1.7e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKE 4
DB 7 AKKE 10

RESULT 7
US-08-156-552A 18
Sequence 18: Application US/58-5652A
Patent No. 5726155
GENERAL INFORMATION:
APPLICANT: Bokoch, Gary M
TITLE OF INVENTION: REGULATION OF OXIDATIVE PEROXIDE USING
TITLE OF INVENTION: LMWG-DERIVED PEPTIDES AND ANALOGS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, 10550 N.
ADDRESS: Patent Counsel
STREET: 13566 No. 5726155th battery (U.S. Pat. 13566
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/156,552A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,944
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Logan, Adell C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: SCRF 491.1
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-100 930A 10

Query Match 36.4% Score 4: DB 1: Length 12:
Best Local Similarity 100.0% Pred. No. 1.9e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 RKDT 10
DB 9 RKDI 12

RESULT 8
US-08-548-540-147
Sequence 147: Application US/08548540
Patent No. 5733731
GENERAL INFORMATION:
APPLICANT: Schatz, Peter J.
APPLICANT: Cull, Milard C.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, William P.C.
APPLICANT: Gates, Christian M.
TITLE OF INVENTION: Peptide Library and Screening Method
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/548,540
FILING DATE: 26-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/290,641
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,423
REFERENCE/DOCKET NUMBER: 165283-00124005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-548-540-147

Query Match 36.4% Score 4: DB 1: Length 12:
Best Local Similarity 100.0% Pred. No. 1.9e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 ERQR 7
DB 8 ERQR 11

RESULT 9
US-08-461-384B-7
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Sequence 7, Application US/08461484B
Patent No. 6025473
GENERAL INFORMATION:
APPLICANT: Cole, Susan P.C.
APPLICANT: Cole, Roger G.
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STATE: Ontario
COUNTRY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,484B
FILING DATE: 05-JUN-95
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,440
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Meinick
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1512
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-461-484B-7

Query Match 36.4% Score 41 DB 3 Length 12
Best Local Similarity 100.0% Prod. No. 1.9e+02
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKE 4
LD 1111
8 AKKE 11

RESULT 1:
US 08-407 207A 4
Sequence 4, Application US/08407207A
Patent No. 6061621
GENERAL INFORMATION:
APPLICANT: Deeley, Roger G.
APPLICANT: Cole, Susan P.C.
TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
STREET: Queen's University at Kingston
CITY: Kingston
STATE: Ontario
COUNTRY: CANADA
ZIP: K7L 3N6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/407,207A
FILING DATE: 20-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/966,923
FILING DATE: 27-OCT-1992
APPLICATION NUMBER: 08/029,440
FILING DATE: 8-MAR-1993
APPLICATION NUMBER: 08/141,893
FILING DATE: 26-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Meinick
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: Q1512
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 545-2342
TELEFAX: (613) 545-6853
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-407-207A-4

Query Match 36.4% Score 41 DB 3 Length 12
Best Local Similarity 100.0% Prod. No. 1.9e+02
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKE 4
LD 1111
8 AKKE 11

RESULT 1:
US-09-035-249A-18
Sequence 18, Application US/09035249A
Patent No. 6184203
GENERAL INFORMATION:
APPLICANT: Bokoch, Gary M.
APPLICANT: Curdutt, John T.
TITLE OF INVENTION: REGULATION OF OXIDATIVE BURST USING
LMWG-DERIVED PEPTIDES AND ANALOGS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESS: Patent Counsel
STREET: 10666 No. 6184203th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,249A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/18/156,552
FILING DATE: 15-NOV-1993
APPLICATION NUMBER: US 08/102,944
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Logan, April C.
REGISTRATION NUMBER: 33,950

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REFERENCE/DOCKET NUMBER: 36.4% Score 4; DB 0; Length 12
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-035-249A-18

Query Match 36.4% Score 4; DB 0; Length 12
Best Local Similarity 100.0% Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RKDT 10
DB 9 RKDT 12

RESULT 12
PCT-US96-09809-147
Sequence 147, Application PC/TJS36G9809
GENERAL INFORMATION:
APPLICANT: Schatz, Peter J.
APPLICANT: Cull, Millard G.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, William P.
APPLICANT: Gates, Christian M.
TITLE OF INVENTION: Peptide Library and Screening Method
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.26
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09809
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,541
FILING DATE: 26-OCT-1995
APPLICATION NUMBER: US 08/230,641
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,342
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 165282-00124005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-09809-147

Query Match 36.4% Score 4; DB 0; Length 12

Best Local Similarity 100.0% Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERQR 7
DB 8 ERQR 11

RESULT 13
US-08-796-598-15
Sequence 15, Application US/08796598
Patent No. 5827659
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
APPLICANT: TARR, GEORGE E.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator - Testa, Hurwitz &
ADDRESSEE: Thibeault
STREET: High Street Tower, 125 High Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,598
FILING DATE: 07-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,055
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FLYNN ESQ., Kerry A.
REGISTRATION NUMBER: 33,693
REFERENCE/DOCKET NUMBER: SYP-115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-796-598-15

Query Match 36.4% Score 4; DB 2; Length 13;
Best Local Similarity 100.0% Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRKD 9
DB 3 QRKD 6

RESULT 14
US-08-447-175A-15
Sequence 15, Application US/08447175A
Patent No. 5869240
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
SPECTROMETRY.
NUMBER OF SEQUENCES: 23

1 CORRESPONDENCE ADDRESS:
 2 ADDRESSEE: Patent Administrator - Testa, Amity &
 3 ADDRESSEE: Thibault, LLP
 4 STREET: High Street Tower, 125 High Street
 5 CITY: Boston
 6 STATE: MA
 7 COUNTRY: USA
 8 ZIP: 02110
 9 COMPUTER READABLE FORM:
 10 MEDIUM TYPE: Floppy disk
 11 COMPUTER: IBM PC compatible
 12 OPERATING SYSTEM: PC-DOS/MS-DOS
 13 SOFTWARE: Patent Release #1.0, Version #1.0
 14 CURRENT APPLICATION DATA:
 15 APPLICATION NUMBER: US/08/447,175A
 16 FILING DATE: 19-MAY-1995
 17 CLASSIFICATION: 422
 18 ATTORNEY/AGENT INFORMATION:
 19 NAME: RAUSCHENBACH, KAT
 20 REGISTRATION NUMBER: 43,147
 21 REFERENCE/DOCKET NUMBER: SYP-114
 22 TELECOMMUNICATION INFORMATION:
 23 TELEPHONE: (617) 248-7000
 24 TELEFAX: (617) 248-7100
 25 INFORMATION FOR SEQ ID NO: 15:
 26 SEQUENCE CHARACTERISTICS:
 27 LENGTH: 13 amino acids
 28 TYPE: amino acid
 29 STRANDEDNESS: single
 30 TOPOLOGY: linear
 31 MOLECULE TYPE: peptide
 32 US-08-447,175A 15
 33
 34 Query Match: 36.4%, Score 4; DB 2; Length 13;
 35 Best Local Similarity: 100.0%; Pred. No. 2e+02;
 36 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 37
 38 QY 6 QKRD 9
 39 DB 1 1111
 40 1 QKRD 6
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 42 RESULT 16
 43 US-09-747-137 77
 44 Sequence 77, Application US/08/447,137
 45 Patent No. 5945013
 46 GENERAL INFORMATION:
 47 APPLICANT: YEN, Richard C.K.
 48 TITLE OF INVENTION: NON-CROSS-LINKED PEPTIDE COMPOUNDS FOR P
 49 TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
 50 NUMBER OF SEQUENCES: 184
 51 CORRESPONDENCE ADDRESS:
 52 ADDRESSEE: Townsend and Townsend
 53 STREET: Two Embarcadero Center, 100 Embarc
 54 CITY: San Francisco
 55 STATE: CA
 56 COUNTRY: USA
 57 ZIP: 94111
 58 COMPUTER READABLE FORM:
 59 MEDIUM TYPE: Floppy disk
 60 COMPUTER: IBM PC compatible
 61 OPERATING SYSTEM: PC-DOS/MS-DOS
 62 SOFTWARE: Patent Release #1.0, Version #1.0
 63 CURRENT APPLICATION DATA:
 64 APPLICATION NUMBER: US/08/747,137
 65 FILING DATE: 12-NOV-1996
 66 CLASSIFICATION: 424
 67 PRIOR APPLICATION DATA:
 68 APPLICATION NUMBER: US 08/212,546
 69 FILING DATE: 14-MAR-1994
 70 PRIOR APPLICATION DATA:
 71 APPLICATION NUMBER: US 08/069,843
 72 FILING DATE: 01-JUN-1993

1 PRIOR APPLICATION DATA:
 2 APPLICATION NUMBER: US 07/959,560
 3 FILING DATE: 13-OCT-1992
 4 PRIOR APPLICATION DATA:
 5 APPLICATION NUMBER: US 07/941,720
 6 FILING DATE: 15-JAN-1991
 7 ATTORNEY/AGENT INFORMATION:
 8 NAME: Apple, Raulolph T.
 9 REGISTRATION NUMBER: 36,429
 10 REFERENCE/DOCKET NUMBER: 016147-0008400US
 11 TELECOMMUNICATION INFORMATION:
 12 TELEPHONE: 415 576-0200
 13 INFORMATION FOR SEQ ID NO: 77:
 14 SEQUENCE CHARACTERISTICS:
 15 LENGTH: 13 amino acids
 16 TYPE: amino acid
 17 STRANDEDNESS: not relevant
 18 TOPOLOGY: not relevant
 19 US-08-747-137-77
 20
 21 Query Match: 36.4%, Score 4; DB 2; Length 13;
 22 Best Local Similarity: 100.0%; Pred. No. 2e+02;
 23 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 24
 25 QY 6 QKRD 9
 26 DB 3 1111
 27 3 QKRD 6
 28
 29 RESULT 16
 30 US-09-400-564 6
 31 Sequence 6, Application US/09400564
 32 Patent No. 6350574
 33 GENERAL INFORMATION:
 34 APPLICANT: Montelaro, Ronald C.
 35 APPLICANT: Tencza, Sarah B.
 36 APPLICANT: Jolley, Michael S.
 37 APPLICANT: Nasir, Mohammad S.
 38 TITLE OF INVENTION: A Fluorescence Polarization-Based Diagnostic Assay
 39 TITLE OF INVENTION: For Equine Infectious Anemia Virus
 40 FILE REFERENCE: Case No. 6350574 99,579
 41 CURRENT APPLICATION NUMBER: US/09/400,564
 42 CURRENT FILING DATE: 1999-09-21
 43 EARLIER APPLICATION NUMBER: US 66/101,553
 44 NUMBER OF SEQ ID NOS: 21
 45 SEQ ID NO 6
 46 LENGTH: 13
 47 TYPE: PPT
 48 ORGANISM: Equine infectious anemia virus
 49 US-09-400-564 6
 50
 51 Query Match: 36.4%, Score 4; DB 4; Length 13;
 52 Best Local Similarity: 100.0%; Pred. No. 2e+02;
 53 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 54
 55 QY 3 KERQ 6
 56 DB 1 1111
 57 1 KERQ 4
 58
 59 RESULT 17
 60 US-09-325-601-44
 61 Sequence 44, Application US/09325601
 62 Patent No. 6573045
 63 GENERAL INFORMATION:
 64 APPLICANT: Karn
 65 APPLICANT: Prescott
 66 TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
 67 FILE REFERENCE: 3550/81245
 68 CURRENT APPLICATION NUMBER: US/09/325,601
 69 CURRENT FILING DATE: 1999-06-03
 70 NUMBER OF SEQ ID NOS: 64
 71 SOFTWARE: FastAlign Ver 2.1

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1 SEQ ID NO 44
2 LENGTH: 13
3 TYPE: PRT
4 ORGANISM: Artificial Sequence
5 FEATURES:
6 OTHER INFORMATION: Description of Artificial Sequence provided from X,
7 OTHER INFORMATION: Q, R-peptideptide identity
8 US-09-425-601-44
9
10 Query Match
11 Best Local Similarity 36.4% Score 4, DB 4, Length 14
12 Matches 4: Conservative 0, Mismatches 0, Gaps 0
13
14 QY 5 EROR 8
15 III
16 4 EROR 7
17
18 RESULT 16
19 US-08-484-905-55
20 Sequence 55, Application US/06444905
21 Patent No. 5976551
22 GENERAL INFORMATION:
23 APPLICANT: Mottez, Estelle
24 APPLICANT: Abastado, Jean-Pierre
25 APPLICANT: Kourilsky, Philippe
26 TITLE OF INVENTION: An Altered Major Histocompatibility
27 TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
28 NUMBER OF SEQUENCES: 127
29 CORRESPONDENCE ADDRESS:
30 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
31 ADDRESSEE: Dunner
32 STREET: 1400 I Street, N.W., Suite 700
33 CITY: Washington
34 STATE: D.C.
35 ZIP: 20005-3315
36 COMPUTER READABLE FORM:
37 MEDIUM TYPE: Floppy disk
38 COMPUTER: IBM PC compatible
39 OPERATING SYSTEM: PC DOS/MS-DOS
40 SOFTWARE: Patent in Release #1.0, Version #1.2
41 CURRENT APPLICATION DATA:
42 APPLICATION NUMBER: US/08/484,905
43 FILING DATE: 07-JUNE-1995
44 CLASSIFICATION: 530
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: US 07/461,818
47 FILING DATE: 05-DEC-1991
48 CLASSIFICATION: 530
49 APPLICATION NUMBER: 530
50 FILING DATE: 15-NOV-1991
51 ATTORNEY/AGENT INFORMATION:
52 NAME: Potter, Jane E. R.
53 REGISTRATION NUMBER: 33,432
54 REFERENCE/DOCKET NUMBER: 34495, 0106-04000
55 TELECOMMUNICATION INFORMATION:
56 TELEPHONE: 202-408-4400
57 TELEFAX: 202-408-4400
58 INFORMATION FOR SEQ ID NO: 55:
59 SEQUENCE CHARACTERISTICS:
60 LENGTH: 14 amino acids
61 TYPE: amino acid
62 TOPOLOGY: linear
63 MOLECULE TYPE: peptide
64 US-08-484-905-55
65
66 Query Match
67 Best Local Similarity 36.4% Score 4, DB 4, Length 14
68 Matches 4: Conservative 0, Mismatches 0, Gaps 0
```

```
QY 4 EROR 7
DB 11 EROR 14

RESULT 17
US-08-481-985B-55
Sequence 55, Application US/08481985B
Patent No. 601114
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1400 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/401,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
APPLICATION NUMBER: 435
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495, 0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4500
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-985B-55

Query Match
Best Local Similarity 36.4% Score 4, DB 3, Length 14:
Matches 4: Conservative 0, Mismatches 0, Indels 0, Gaps 0:

QY 4 EROR 7
DB 11 EROR 14

RESULT 20
US-08-370-476-55
Sequence 55, Application US/08370476
Patent No. 615408
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lone, Yu-Chan
```

APPLICANT: O'Brien, David
APPLICANT: Casinger, Amanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
FILE REFERENCE: superantigen
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farrel W. Bartlett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-4335
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476-405A
FILING DATE: 05-DEC-1991
CLASSIFICATION: 445
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/417,595
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/572,747
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/611,817
FILING DATE: 05-DEC-1991
APPLICATION NUMBER: US 07/793,478
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 5243, 101, 01600
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: peptide
US-08-476-476-55

Query Match: 96.4% Score 4: 1P 1 Length 14;
Best Local Similarity 100.0% Pred. No. 2.1e+02;
Matches 4: Conservative 0; Mismatches 0; Gaps 0

QY 4 ERROR 7
1b 11 ERROR 14

RESULT 21
US-08-992-877-45
Sequence 35, Application US/08992877
Patent No. 640461
GENERAL INFORMATION:
APPLICANT: Torman, David S
TITLE OF INVENTION: SUPERANTIGEN BASE METHOD IS AN COMPOSITIONS FOR
TREATMENT OF INFECTIOUS DISEASE
FILE REFERENCE: superantigen
CURRENT APPLICATION NUMBER: US/08/992,877
CURRENT FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/044,074
PRIOR FILING DATE: 1997-04-17
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 14

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antigen
OTHER INFORMATION: sequences
US-08-992-877-45

Query Match: 96.4% Score 4: 1P 1 Length 14;
Best Local Similarity 100.0% Pred. No. 2.1e+02;
Matches 4: Conservative 0; Mismatches 0; Gaps 0

QY 4 ERROR 7
1b 11 ERROR 14

RESULT 22
US-08-476-405A-24
Sequence 23, Application US/08476405A
Patent No. 5776459
GENERAL INFORMATION:
APPLICANT: Vandenbark, Arthur A.
TITLE OF INVENTION: Method of Treatment Using TCR VBeta5 Peptides
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connective Therapeutics, Inc.
STREET: 3400 West Bayshore Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,405A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,020
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,612
FILING DATE: 16-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/708,022
FILING DATE: 31-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,529
FILING DATE: 19-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/467,577
FILING DATE: 19-JAN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/382,804
FILING DATE: 19-JUL-1989
ATTORNEY/AGENT INFORMATION:
NAME: Lowin, David A.
REGISTRATION NUMBER: 25,326
REFERENCE/DOCKET NUMBER: 886 #15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-2800
TELEFAX: 415-843-2899
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-405A-24

Query Match 36.4% Score 4: DB 1: Length 15;
Best Local Similarity 100.0% Pred. No. 2.2e+02;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 4 ERQR 7
DB 9 ERQR 12

RESULT 23
US-08-466-860-12
Sequence 12: Application US/08466860
Patent No. 5985562
GENERAL INFORMATION:
APPLICANT: HOWELL, MARK D.
APPLICANT: BROSTOFF, STEVEN W.
APPLICANT: CARLO, DENNIS J.
TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466-860
FILING DATE:
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/915,567
FILING DATE: 24-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P 1M 9100
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-466-860-12

Query Match 36.4% Score 4: DB 1: Length 15;
Best Local Similarity 100.0% Pred. No. 2.2e+02;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 2 KKER 5
DB 9 KKER 12

RESULT 24
US-08-559-397A-13
Sequence 33: Application US/08559397A
Patent No. 6083713
GENERAL INFORMATION:
APPLICANT: Madly, Susan P.
APPLICANT: Kozlowski, Michael R.

Query Match 36.4% Score 4: DB 3: Length 15;
Best Local Similarity 100.0% Pred. No. 2.2e+02;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 5 RGRK 8
DB 4 RGRK 7

RESULT 25
US-08-472-040A-12
Sequence 12: Application US/08472040A
Patent No. 6093387
GENERAL INFORMATION:
APPLICANT: HOWELL, MARK D.
APPLICANT: BROSTOFF, STEVEN W.
APPLICANT: CARLO, DENNIS J.
TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,040A
FILING DATE: 06-JUN-1995

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/Docket NUMBER: P-1M 9107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-472-040A-12

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Prod. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKER 5
DB 9 KKER 12

RESULT 25
US-08-276-776-12
Sequence 12, Application US/08-276776
Patent No. 6207645
GENERAL INFORMATION:
APPLICANT: HOWELL, MARK D.
APPLICANT: BROSTOFF, STEVEN W.
APPLICANT: CARLO, DENNIS J.
TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESS: CAMPBELL AND FLORES
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,776
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,867
FILING DATE: 24-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/Docket NUMBER: P-1M 9107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-276-776-12

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Prod. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKER 5
DB 9 KKER 12

RESULT 27
US-08-471-209-12
Sequence 12, Application US/08-471209
Patent No. 6221952
GENERAL INFORMATION:
APPLICANT: HOWELL, MARK D.
APPLICANT: BROSTOFF, STEVEN W.
APPLICANT: CARLO, DENNIS J.
TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESS: CAMPBELL AND FLORES
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,209
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,867
FILING DATE: 24-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/Docket NUMBER: P-1M 9107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-471-209-12

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Prod. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKER 5
DB 9 KKER 12

RESULT 28
US-09-308-935-14
Sequence 14, Application US/09308935
Patent No. 6268334
GENERAL INFORMATION:
APPLICANT: La Thaque, Nicholas H
APPLICANT: Randara, Sasanthia R
TITLE OF INVENTION: Peptide antagonists of DP transcription factors

FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/99/308,965
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: PCI/3997/0600E
EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: GB 9626589 7
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US 09-308-965-14

Query Match 36.4% Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERROR 7
DB 3 ERROR 6

RESULT 29
US-09-009-953-240
Sequence 240, Application US/00/09953;
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Free LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/009,953
FILING DATE: 21-JAN-1998
CLASSIFICATION: <unknown>
PRT
APPLICATION DATA:
APPLICATION NUMBER: US 60/216,133
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/297,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Laurel
REGISTRATION NUMBER: 32,782
REFERENCE/DOCKET NUMBER: 018623 0112 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 240:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 240:
US-09-009-953-240

Query Match 36.4% Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQRK 8
DB 6 RQRK 9

RESULT 30
US-09-311-784A-319
Sequence 319, Application US/00/11784A
Patent No. 6534482
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/99/311,784A
CURRENT FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 319
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV VPU 31 (peptide 35.0135)
US-09-311-784A-319

Query Match 36.4% Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQRK 8
DB 6 RQRK 9

RESULT 31
US-08-103-490A-6
Sequence 6, Application US/08103490A
Patent No. 5422341
GENERAL INFORMATION:
APPLICANT: Macielag, Mark J.
TITLE OF INVENTION: Motilin-like Polypeptides With
Gastrointestinal Motor Stimulating Activity
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: The BOC Group, Inc.
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/103,490A
FILING DATE: 06-AUG-1993
CLASSIFICATION: 514

```

1  ALPHEV/AGENT INFORMATION:
2  NAME: Swoppe, R. Bain
3  REGISTRATION NUMBER: 24,864
4  REFERENCE/DOCKET NUMBER: 92HR17
5  TELECOMMUNICATION INFORMATION:
6  TELEPHONE: 908-771-6292
7  TELEFAX: 908-771-6159
8  INFORMATION FOR SEQ ID NO: 6:
9  SEQUENCE CHARACTERISTICS:
10 LENGTH: 8 amino acids
11 TYPE: amino acid
12 STRANDEDNESS: unknown
13 COMPLETENESS: unknown
14 MODIFIER TYPE: peptide
15 US 08 103 496A 6
16
17 Query Match: 27.0% Score 5: 100.0% Length 8:
18 Best Local Similarity 100.0%, Prod. No. 2 50000
19 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
20
21 QY 5 KER 5
22 III
23 5 KER 7
24
25 RESULT 42
26 US 08 246 240 5
27 Sequence 3: Application US/08246240
28 Patent No. 6446124
29 GENERAL INFORMATION:
30 APPLICANT: Kahn, Michael
31 TITLE OF INVENTION: Alpha-helix motifs and methods
32 FIELD OF INVENTION: Relating Therapeutics
33 NUMBER OF SEQUENCES: 9
34 CORRESPONDENCE ADDRESS:
35 ADDRESSEE: Seed and Berry
36 STREET: 610 Columbia Street, 7th Floor, Seattle
37 CITY: Seattle
38 STATE: Washington
39 COUNTRY: USA
40 ZIP: 98104
41 COMPUTER READABLE FORM:
42 MEDIUM TYPE: Floppy disk
43 COMPUTER: IBM PC compatible
44 OPERATING SYSTEM: PC DOS/MS-DOS
45 SOFTWARE: Patent In Release #1.0, Version #1.25
46 CURRENT APPLICATION DATA:
47 APPLICATION NUMBER: US/08/246,240
48 FILING DATE:
49 CLASSIFICATION: 514
50 ATTORNEY/AGENT INFORMATION:
51 NAME: Swoppe, R. Bain
52 REGISTRATION NUMBER: 24,864
53 REFERENCE/DOCKET NUMBER: 92HR17
54 TELECOMMUNICATION INFORMATION:
55 TELEPHONE: 908-771-6292
56 TELEFAX: 908-771-6159
57 INFORMATION FOR SEQ ID NO: 4:
58 SEQUENCE CHARACTERISTICS:
59 LENGTH: 8 amino acids
60 TYPE: amino acid
61 STRANDEDNESS: unknown
62 COMPLETENESS: unknown
63 MODIFIER TYPE: peptide
64 US 08 103 496A 6
65
66 Query Match: 27.0% Score 5: 100.0% Length 8:
67 Best Local Similarity 100.0%, Prod. No. 2 50000
68 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
69
70 QY 5 KER 5
71 III
72 5 KER 7
73
74 RESULT 43
75 US 08 103 489A 6
76 Sequence 5: Application US/08064395A
77 Patent No. 6446719
78 GENERAL INFORMATION:
79 APPLICANT: YAMADA, YUKIO
80 APPLICANT: ASAMI, OSAMU
81 APPLICANT: SUGIYAMA, HIROHIKO
82 APPLICANT: IZUKAWA, CHIE
83 APPLICANT: FUSHINO, FUMIHIKO
84 APPLICANT: HIRAI, MASANA
85 APPLICANT: KATUNO, ISUTOMU
86 APPLICANT: OMAEDA, TAKAO
87 APPLICANT: SARAI, KIYOKO
88 TITLE OF INVENTION: POLYPEPTIDE POSSESSING PROTEIN DISULFIDE
89 FIELD OF INVENTION: ISOLATED ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR
90 NUMBER OF SEQUENCES: 5
91 COMPLETENESS: 100.0%
92

```

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1  ALPHEV/AGENT INFORMATION:
2  NAME: Swoppe, R. Bain
3  REGISTRATION NUMBER: 24,864
4  REFERENCE/DOCKET NUMBER: 92HR17
5  TELECOMMUNICATION INFORMATION:
6  TELEPHONE: 908-771-6292
7  TELEFAX: 908-771-6159
8  INFORMATION FOR SEQ ID NO: 6:
9  SEQUENCE CHARACTERISTICS:
10 LENGTH: 8 amino acids
11 TYPE: amino acid
12 STRANDEDNESS: unknown
13 COMPLETENESS: unknown
14 MODIFIER TYPE: peptide
15 US 08 103 496A 6
16
17 Query Match: 27.0% Score 5: 100.0% Length 8:
18 Best Local Similarity 100.0%, Prod. No. 2 50000
19 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
20
21 QY 5 KER 5
22 III
23 5 KER 7
24
25 RESULT 43
26 US 08 103 489A 6
27 Sequence 5: Application US/08064395A
28 Patent No. 6446719
29 GENERAL INFORMATION:
30 APPLICANT: YAMADA, YUKIO
31 APPLICANT: ASAMI, OSAMU
32 APPLICANT: SUGIYAMA, HIROHIKO
33 APPLICANT: IZUKAWA, CHIE
34 APPLICANT: FUSHINO, FUMIHIKO
35 APPLICANT: HIRAI, MASANA
36 APPLICANT: KATUNO, ISUTOMU
37 APPLICANT: OMAEDA, TAKAO
38 APPLICANT: SARAI, KIYOKO
39 TITLE OF INVENTION: POLYPEPTIDE POSSESSING PROTEIN DISULFIDE
40 FIELD OF INVENTION: ISOLATED ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR
41 NUMBER OF SEQUENCES: 5
42 COMPLETENESS: 100.0%
43

```


ATTORNEY/AGENT INFORMATION:
 NAME: Tsai, Christine H
 REGISTRATION NUMBER: 34,266
 REFERENCE/DOCKET NUMBER: LUD 5250.4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 688-3884
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 FEATURE: OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 US-08-046 555b 15

Query Match 27.3% Score 3: DB 1: Length 8:
 Best Local Similarity 100.0% Pred No 2.5e+05;
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKK 3
 III
 DE 6 AKK 8

RESULT 47
 US-08-201-046A 27
 Sequence 27, Application US/04261032A
 Patent No. 5945719
 GENERAL INFORMATION:
 APPLICANT: Shasouna, Victor E
 TITLE OF INVENTION: NERVE GROWTH RECEPTORS AND USES THEREOF
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WOLL, Greenfield & Sparks, P.C.
 STREET: 600 Atlantic Ave.
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #100, Version #1.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/201-046A
 FILING DATE: 24-FEB-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Fluor, Elizabeth R.
 REGISTRATION NUMBER: 36,647
 REFERENCE/DOCKET NUMBER: N0260/7014
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 517-720-3500
 TELEFAX: 517-720-2441
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 FEATURE: OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 US-08-201-046A-27

Query Match 27.3% Score 3: DB 1: Length 8:
 Best Local Similarity 100.0% Pred No 2.5e+05;
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 KKE 4
 III
 DE 3 KKE 3

RESULT 38
 US-08-459-569-15
 Sequence 15, Application US/08459504
 Patent No. 5506032
 GENERAL INFORMATION:
 APPLICANT: Goodheart, Andrew; Stroubant, Paul;
 APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
 APPLICANT: Chen, Mao Su; Hiles, Ian
 TITLE OF INVENTION: Glial Mitogenic Factors, Their
 PREPARATION AND USE
 NUMBER OF SEQUENCES: 184
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felie & Lyet
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,569
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/046,555
 FILING DATE: 24-MAR-1994
 APPLICATION NUMBER: 07/965,173
 FILING DATE: 23-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/940,389
 FILING DATE: 03-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/907,138
 FILING DATE: 30-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/864,703
 FILING DATE: 04-APRIL-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/041,075
 FILING DATE: 10-APRIL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Tsai, Christine H.
 REGISTRATION NUMBER: 34,266
 REFERENCE/DOCKET NUMBER: LUD 5250.4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 688-3884
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 FEATURE: OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 US-08-459-569-15

Query Match 27.3% Score 3: DB 1: Length 8:
 Best Local Similarity 100.0% Pred No 2.5e+05;
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKK 3
 III
 DE 6 AKK 8

RESULT 39

```

US-08-472-952-3
: Sequence 3, Application US/08372952
: Patent No. 5645837
: GENERAL INFORMATION:
: APPLICANT: Jamieson, Bradford A.
: APPLICANT: Choksi, Swati
: APPLICANT: Koringold, Robert
: TITLE OF INVENTION: CD8 Antagonists
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Markiewicz &
: STREET: One Liberty Place, 40th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/372,952
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: DeLuca, Mark
: REGISTRATION NUMBER: 34,229
: REFERENCE/DOCKET NUMBER: TJU-1440
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-568-3100
: TELEFAX: 215-568-3439
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-472-952-3

Query Match 27.3% Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
Db 1 1
5 DTQ 7

RESULT 40
US-08-475-6450-9
: Sequence 9, Application US/084556450
: Patent No. 5650487
: GENERAL INFORMATION:
: APPLICANT: Chang, Y-H.
: APPLICANT: Abraham, E.
: TITLE OF INVENTION: Serum Immunoregulatory Polypeptide and
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pons, Smith, Lande & Rose
: STREET: 2029 Century Park East, Suite 400
: CITY: Los Angeles
: STATE: CA
: COUNTRY: USA
: ZIP: 90067
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/455,645D
: FILING DATE: May 31, 1995
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/204,486
: FILING DATE: March 2, 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Oldenkamp, David J.
: REGISTRATION NUMBER: 29,421
: REFERENCE/DOCKET NUMBER: 109-175
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (310) 788-5000
: TELEFAX: (310) 277-1297
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY:
: LOCATION:
: IDENTIFICATION METHOD:
: US-08-455-645D-9

Query Match 27.3% Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RKD 9
Db 4 RKD 6

RESULT 41
US-08-249-387-2
: Sequence 2, Application US/08249387
: Patent No. 5681700
: GENERAL INFORMATION:
: APPLICANT: Reichlin, Morris
: APPLICANT: Koren, Eugen
: TITLE OF INVENTION: Assay for Pathogenicity of Anti-DNA
: TITLE OF INVENTION: Antibodies
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Patrea I. Pabst
: STREET: 1100 Peachtree Street, Suite 2800
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30309-4530
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/249,387
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Pabst, Patrea I.
: REGISTRATION NUMBER: 31,284
: REFERENCE/DOCKET NUMBER: OMRF145
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404) 815-6508
: TELEFAX: (404) 815-6555
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:

```

: LENGTH: 8 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 : HYPOTHETICAL: NO
 : ANTI-SENSE: NO
 : FRAGMENT TYPE: Internal
 : US-08-249-387-2

Query Match 27.3% Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AKK 4
 ID 6 AKK 8

RESULT 42
 : US 08 464 365-5
 : Sequence 5, Application US/08464365
 : Patent No. 5700659

: GENERAL INFORMATION:
 : APPLICANT: YAMADA, YUKIO
 : APPLICANT: ASAMI, OSAMU
 : APPLICANT: SUGIYAMA, HIDEHIKO
 : APPLICANT: IDEKUBA, CHIE
 : APPLICANT: HOSHINO, FUMHIKO
 : APPLICANT: HIRAI, MASANA
 : APPLICANT: KAJINO, TSUTOMU
 : APPLICANT: IMAEDA, TAKAO
 : APPLICANT: SARAI, KIYOKO
 : TITLE OF INVENTION: POLYPEPTIDE PROCESSING PROTEIN C-SUBCLIF
 : TITLE OF INVENTION: ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR
 : TITLE OF INVENTION: PRODUCING THE SAME
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATHER & NEUSTADT
 : ADDRESS: P.C.
 : STREET: 1755 S. Jefferson Davis Highway, Suite 400
 : CITY: Arlington
 : STATE: Virginia
 : COUNTRY: U.S.A.
 : ZIP: 22202

: COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #10, Version #1.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/464,365
 : FILING DATE:

: CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: JP 4 135254
 : FILING DATE: 27-MAY-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: JP 5-44-113
 : FILING DATE: 04-MAR-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: JP 5-44014
 : FILING DATE: 04-MAR-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Oblon, No. 5700659man P.
 : REGISTRATION NUMBER: 24,618
 : REFERENCE/DOCKET NUMBER: 68-228-C
 : TELEPHONE: (703) 413-3000
 : TELEFAX: (703) 413-2220
 : TELEX: 248855 OPAT UR
 : INFORMATION FOR SEQ ID NO: 5:
 : SEQUENCE CHARACTERISTICS:

: LENGTH: 8 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 : US-08-464-365-5

Query Match 27.3% Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 8 KDT 16
 ID 1 KDT 3

RESULT 43
 : US-08-249-322A-15
 : Sequence 15, Application US/08249322A
 : Patent No. 5716930

: GENERAL INFORMATION:
 : APPLICANT: Goodheart, Andrew; Strobant, Paul;
 : APPLICANT: Minnetti, Luisa; Waterfield, Michael; Marchioni, Mark;
 : APPLICANT: Chen, Maio Su; Hiles, Ian
 : TITLE OF INVENTION: Glial Mitogenic Factors, Their
 : TITLE OF INVENTION: Preparation and Use
 : NUMBER OF SEQUENCES: 184
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Felfe & Lynch
 : STREET: 805 Third Avenue
 : CITY: New York City
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10022

: COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 : COMPUTER: IBM
 : OPERATING SYSTEM: PC-DOS
 : SOFTWARE: Wordperfect
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/249,322A
 : FILING DATE: 26-MAY-1994

: CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/036,555
 : FILING DATE: 24-MAR-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/965,174
 : FILING DATE: 23-OCT-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/940,389
 : FILING DATE: 03-SEP-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/907,138
 : FILING DATE: 30-JUN-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/863,703
 : FILING DATE: 03-APRIL-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: U.K. 91 07566.3
 : FILING DATE: 10-APRIL-1991
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Tsai, Christine H.
 : REGISTRATION NUMBER: 34,266
 : REFERENCE/DOCKET NUMBER: LMD 250.4
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212) 688-9200
 : TELEFAX: (212) 838-3884
 : INFORMATION FOR SEQ ID NO: 15:
 : SEQUENCE CHARACTERISTICS:

: LENGTH: 8
 : TYPE: amino acid
 : STRANDEDNESS:
 : TOPOLOGY: linear

1 FEATURE:
2 OTHER INFORMATION: Xaa at position 1 is Cysteine or Arginine.
3 US-08 249-322A-15

Query Match: 27.4%, Score 3, DB 1, Length 8
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
1-1
DB 6 AKK 8

RESULT 44
US-08-461-597-8
2 Sequence 8, Application US/084-1597
3 Patent No. 5759834
4 GENERAL INFORMATION:
5 APPLICANT: ALASSI, M. Zohair
6 TITLE OF INVENTION: Synthetic Sterically Constrained
7 CATALYSTS
8 NUMBER OF SEQUENCES: 8
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Thomas D. Paul
11 STREET: 1401 McKinney, Suite 5100
12 CITY: Houston
13 STATE: Texas
14 COUNTRY: USA
15 ZIP: 77010-4095
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/461-597
23 FILING DATE:
24 CLASSIFICATION: 435
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US/08/00,114
27 FILING DATE: 18-MAY-1993
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Paul, Thomas D.
30 REGISTRATION NUMBER: 42,711
31 REFERENCE/DRAWET NUMBER: 1-1-1
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: 713/651-5345
34 TELEFAX: 713/651-4246
35 INFORMATION FOR SEQ ID NO: 8:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 8 amino acids
38 TYPE: amino acid
39 STRANDEDNESS: single
40 TOPOLOGY: linear
41 MOLECULE TYPE: peptide
42 HYDROPHILIC: NO
43 ANTI-SENSE: NO
44 FRAGMENT TYPE: not applicable
45 US-08-461-597-8

Query Match: 27.4%, Score 3, DB 1, Length 8
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
1-1
DB 6 AKK 8

RESULT 45
US-08-461-526A-15
2 Sequence 15, Application US/08469-26A
3 Patent No. 5792849
4 GENERAL INFORMATION:
5 APPLICANT: Goodell, Andrew
6 APPLICANT: Stroobant, Paul
7 APPLICANT: Minghetti, Luisa
8 APPLICANT: Waterfield, Michael
9 APPLICANT: Marchionni, Mark
10 APPLICANT: Chen, Mao SC
11 APPLICANT: Biles, Ian
12 TITLE OF INVENTION: GLOBAL MITOGENIC FACTORS, THEIR
13 PREPARATION AND USE
14 NUMBER OF SEQUENCES: 187
15 CORRESPONDENCE ADDRESS:
16 ADDRESSEE: Mark S. Biles, M.D.
17 STREET: 7700 Eastfield Street
18 CITY: Houston

Query Match: 27.4%, Score 3, DB 1, Length 8
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
1-1
DB 6 AKK 8

GENERAL INFORMATION:
1 APPLICANT: KIMACHI, Kazuhiko
2 APPLICANT: MAEDA, Hiroaki
3 APPLICANT: NISHIYAMA, Kiyoto
4 APPLICANT: TOKIYOSHI, Sachio
5 APPLICANT: TOHYA, Y. Kingo
6 APPLICANT: MIKAMI, Takeshi
7 TITLE OF INVENTION: ANTI-PELINE CALCIVIRUS RECOMBINANT
8 ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
9 NUMBER OF SEQUENCES: 23
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
12 STREET: 1235 20th Street, N.W., Suite 300
13 CITY: Washington
14 STATE: D.C.
15 COUNTRY: U.S.A.
16 ZIP: 20036-8218
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: PatentIn Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/024-253
24 FILING DATE: 19930301
25 CLASSIFICATION: 424
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: JP 79189/1992
28 FILING DATE: 28-FEB-1992
29 ATTORNEY/AGENT INFORMATION:
30 NAME: CANTOR, Herbert J.
31 REGISTRATION NUMBER: 24,142
32 REFERENCE/DRAWET NUMBER: P-500-23744
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (202) 887-0400
35 TELEFAX: (202) 845-0995
36 TELEX: 440706 WEGUR
37 INFORMATION FOR SEQ ID NO: 13:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 8 amino acids
40 TYPE: amino acid
41 TOPOLOGY: unknown
42 MOLECULE TYPE: protein
43 US-08-024-253-13

Query Match: 27.4%, Score 3, DB 1, Length 8
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KDI 10
1-1
DB 6 KDI 5

RESULT 46
US-08-461-526A-15
2 Sequence 15, Application US/08469-26A
3 Patent No. 5792849
4 GENERAL INFORMATION:
5 APPLICANT: Goodell, Andrew
6 APPLICANT: Stroobant, Paul
7 APPLICANT: Minghetti, Luisa
8 APPLICANT: Waterfield, Michael
9 APPLICANT: Marchionni, Mark
10 APPLICANT: Chen, Mao SC
11 APPLICANT: Biles, Ian
12 TITLE OF INVENTION: GLOBAL MITOGENIC FACTORS, THEIR
13 PREPARATION AND USE
14 NUMBER OF SEQUENCES: 187
15 CORRESPONDENCE ADDRESS:
16 ADDRESSEE: Mark S. Biles, M.D.
17 STREET: 7700 Eastfield Street
18 CITY: Houston

Query Match: 27.4%, Score 3, DB 1, Length 8
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KDI 10
1-1
DB 6 KDI 5

RESULT 47
US-08-461-526A-15
2 Sequence 15, Application US/08469-26A
3 Patent No. 5792849
4 GENERAL INFORMATION:
5 APPLICANT: Goodell, Andrew
6 APPLICANT: Stroobant, Paul
7 APPLICANT: Minghetti, Luisa
8 APPLICANT: Waterfield, Michael
9 APPLICANT: Marchionni, Mark
10 APPLICANT: Chen, Mao SC
11 APPLICANT: Biles, Ian
12 TITLE OF INVENTION: GLOBAL MITOGENIC FACTORS, THEIR
13 PREPARATION AND USE
14 NUMBER OF SEQUENCES: 187
15 CORRESPONDENCE ADDRESS:
16 ADDRESSEE: Mark S. Biles, M.D.
17 STREET: 7700 Eastfield Street
18 CITY: Houston

Query Match: 27.4%, Score 3, DB 1, Length 8
Best Local Similarity 100.0%, Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KDI 10
1-1
DB 6 KDI 5


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1  STATE: MA
2  COUNTRY: USA
3  ZIP: 02110
4  COMPUTER READABLE FORM:
5  MEDIUM TYPE: Diskette
6  COMPUTER: IBM Compatible
7  OPERATING SYSTEM: DOS
8  SOFTWARE: FASTSEQ for Windows Version 1.5
9  CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/08/429,527A
11 FILING DATE: 06 June 1995
12 CLASSIFICATION: 445
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: 08/036,555
15 FILING DATE: 24-MAR-1993
16 APPLICATION NUMBER: 07/905,173
17 FILING DATE: 23-OCT-1992
18 APPLICATION NUMBER: 07/940,339
19 FILING DATE: 03-SEP-1992
20 APPLICATION NUMBER: 07/907,138
21 FILING DATE: 03-JUN-1992
22 APPLICATION NUMBER: 07/963,703
23 FILING DATE: 03-APR-1992
24 APPLICATION NUMBER: 01-K-9,07566.3
25 FILING DATE: 10-APR-1991
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Broker Brady, Kristina
28 REGISTRATION NUMBER: 39,109
29 REFERENCE/DOCKET NUMBER: 04505/0209A
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 617-428-0200
32 TELEFAX: 617-428-7045
33 INFORMATION FOR SEQ ID NO: 15:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 8
36 TYPE: amino acid
37 STRANDEDNESS: Single
38 TOPOLOGY: Linear
39 FEATURE:
40 OTHER INFORMATION: Xaa is position 15 in position 1
41 OTHER INFORMATION: Arginine
42 US 09 469 526A-15
43
44 Query Match 27.3%, Score 3, ID 15, Length 8
45 Best local Similarity 100.0%, Pred. No. 2.5e+05
46 Matches 3, Conservative 0, Mismatches 0, Gaps 0
47
48 QY 1 AKK 3
49 ID 6 AKK 8
50
51 RESULT 47
52 US-08-373,193-A6
53 Sequence 46, Application US/08/373193
54 Patent No. 5851829
55 GENERAL INFORMATION:
56 APPLICANT: PARASCO, WAYNE
57 APPLICANT: HASELTINE, WILLIAM
58 TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS
59 NUMBER OF SEQUENCES: 79
60 CORRESPONDENCE ADDRESS:
61 ADDRESSEE: DIKE, BRONSTEIN, KUBERTS & FLYNNMAN
62 STREET: 140 WATER STREET
63 CITY: BOSTON
64 STATE: MA
65 COUNTRY: US
66 ZIP: 02109
67 COMPUTER READABLE FORM:
68 MEDIUM TYPE: Diskette
69 COMPUTER: IBM Compatible
70 OPERATING SYSTEM: DOS
71 SOFTWARE: FASTSEQ Version 1.5

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1  CURRENT APPLICATION DATA:
2  APPLICATION NUMBER: US/08/374,190
3  FILING DATE: 17 JAN-1995
4  CLASSIFICATION: 445
5  PRIOR APPLICATION DATA:
6  APPLICATION NUMBER: 01/US94/06335
7  FILING DATE: 16 JUL 1994
8  ATTORNEY/AGENT INFORMATION:
9  NAME: RESNICK, DAVID S
10 REGISTRATION NUMBER: 34,245
11 REFERENCE/DOCKET NUMBER: 41954 1P1 US
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 617 523 3400
14 TELEFAX: 617 523 6446
15 TEXT: SEQ ID NO: 41:
16 INFORMATION FOR SEQ ID NO: 41:
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 8 amino acids
19 TYPE: amino acid
20 STRANDEDNESS: Single
21 TOPOLOGY: Linear
22 MOLECULE TYPE: peptide
23 HYPOTHEICAL: NO
24 ANTI-SENSE: NO
25 FRAGMENT TYPE: N-terminal
26 ORIGINAL SOURCE:
27 US-08-373-190-46
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29 Query Match 27.3%, Score 3, ID 2, Length 8
30 Best local Similarity 100.0%, Pred. No. 2.5e+05
31 Matches 3, Conservative 0, Mismatches 0, Gaps 0
32
33 QY 1 AKK 3
34 ID 6 AKK 8
35
36 RESULT 48
37 US-08-734,591-A 15
38 Sequence 15, Application US/08/734591A
39 Patent No. 5854220
40 GENERAL INFORMATION:
41 APPLICANT: Godeart, Andrew
42 APPLICANT: Strobant, Paul
43 APPLICANT: Minthell, Luisa
44 APPLICANT: Watterfield, Michael
45 APPLICANT: Biles, Ian
46 APPLICANT: Marchionni, Mark
47 APPLICANT: Chen, Marie
48 TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
49 PREPARATION AND USE
50 NUMBER OF SEQUENCES: 187
51 CORRESPONDENCE ADDRESS:
52 ADDRESSEE: Clark & Elding LLP
53 STREET: 175 Federal Street
54 CITY: Boston
55 STATE: Massachusetts
56 COUNTRY: U.S.A.
57 ZIP: 02110
58 COMPUTER READABLE FORM:
59 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
60 COMPUTER: IBM Compatible Pentium
61 OPERATING SYSTEM: Windows95
62 SOFTWARE: WordPerfect (Version 7.0)
63 CURRENT APPLICATION DATA:
64 APPLICATION NUMBER: US/08/734,591A
65 FILING DATE: 22 OCT-1996
66 CLASSIFICATION: 536
67 PRIOR APPLICATION DATA:
68 APPLICATION NUMBER: 08/470,445
69 FILING DATE: 06 JUN 1995
70 PRIOR APPLICATION DATA:
71 APPLICATION NUMBER: 08/046,555

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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/965,174
: FILING DATE: 23-OCT-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/940,149
: FILING DATE: 03-SEP-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/907,118
: FILING DATE: 30-JUN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/864,703
: FILING DATE: 03-APR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: UK 91 07566,3
: FILING DATE: 10-APR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Bleker-Brady, Kristina
: REGISTRATION NUMBER: 39,709
: REFERENCE/DOCKET NUMBER: 04585/00200P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 428-0200
: TELEFAX: (617) 428-7045
: TELEX:
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: FEATURE:
: OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
US 08 734-591A-15

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Query Match 27.3% Score 3: DB 2: Length 8:
Best Local Similarity 100.0%: Pred. No. 2.5e+05:
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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CY 1 AKK 3
DB 6 AKK 8

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RESULT 47
US 08-545-298-15
: Sequence 15: Application US/08/545298
: Patent No. 5861477
: GENERAL INFORMATION:
: APPLICANT: Atassi, Zouhair
: TITLE OF INVENTION: Synthetic Stereocatalysts
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: C. Steven McDaniel
: STREET: 600 Travis Street, Suite 1400
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77002-2912
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Microsoft Word 97 (running under MS Windows 95)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/545,298
: FILING DATE: 19-JUNE-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: C. Steven McDaniel
: REGISTRATION NUMBER: 33,962
: REFERENCE/DOCKET NUMBER: 1515-0310A
: TELECOMMUNICATION INFORMATION:

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: TELEPHONE: 714/248 8000
: TELEFAX: 714/248-8008
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: not applicable
US-08 545-298-10

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Query Match 27.3% Score 3: DB 2: Length 8:
Best Local Similarity 100.0%: Pred. No. 2.5e+05:
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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CY 1 AKK 3
DB 1 AKK 3

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RESULT 50
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: Sequence 15: Application US/08469660
: Patent No. 5876973
: GENERAL INFORMATION:
: APPLICANT: Gwynne, David I.; Marchionni, Mark;
: APPLICANT: McBurney, Robert N.
: TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
: TITLE OF INVENTION: THEIR PREPARATION AND USE
: NUMBER OF SEQUENCES: 184
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: Massachusetts
: ZIP: 02111-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
: COMPUTER: IBM
: OPERATING SYSTEM: PC DOS
: SOFTWARE: Wordperfect
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/469,660
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/011,196
: FILING DATE: 29-JAN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/984,085
: FILING DATE: 01-OCT-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/951,747
: FILING DATE: 25-SEP-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/927,337
: FILING DATE: 10-AUG-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,162
: REFERENCE/DOCKET NUMBER: 04585/017004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-5070
: TELEFAX: 200154
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear

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: FEATURE:
: OTHER INFORMATION: Xaa in position 1 is Lysine or
: OTHER INFORMATION: Arginine.
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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKK 3
Db 6 AKK 8
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Search completed: September 30, 2003, 10:28:28
Job time : 16.9167 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2003, 10:10:03 : Search time 21.5 Seconds

(without alignments)
77.413 Million cell updates/sec

Title: US-09-787-443-2

Perfect score: 11

Sequence: 1 AKKERQKDIQ 11

Scoring table: OLICO

Gapop 60.0 , Gapext 60.0

Searched: 566894 seqs, 151307093 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68387

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : Published_Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	4	36.4	8	11	US-09-876-904A-439
5	4	36.4	10	11	US-09-922-226-84
6	4	36.4	11	9	US-09-876-946-10
7	4	36.4	11	12	US-10-304-443-118
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9	4	36.4	13	10	US-09-746-170-33
10	4	36.4	13	11	US-09-820-053A-88
11	4	36.4	13	12	US-10-304-443-113
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19	3	27.3	8	10	US-09-792-480-11	Sequence 11, Appl
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44	3	27.3	8	14	US-10-024-935-19	Sequence 19, Appl
45	3	27.3	8	14	US-10-040-572-8	Sequence 8, Appl
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50	3	27.3	8	14	US-10-061-395-65	Sequence 65, Appl
51	3	27.3	8	14	US-10-115-704-5	Sequence 5, Appl
52	3	27.3	8	15	US-10-083-815-10	Sequence 10, Appl
53	3	27.3	8	15	US-10-039-831-15	Sequence 15, Appl
54	3	27.3	8	15	US-10-097-065-643	Sequence 643, App
55	3	27.3	8	15	US-10-174-105A-48	Sequence 48, Appl
56	3	27.3	8	15	US-10-006-869-528	Sequence 528, App
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80	3	27.3	8	15	US-10-006-869-3500	Sequence 3500, Ap
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104	3	27.3	9	9	US-09-834-765-319	Sequence 318, App	177	3	27.3	9	11	US-09-857-844-10	Sequence 10, Appl
105	3	27.3	9	9	US-09-834-765-451	Sequence 451, App	178	3	27.3	9	11	US-09-857-823-6	Sequence 6, Appl
106	3	27.3	9	9	US-09-834-765-645	Sequence 645, App	179	3	27.3	9	11	US-09-989-994-5	Sequence 5, Appl
107	3	27.3	9	9	US-09-989-789-5	Sequence 5, Appl	180	3	27.3	9	12	US-09-932-165-438	Sequence 438, App
108	3	27.3	9	9	US-09-192-854-42	Sequence 42, Appl	181	3	27.3	9	12	US-09-932-165-650	Sequence 650, App
109	3	27.3	9	9	US-09-192-854-99	Sequence 92, App	182	3	27.3	9	12	US-09-932-165-1175	Sequence 1175, App
110	3	27.3	9	9	US-09-192-854-160	Sequence 160, App	183	3	27.3	9	12	US-10-039-183A-12	Sequence 12, Appl
111	3	27.3	9	9	US-09-481-490-176	Sequence 176, App	184	3	27.3	9	12	US-10-291-250-10	Sequence 10, Appl
112	3	27.3	9	9	US-09-925-796-10	Sequence 10, Appl	185	3	27.3	9	12	US-10-291-250-13	Sequence 13, Appl
113	3	27.3	9	9	US-09-874-666-3	Sequence 3, Appl	186	3	27.3	9	12	US-10-291-250-15	Sequence 15, Appl
114	3	27.3	9	9	US-09-941-453-10	Sequence 10, Appl	187	3	27.3	9	12	US-09-968-744A-66	Sequence 66, Appl
115	3	27.3	9	10	US-09-984-056-10	Sequence 10, Appl	188	3	27.3	9	12	US-09-968-744A-182	Sequence 182, App
116	3	27.3	9	10	US-09-872-1856-15	Sequence 15, Appl	189	3	27.3	9	12	US-09-968-744A-282	Sequence 282, App
117	3	27.3	9	10	US-09-792-480-8	Sequence 8, Appl	190	3	27.3	9	12	US-10-172-425B-22	Sequence 22, Appl
118	3	27.3	9	10	US-09-792-480-14	Sequence 14, Appl	191	3	27.3	9	12	US-10-190-082-270	Sequence 270, App
119	3	27.3	9	10	US-09-792-480-14	Sequence 14, Appl	192	3	27.3	9	12	US-10-201-389A-18	Sequence 18, Appl
120	3	27.3	9	10	US-09-792-480-15	Sequence 15, Appl	193	3	27.3	9	12	US-10-169-223-6	Sequence 6, Appl
121	3	27.3	9	10	US-09-792-480-16	Sequence 16, Appl	194	3	27.3	9	12	US-09-793-451-522	Sequence 522, App
122	3	27.3	9	10	US-09-792-480-20	Sequence 20, Appl	195	3	27.3	9	12	US-09-793-451-643	Sequence 643, App
123	3	27.3	9	10	US-09-792-480-21	Sequence 21, Appl	196	3	27.3	9	12	US-10-169-351-26	Sequence 26, Appl
124	3	27.3	9	10	US-09-792-480-22	Sequence 22, Appl	197	3	27.3	9	12	US-10-308-967-22	Sequence 22, Appl
125	3	27.3	9	10	US-09-792-480-28	Sequence 28, Appl	198	3	27.3	9	12	US-10-308-967-26	Sequence 26, Appl
126	3	27.3	9	10	US-09-731-558-8	Sequence 8, Appl	199	3	27.3	9	12	US-10-338-348-1	Sequence 1, Appl
127	3	27.3	9	10	US-09-779-308-182	Sequence 182, App	200	3	27.3	9	12	US-10-022-066-21	Sequence 21, Appl
128	3	27.3	9	10	US-09-779-308-196	Sequence 196, App	201	3	27.3	9	12	US-10-022-066-158	Sequence 158, App
129	3	27.3	9	10	US-09-779-308-407	Sequence 407, App	202	3	27.3	9	12	US-10-077-106-13	Sequence 13, Appl
130	3	27.3	9	10	US-09-779-308-481	Sequence 481, App	203	3	27.3	9	12	US-10-077-106-15	Sequence 15, Appl
131	3	27.3	9	10	US-09-984-057-10	Sequence 10, Appl	204	3	27.3	9	12	US-10-077-106-15	Sequence 15, Appl
132	3	27.3	9	10	US-09-942-587A-10	Sequence 10, Appl	205	3	27.3	9	12	US-10-245-415B-10	Sequence 10, Appl
133	3	27.3	9	10	US-09-942-590-17	Sequence 17, Appl	206	3	27.3	9	12	US-10-262-435-4	Sequence 4, Appl
134	3	27.3	9	10	US-09-966-561A-16	Sequence 66, App	207	3	27.3	9	12	US-09-942-052-15	Sequence 15, Appl
135	3	27.3	9	10	US-09-968-641A-142	Sequence 162, App	208	3	27.3	9	12	US-09-942-052-47	Sequence 47, Appl
136	3	27.3	9	10	US-09-968-641A-262	Sequence 282, App	209	3	27.3	9	12	US-09-942-052-115	Sequence 115, App
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138	3	27.3	9	10	US-09-968-641A-262	Sequence 23, App	211	3	27.3	9	12	US-09-942-052-220	Sequence 220, App
139	3	27.3	9	10	US-09-968-641A-262	Sequence 22, App	212	3	27.3	9	12	US-09-942-052-224	Sequence 224, App
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141	3	27.3	9	11	US-09-864-291-17	Sequence 67, Appl	214	3	27.3	9	12	US-09-942-052-528	Sequence 528, App
142	3	27.3	9	11	US-09-846-034B-214	Sequence 214, App	215	3	27.3	9	12	US-09-942-052-617	Sequence 617, App
143	3	27.3	9	11	US-09-925-179-11	Sequence 11, Appl	216	3	27.3	9	12	US-10-280-137-237	Sequence 237, App
144	3	27.3	9	11	US-09-925-179-28	Sequence 28, Appl	217	3	27.3	9	12	US-10-304-443-112	Sequence 112, App
145	3	27.3	9	11	US-09-990-186-6	Sequence 5, Appl	218	3	27.3	9	12	US-10-239-313A-692	Sequence 692, App
146	3	27.3	9	11	US-09-936-854-46	Sequence 46, App	219	3	27.3	9	12	US-10-353-929-13	Sequence 13, Appl
147	3	27.3	9	11	US-09-936-854-80	Sequence 80, Appl	220	3	27.3	9	12	US-10-353-929-163	Sequence 163, App
148	3	27.3	9	11	US-09-938-864-128	Sequence 128, App	221	3	27.3	9	12	US-10-412-105-33	Sequence 33, Appl
149	3	27.3	9	11	US-09-938-864-164	Sequence 163, App	222	3	27.3	9	14	US-10-011-321-4	Sequence 1, Appl
150	3	27.3	9	11	US-09-938-864-172	Sequence 172, App	223	3	27.3	9	14	US-10-114-176-1	Sequence 4, Appl
151	3	27.3	9	11	US-09-938-864-219	Sequence 219, App	224	3	27.3	9	15	US-10-211-207-13	Sequence 13, Appl
152	3	27.3	9	11	US-09-938-864-300	Sequence 300, App	225	3	27.3	9	15	US-10-211-207-14	Sequence 14, Appl
153	3	27.3	9	11	US-09-876-904A-272	Sequence 272, App	226	3	27.3	9	15	US-10-211-207-15	Sequence 15, Appl
154	3	27.3	9	11	US-09-876-904A-276	Sequence 276, App	227	3	27.3	9	15	US-10-006-069A-214	Sequence 214, App
155	3	27.3	9	11	US-09-876-904A-466	Sequence 466, App	228	3	27.3	9	15	US-10-125-635A-46	Sequence 46, Appl
156	3	27.3	9	11	US-09-876-904A-589	Sequence 589, App	229	3	27.3	9	15	US-10-125-635A-80	Sequence 80, Appl
157	3	27.3	9	11	US-09-876-904A-596	Sequence 596, App	230	3	27.3	9	15	US-10-125-635A-128	Sequence 128, App
158	3	27.3	9	11	US-09-791-477-46	Sequence 46, Appl	231	3	27.3	9	15	US-10-125-635A-163	Sequence 163, App
159	3	27.3	9	11	US-09-791-477-80	Sequence 80, Appl	232	3	27.3	9	15	US-10-125-635A-172	Sequence 172, App
160	3	27.3	9	11	US-09-791-477-128	Sequence 128, App	233	3	27.3	9	15	US-10-125-635A-219	Sequence 219, App
161	3	27.3	9	11	US-09-791-477-164	Sequence 163, App	234	3	27.3	9	15	US-10-125-635A-300	Sequence 300, App

235	9	15	US-10-039-831-16	Sequence 16, Appl	308	3	27.3	9	15	US-10-001-459-1966	Sequence 1566, Ap
236	3	27.3	US-10-055-713-8	Sequence 8, Appl1	309	3	27.3	9	15	US-10-001-469-2007	Sequence 2007, Ap
237	9	15	US-10-239-804-1	Sequence 1, Appl1	310	3	27.3	9	15	US-10-001-469-2008	Sequence 2008, Ap
238	3	27.3	US-10-084-813-987	Sequence 987, App	311	3	27.3	9	15	US-10-001-469-2013	Sequence 2013, Ap
239	9	15	US-10-084-813-988	Sequence 988, App	312	3	27.3	9	15	US-10-001-469-2062	Sequence 2062, Ap
240	3	27.3	US-10-084-813-989	Sequence 989, App	313	3	27.3	9	15	US-10-001-469-2063	Sequence 2063, Ap
241	9	15	US-10-084-813-990	Sequence 990, App	314	3	27.3	9	15	US-10-001-469-2132	Sequence 2132, Ap
242	3	27.3	US-10-084-813-991	Sequence 991, App	315	3	27.3	9	15	US-10-105-901-29	Sequence 29, Appl
243	3	27.3	US-10-084-813-992	Sequence 992, App	316	3	27.3	9	15	US-10-023-282-832	Sequence 832, App
244	9	15	US-10-084-813-993	Sequence 993, App	317	3	27.3	9	15	US-10-002-603-46	Sequence 46, Appl
245	3	27.3	US-10-090-013-4	Sequence 4, Appl1	318	3	27.3	9	15	US-10-002-603-80	Sequence 80, Appl
246	9	15	US-10-059-261-239	Sequence 239, App	319	3	27.3	9	15	US-10-002-603-128	Sequence 128, App
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251	9	15	US-10-006-869-545	Sequence 545, App	324	3	27.3	9	15	US-10-133-210-58	Sequence 58, Appl
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255	9	15	US-10-006-869-531	Sequence 3151, App	328	3	27.3	9	15	US-10-091-724-49	Sequence 49, Appl
256	3	27.3	US-10-006-869-531	Sequence 3194, App	329	3	27.3	9	15	US-10-113-424-5	Sequence 5, Appl1
257	9	15	US-10-006-869-531	Sequence 3196, App	330	3	27.3	9	15	US-10-165-250A-9	Sequence 9, Appl1
258	3	27.3	US-10-006-869-531	Sequence 3249, App	331	3	27.3	9	15	US-10-165-250A-10	Sequence 10, Appl1
259	9	15	US-10-006-869-531	Sequence 3247, App	332	3	27.3	9	15	US-10-055-711-8	Sequence 8, Appl1
260	3	27.3	US-10-006-869-531	Sequence 3284, App	333	3	27.3	9	15	US-10-136-738-46	Sequence 46, Appl1
261	9	15	US-10-006-869-531	Sequence 3286, App	334	3	27.3	9	15	US-10-109-171-40	Sequence 40, Appl1
262	3	27.3	US-10-006-869-531	Sequence 3326, App	335	3	27.3	9	15	US-10-109-171-122	Sequence 122, App
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264	3	27.3	US-10-006-869-531	Sequence 3337, App	337	3	27.3	9	15	US-10-109-171-135	Sequence 135, App
265	9	15	US-10-006-869-531	Sequence 3337, App	338	3	27.3	9	15	US-10-109-171-136	Sequence 136, App
266	3	27.3	US-10-006-869-531	Sequence 3339, App	339	3	27.3	9	15	US-10-301-644-16	Sequence 16, Appl
267	9	15	US-10-006-869-531	Sequence 3419, App	340	3	27.3	9	15	US-10-301-644-17	Sequence 17, Appl
268	3	27.3	US-10-006-869-531	Sequence 3421, App	341	3	27.3	9	15	US-10-012-806A-43	Sequence 43, Appl
269	9	15	US-10-006-869-531	Sequence 3461, App	342	3	27.3	9	15	US-10-201-394A-18	Sequence 18, Appl
270	3	27.3	US-10-006-869-531	Sequence 3503, App	343	3	27.3	10	8	US-08-927-939-27	Sequence 27, Appl
271	9	15	US-10-006-869-531	Sequence 3505, App	344	3	27.3	10	8	US-08-873-601-5	Sequence 5, Appl1
272	3	27.3	US-10-006-869-531	Sequence 3545, App	345	3	27.3	10	9	US-09-157-748-12	Sequence 12, Appl
273	9	15	US-10-209-421-11	Sequence 9, Appl1	346	3	27.3	10	9	US-09-010-714-4	Sequence 4, Appl1
274	3	27.3	US-10-209-421-11	Sequence 11, Appl	347	3	27.3	10	9	US-09-834-765-487	Sequence 487, App
275	9	15	US-10-209-421-28	Sequence 28, Appl	348	3	27.3	10	9	US-09-834-765-606	Sequence 606, App
276	3	27.3	US-10-229-915-26	Sequence 26, Appl	349	3	27.3	10	9	US-09-834-765-672	Sequence 672, App
277	9	15	US-10-229-915-31	Sequence 31, Appl	350	3	27.3	10	9	US-09-802-109-10	Sequence 10, Appl
278	3	27.3	US-10-001-469-844	Sequence 462, App	351	3	27.3	10	10	US-09-950-692-4	Sequence 4, Appl1
279	9	15	US-10-001-469-844	Sequence 462, App	352	3	27.3	10	10	US-09-972-016-2	Sequence 2, Appl1
280	3	27.3	US-10-001-469-844	Sequence 479, App	353	3	27.3	10	10	US-09-972-016-3	Sequence 3, Appl1
281	9	15	US-10-001-469-844	Sequence 491, App	354	3	27.3	10	10	US-09-977-831-36	Sequence 36, Appl
282	3	27.3	US-10-001-469-844	Sequence 615, App	355	3	27.3	10	10	US-09-984-056-91	Sequence 91, Appl
283	9	15	US-10-001-469-844	Sequence 629, App	356	3	27.3	10	10	US-09-963-206B-14	Sequence 14, Appl
284	3	27.3	US-10-001-469-844	Sequence 634, App	357	3	27.3	10	10	US-09-916-940-9	Sequence 9, Appl1
285	9	15	US-10-001-469-844	Sequence 852, App	358	3	27.3	10	10	US-09-970-515-7	Sequence 7, Appl1
286	3	27.3	US-10-001-469-844	Sequence 897, App	359	3	27.3	10	10	US-09-824-588-5	Sequence 5, Appl1
287	9	15	US-10-001-469-844	Sequence 1004, App	360	3	27.3	10	10	US-09-779-308-150	Sequence 150, App
288	3	27.3	US-10-001-469-844	Sequence 1067, App	361	3	27.3	10	10	US-09-779-308-356	Sequence 356, App
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290	3	27.3	US-10-001-469-844	Sequence 1498, App	363	3	27.3	10	10	US-09-254-590-18	Sequence 18, Appl
291	9	15	US-10-001-469-844	Sequence 1595, App	364	3	27.3	10	10	US-09-792-630-58	Sequence 58, Appl
292	3	27.3	US-10-001-469-844	Sequence 1674, App	365	3	27.3	10	10	US-09-966-976A-14	Sequence 14, Appl
293	9	15	US-10-001-469-844	Sequence 1739, App	366	3	27.3	10	10	US-09-910-552-55	Sequence 55, Appl
294	3	27.3	US-10-001-469-844	Sequence 1740, App	367	3	27.3	10	10	US-09-978-178-1	Sequence 1, Appl1
295	9	15	US-10-001-469-844	Sequence 1763, App	368	3	27.3	10	10	US-09-959-845-8	Sequence 8, Appl1
296	3	27.3	US-10-001-469-844	Sequence 1826, App	369	3	27.3	10	10	US-09-882-774-12	Sequence 12, Appl
297	9	15	US-10-001-469-844	Sequence 1853, App	370	3	27.3	10	10	US-09-782-672-47	Sequence 47, Appl
298	3	27.3	US-10-001-469-844	Sequence 1894, App	371	3	27.3	10	10	US-09-994-595-26	Sequence 26, Appl
299	9	15	US-10-001-469-844	Sequence 1827, App	372	3	27.3	10	10	US-09-994-595-63	Sequence 63, Appl
300	3	27.3	US-10-001-469-844	Sequence 1853, App	373	3	27.3	10	10	US-09-994-595-67	Sequence 67, Appl
301	9	15	US-10-001-469-844	Sequence 1894, App	374	3	27.3	10	10	US-09-994-595-83	Sequence 83, Appl
302	3	27.3	US-10-001-469-844	Sequence 1898, App	375	3	27.3	10	10	US-09-866-512A-15	Sequence 15, Appl
303	9	15	US-10-001-469-844	Sequence 1906, App	376	3	27.3	10	10	US-09-876-904A-41	Sequence 41, Appl
304	3	27.3	US-10-001-469-844	Sequence 1943, App	377	3	27.3	10	10	US-09-876-904A-87	Sequence 87, Appl
305	9	15	US-10-001-469-844	Sequence 1943, App	378	3	27.3	10	10	US-09-876-904A-90	Sequence 90, Appl
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385	3	27.3	10	11	US-09-572-404B-250	Sequence 250, App	458	3	27.3	10	12	US-10-262-435-29	Sequence 29, App
386	3	27.3	10	11	US-09-572-404B-252	Sequence 252, App	459	3	27.3	10	12	US-10-262-435-52	Sequence 52, App
387	3	27.3	10	11	US-09-572-404B-820	Sequence 820, App	460	3	27.3	10	12	US-10-262-435-53	Sequence 53, App
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390	3	27.3	10	11	US-09-572-404B-1183	Sequence 1181, App	463	3	27.3	10	12	US-10-262-435-61	Sequence 61, App
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396	3	27.3	10	11	US-09-572-404B-1724	Sequence 1724, App	469	3	27.3	10	12	US-10-262-435-82	Sequence 82, App
397	3	27.3	10	11	US-09-572-404B-1842	Sequence 1842, App	470	3	27.3	10	12	US-10-262-435-83	Sequence 83, App
398	3	27.3	10	11	US-09-572-404B-1942	Sequence 1942, App	471	3	27.3	10	12	US-10-262-435-107	Sequence 0, App
399	3	27.3	10	11	US-09-572-404B-1947	Sequence 1947, App	472	3	27.3	10	12	US-09-942-052-52	Sequence 52, App
400	3	27.3	10	11	US-09-572-404B-1947	Sequence 1949, App	473	3	27.3	10	12	US-09-942-052-167	Sequence 167, App
401	3	27.3	10	11	US-09-572-404B-2141	Sequence 2141, App	474	3	27.3	10	12	US-09-942-052-180	Sequence 180, App
402	3	27.3	10	11	US-09-572-404B-2152	Sequence 2152, App	475	3	27.3	10	12	US-09-942-052-200	Sequence 200, App
403	3	27.3	10	11	US-09-572-404B-2171	Sequence 2171, App	476	3	27.3	10	12	US-09-942-052-253	Sequence 253, App
404	3	27.3	10	11	US-09-572-404B-2176	Sequence 2178, App	477	3	27.3	10	12	US-09-942-052-298	Sequence 298, App
405	3	27.3	10	11	US-09-572-404B-2183	Sequence 2183, App	478	3	27.3	10	12	US-09-942-052-354	Sequence 354, App
406	3	27.3	10	11	US-09-572-404B-2520	Sequence 2520, App	479	3	27.3	10	12	US-09-942-052-376	Sequence 376, App
407	3	27.3	10	11	US-09-572-404B-2522	Sequence 2522, App	480	3	27.3	10	12	US-09-942-052-587	Sequence 587, App
408	3	27.3	10	11	US-09-572-404B-4116	Sequence 2616, App	481	3	27.3	10	12	US-09-942-052-661	Sequence 661, App
409	3	27.3	10	11	US-09-820-553A-37	Sequence 57, App	482	3	27.3	10	12	US-10-096-550-9	Sequence 9, App
410	3	27.3	10	11	US-09-820-553A-38	Sequence 58, App	483	3	27.3	10	12	US-10-280-137-114	Sequence 114, App
411	3	27.3	10	11	US-09-820-553A-143	Sequence 59, App	484	3	27.3	10	12	US-10-155-693-26	Sequence 26, App
412	3	27.3	10	11	US-09-820-553A-143	Sequence 54, App	485	3	27.3	10	12	US-10-239-313A-458	Sequence 458, App
413	3	27.3	10	11	US-09-952-406A-54	Sequence 54, App	486	3	27.3	10	12	US-10-315-920-11	Sequence 11, App
414	3	27.3	10	12	US-09-132-145-549	Sequence 539, App	487	3	27.3	10	14	US-10-007-761-9	Sequence 9, App
415	3	27.3	10	12	US-09-321-982-26	Sequence 26, App	488	3	27.3	10	14	US-10-117-476-6	Sequence 6, App
416	3	27.3	10	12	US-10-177-725-138	Sequence 138, App	489	3	27.3	10	14	US-10-080-378-58	Sequence 58, App
417	3	27.3	10	12	US-10-426-877A-14	Sequence 14, App	490	3	27.3	10	14	US-10-006-395-6	Sequence 6, App
418	3	27.3	10	12	US-09-572-270A-102	Sequence 102, App	491	3	27.3	10	14	US-10-061-395-6	Sequence 6, App
419	3	27.3	10	12	US-09-572-270A-184	Sequence 49, App	492	3	27.3	10	14	US-10-115-695-18	Sequence 18, App
420	3	27.3	10	12	US-09-572-270A-41	Sequence 41, App	493	3	27.3	10	15	US-10-096-339-5	Sequence 5, App
421	3	27.3	10	12	US-09-572-270A-52	Sequence 52, App	494	3	27.3	10	15	US-10-165-015-16	Sequence 16, App
422	3	27.3	10	12	US-09-572-270A-57	Sequence 56, App	495	3	27.3	10	15	US-10-108-795-13	Sequence 13, App
423	3	27.3	10	12	US-09-572-270A-59	Sequence 60, App	496	3	27.3	10	15	US-10-116-561-18	Sequence 18, App
424	3	27.3	10	12	US-09-572-270A-14	Sequence 64, App	497	3	27.3	10	15	US-10-012-542-405	Sequence 405, App
425	3	27.3	10	12	US-09-572-270A-74	Sequence 68, App	498	3	27.3	10	15	US-10-115-671-18	Sequence 18, App
426	3	27.3	10	12	US-09-572-270A-74	Sequence 72, App	499	3	27.3	10	15	US-10-194-155-3	Sequence 3, App
427	3	27.3	10	12	US-09-572-270A-74	Sequence 89, App	500	3	27.3	10	15	US-10-043-487-495	Sequence 495, App
428	3	27.3	10	12	US-09-572-270A-74	Sequence 97, App							
429	3	27.3	10	12	US-09-572-270A-74	Sequence 99, App							
430	3	27.3	10	12	US-09-572-270A-74	Sequence 318, App							
431	3	27.3	10	12	US-09-572-270A-74	Sequence 420, App							
432	3	27.3	10	12	US-09-572-270A-74	Sequence 428, App							
433	3	27.3	10	12	US-09-572-270A-74	Sequence 438, App							
434	3	27.3	10	12	US-09-572-270A-74	Sequence 441, App							
435	3	27.3	10	12	US-09-572-270A-74	Sequence 443, App							
436	3	27.3	10	12	US-09-572-270A-74	Sequence 445, App							
437	3	27.3	10	12	US-09-572-270A-74	Sequence 447, App							
438	3	27.3	10	12	US-09-572-270A-74	Sequence 449, App							
439	3	27.3	10	12	US-09-572-270A-74	Sequence 451, App							
440	3	27.3	10	12	US-09-572-270A-74	Sequence 453, App							
441	3	27.3	10	12	US-09-572-270A-74	Sequence 455, App							
442	3	27.3	10	12	US-10-133-973-33	Sequence 33, App							
443	3	27.3	10	12	US-10-169-423-24	Sequence 44, App							
444	3	27.3	10	12	US-10-295-73-1	Sequence 2, App							
445	3	27.3	10	12	US-09-793-11-124	Sequence 570, App							
446	3	27.3	10	12	US-09-793-11-124	Sequence 576, App							
447	3	27.3	10	12	US-09-793-11-124	Sequence 578, App							
448	3	27.3	10	12	US-09-793-11-124	Sequence 580, App							
449	3	27.3	10	12	US-09-793-11-124	Sequence 582, App							
450	3	27.3	10	12	US-09-793-11-124	Sequence 584, App							
451	3	27.3	10	12	US-09-793-11-124	Sequence 586, App							
452	3	27.3	10	12	US-09-793-11-124	Sequence 588, App							
453	3	27.3	10	12	US-09-793-11-124	Sequence 590, App							
454	3	27.3	10	12	US-09-793-11-124	Sequence 592, App							
455	3	27.3	10	12	US-09-793-11-124	Sequence 594, App							
456	3	27.3	10	12	US-09-793-11-124	Sequence 596, App							
457	3	27.3	10	12	US-09-793-11-124	Sequence 598, App							

ALIGNMENTS

RESULT: 1

US-09-876-904A-215

1 Sequence 215, Application: US/09876904A

2 Publication No. US20030072794A2

3 GENERAL INFORMATION:

4 APPLICANT: BELLKAS, INC.

5 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/LIPOGENIC PEPTIDE

6 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOE COMPLEXES

7 FILE REFERENCE: IB-2002.00

8 CURRENT APPLICATION NUMBER: US/09/876,904A

9 CURRENT FILING DATE: 2001 06 08

10 PRIOR APPLICATION NUMBER: US 60/210,925

11 PRIOR FILING DATE: 2000 06 09

12 NUMBER OF SEQ ID NOS: 529

13 SOFTWARE: Patent In. Ver. 2.1

14 SEQ ID NO: 215

15 TYPE: CDS

16 ORGANISM: Homo sapiens

17 US 09-876-904A-215

```

Query Match      45.5%: Score 5; DB 11; Length 8;
Best Local Similarity 100.0%: Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RORKE 9
DB 9 RORKE 13

RESULT 2
US-09-876-904A-426
; Sequence 426; Application US/09/876-904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BULLIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002-00
; CURRENT APPLICATION NUMBER: US/09/876-904A
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 426
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TFE3 binds to both enhancers.
US-09-876-904A-426

Query Match      36.4%: Score 4; DB 11; Length 8;
Best Local Similarity 100.0%: Pred. No. 5+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKER 6
DB 2 KKER 5

RESULT 3
US-09-876-904A-428
; Sequence 428; Application US/09/876-904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BULLIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002-00
; CURRENT APPLICATION NUMBER: US/09/876-904A
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 428
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TFE3 (536 aa).
US-09-876-904A-428

Query Match      36.4%: Score 4; DB 11; Length 8;
Best Local Similarity 100.0%: Pred. No. 5+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKER 6
DB 1 KKER 5

RESULT 4
US-09-876-904A-439
; Sequence 439; Application US/09/876-904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BULLIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002-00
; CURRENT APPLICATION NUMBER: US/09/876-904A
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 439
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Yeast NFI1 transcription protein factor (1359 aa)
US-09-876-904A-439

Query Match      36.4%: Score 4; DB 11; Length 8;
Best Local Similarity 100.0%: Pred. No. 5+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKER 4
DB 4 KKER 7

RESULT 5
US-09-922-226-84
; Sequence 84; Application US/09/922-226
; Publication No. US2003037764A1
; GENERAL INFORMATION:
; APPLICANT: Zhao, YJ
; APPLICANT: Thatcher, Scott M.
; APPLICANT: Xiao, Jia-Bao
; APPLICANT: Kusari, Jyotirmoy
; APPLICANT: Chandraharan, Roshantha A.
; TITLE OF INVENTION: Methods of Screening For Compounds That
; TITLE OF INVENTION: Modulate Hormone Receptor Activity
; FILE REFERENCE: P-AR 4681
; CURRENT APPLICATION NUMBER: US/09/922-226
; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/284,797
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 10
; TYPE: PRI
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-922-226-84

Query Match      36.4%: Score 4; DB 11; Length 10;
Best Local Similarity 100.0%: Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKER 10
DB 4 KKER 7

```



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RESULT 5
US-09-879-946-10
: Sequence 10, Application US/09879936
: Patent No. US20020045564A1
: GENERAL INFORMATION:
: TITLE OF INVENTION: METHODS OF MODULATING MUSCLE CONTRACTION
: APPLICANT: Van Eyk, Jennifer E.
: APPLICANT: Mak, Alan S.
: APPLICANT: Cote, Graham P.
: FILE REFERENCE: 1997-021-030S
: CURRENT APPLICATION NUMBER: US/09/879,936
: PRIOR FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: 60/050,478
: PRIOR FILING DATE: 1997-06-23
: PRIOR APPLICATION NUMBER: 60/089,505
: PRIOR FILING DATE: 1998-06-16
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 10
: LENGTH: 11
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: NAME/KEY: PEPTIDE
: LOCATION: (1)...(11)
: OTHER INFORMATION: Residues 423 to 433 of chickenizzard caldesmon.
: NAME/KEY: PEPTIDE
: LOCATION: (11)
: OTHER INFORMATION: Targeted Ser phospho-amino acid
: US-09-879-936-10

Query Match          36.4%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKKE 4
DB      1111
       7 AKKE 10

RESULT 7
US-10-304-443-118
: Sequence 118, Application US/10304443
: Publication No. US20030170229A1
: GENERAL INFORMATION:
: APPLICANT: Smithkline Beecham Pharmaceuticals S.A.
: APPLICANT: Peptide Therapeutics Ltd.
: TITLE OF INVENTION: Vaccine
: FILE REFERENCE: B45173CIP
: CURRENT APPLICATION NUMBER: US/10/304,443
: CURRENT FILING DATE: 2002-11-25
: PRIOR APPLICATION NUMBER: US/09/698,976A
: PRIOR FILING DATE: 2001-02-20
: NUMBER OF SEQ ID NOS: 121
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 118
: LENGTH: 11
: TYPE: PRT
: ORGANISM: Human peptide sequence
: US-10-304-443-118

Query Match          36.4%; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 EKQR 7
DB      1111
       2 EKQR 5

RESULT 8
US-09-876-904A-285
: Sequence 285, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, IENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOsome COMPLEXES
: FILE REFERENCE: FR 2402,00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 285
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
: US-09-876-904A-285

Query Match          36.4%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KQRK 8
DB      1111
       1 KQRK 4

RESULT 9
US-09-746-170-33
: Sequence 33, Application US/09746170
: Patent No. US20020127543A1
: GENERAL INFORMATION:
: APPLICANT: Kato, Jonathan
: APPLICANT: Walker, Stephen
: TITLE OF INVENTION: Methods
: FILE REFERENCE: 22623/1280
: CURRENT APPLICATION NUMBER: US/09/746,170
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/171,804
: PRIOR FILING DATE: 1999-12-22
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: Patent In version 3.0
: SEQ ID NO 33
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Hepatitis C virus
: US-09-746-170-33

Query Match          36.4%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KQRK 6
DB      1111
       4 KQRK 7

RESULT 10
US-09-820-053A-88
: Sequence 88, Application US/09820053A
: Publication No. US20030083243A1
: GENERAL INFORMATION:
: APPLICANT: Owen, Donald R.
: TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
: FILE REFERENCE: HELX027
: CURRENT APPLICATION NUMBER: US/09/820,053A
: CURRENT FILING DATE: 2001-03-28
: NUMBER OF SEQ ID NOS: 165
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 88
: LENGTH: 13
: TYPE: PRT
```

```

: ORGANISM: ARTIFICIAL SEQUENCE
: FEATURE:
: OTHER INFORMATION: SYNTHETIC SEQUENCE
: NAME/KEY: MOD_RES
: LOCATION: (13)
: OTHER INFORMATION: AMIDATION
US 09-820-053A-88

Query Match          36.4%; Score 4; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKE 4
DB 9 AKKE 12

RESULT 11
US-10-304-443-113
: Sequence 113, Application US/12304443
: Publication No. US20030170229A1
: GENERAL INFORMATION:
: APPLICANT: SmithKline Beecham Biologicals S.A.
: TITLE OF INVENTION: Vaccine
: FILE REFERENCE: R45173C1P
: CURRENT APPLICATION NUMBER: US/10/304,443
: PRIOR FILING DATE: 2002-11-26
: PRIOR APPLICATION NUMBER: US/95/698,906A
: PRIOR FILING DATE: 2001-02-20
: NUMBER OF SEQ ID NOS: 121
: SOFTWARE: FastSeq for Windows Version: 4.0
: SEQ ID NO 113
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Human peptide sequence
US-10-304-443-113

Query Match          36.4%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EROR 7
DB 3 EROR 6

RESULT 12
US-10-109-171-88
: Sequence 68, Application US/10159171
: Publication No. US20030109452A1
: GENERAL INFORMATION:
: APPLICANT: Owen, Donald R.
: TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
: FILE REFERENCE: HELX028
: CURRENT APPLICATION NUMBER: US/10/109,171
: CURRENT FILING DATE: 2002-03-28
: NUMBER OF SEQ ID NOS: 165
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 88
: LENGTH: 13
: TYPE: PRT
: ORGANISM: ARTIFICIAL SEQUENCE
: FEATURE:
: OTHER INFORMATION: SYNTHETIC SEQUENCE
: NAME/KEY: MOD_RES
: LOCATION: (13)
: OTHER INFORMATION: AMIDATION
US 10-109-171-88

Query Match          36.4%; Score 4; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKE 4
DB 9 AKKE 12

RESULT 13
US-09-900-147-14
: Sequence 14, Application US/09900147
: Patent No. US20020103121A1
: GENERAL INFORMATION:
: APPLICANT: La Thangue, Nicholas B
: APPLICANT: Bandaru, Laxantha R
: TITLE OF INVENTION: Peptide antagonists of DP transcription factors
: FILE REFERENCE: 620-67
: CURRENT APPLICATION NUMBER: US/09/900,147
: PRIOR FILING DATE: 2001-07-09
: PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-05-27
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7
: PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 14
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-900-147-14

Query Match          36.4%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EROR 7
DB 3 EROR 6

RESULT 14
US-09-894-018-203
: Sequence 203, Application US/09894018
: Patent No. US20020119127A1
: GENERAL INFORMATION:
: APPLICANT: EPIMUNE, Inc.
: APPLICANT: Settle, Alessandro
: APPLICANT: Chestnut, Robert
: APPLICANT: Livingston, Brian
: APPLICANT: Baker, Dennis
: APPLICANT: Newman, Mark
: APPLICANT: Brown, David
: TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
: TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
: FILE REFERENCE: 39963-20033.00
: CURRENT APPLICATION NUMBER: US/09/894,018
: CURRENT FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: PCT/US00/35568
: PRIOR FILING DATE: 2000-12-28
: PRIOR APPLICATION NUMBER: US 60/173,390
: PRIOR FILING DATE: 1999-12-28
: PRIOR APPLICATION NUMBER: US 60/284,221
: PRIOR FILING DATE: 2001-04-16
: NUMBER OF SEQ ID NOS: 368
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 203
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Transgenic mouse
US-09-894-018-203

Query Match          36.4%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
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Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 RQR 8
DB 5 RQR 9

RESULT 15
US-08-841-310-14
: Sequence 15, Application US/0941310
: Publication No. US2002026035A1
: GENERAL INFORMATION:
: APPLICANT: Kleantous, Harold et al
: TITLE OF INVENTION: Helicobacter GABA_A R₁ and
: TITLE OF INVENTION: GABA_A 750 Polypeptides and Corresponding Polypeptides
: NUMBER OF SEQUENCES: 18
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Clark & Elbing LLP
: STREET: 176 Federal Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02110
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/841,310
: FILING DATE: 01-APR-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,175
: REFERENCE/DOCKET NUMBER: 66142/67001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-428-0200
: TELEFAX: 617-428-7045
: TELEX:
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Peptide
US-08-841-310-14

Query Match 27.4% Score 4: DB 9: Length 4:
Best Local Similarity 100.0% Pred. No. 5e-05:
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKK 3
DB 3 AKK 5

RESULT 16
US-09-813-653-5
: Sequence 5, Application US/0981653
: Patent No. US20020064770A1
: GENERAL INFORMATION:
: APPLICANT: Nestor, John
: APPLICANT: Wilson, Carol
: APPLICANT: See, Raymond
: APPLICANT: Ian Hehir, Christina
: TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
: FILE REFERENCE: CNS-005
: CURRENT APPLICATION NUMBER: US/09/813,653
: CURRENT FILING DATE: 2001-03-20
: PRIOR APPLICATION NUMBER: US 60/190,946
: PRIOR FILING DATE: 2000-03-21

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 RQR 8
DB 5 RQR 9

RESULT 17
US-09-875-519A-34
: Sequence 34, Application US/09875519A
: Patent No. US20020068059A1
: GENERAL INFORMATION:
: APPLICANT: Parries, Timothy C.
: APPLICANT: Harrison, Richard A.
: TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
: FILE REFERENCE: 4-30443/A/IMU/PC1
: CURRENT APPLICATION NUMBER: US/09/875,519A
: CURRENT FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: PC1/CB97/00603
: PRIOR FILING DATE: 1997-03-04
: NUMBER OF SEQ ID NOS: 35
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 34
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: replacement
: OTHER INFORMATION: sequence
US-09-875-519A-34

Query Match 27.4% Score 3: DB 9: Length 8:
Best Local Similarity 100.0% Pred. No. 5e-05:
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 RQR 7
DB 4 RQR 6

RESULT 18
US-09-792-480-9
: Sequence 9, Application US/09792480
: Patent No. US20020127198A1
: GENERAL INFORMATION:
: APPLICANT: Rothbard, Jonathan B.
: APPLICANT: Wender, Paul A.
: APPLICANT: McGrane, P. Leo
: APPLICANT: Sista, Lalitha V.S.
: APPLICANT: Kirschberg, Thorsten A.
: APPLICANT: CellGate, Inc.
: TITLE OF INVENTION: Compositions and Methods for Enhancing Drug Delivery
: FILE REFERENCE: 019801-0002300S
: CURRENT APPLICATION NUMBER: US/09/792,480
: CURRENT FILING DATE: 2001-02-23
: PRIOR APPLICATION NUMBER: US 09/648,400

1 PRIOR FILING DATE: 2000-08-24
2 PRIOR APPLICATION NUMBER: US 60/150,510
3 PRIOR FILING DATE: 1999-08-24
4 NUMBER OF SEQ ID NOS: 57
5 SOFTWARE: PatentIn Ver. 2.1
6 SEQ ID NO 9
7 LENGTH: 8
8 TYPE: PRT
9 ORGANISM: Artificial Sequence
10 FEATURE:
11 OTHER INFORMATION: Description of Artificial Sequence: Tat-49-56
12 OTHER INFORMATION: truncated analog of HIV-1 tat protein basic region
13 OTHER INFORMATION: Tat-49-57
14 NAME/KEY: MOD_RES
15 LOCATION: (1)
16 OTHER INFORMATION: Xaa = fluorosulfon linked to amino group of
17 OTHER INFORMATION: aminohexanoic acid (F1 aux) attached to the
18 OTHER INFORMATION: N-terminal amino group of Arg
19 US-09-792-480-9

Query Match 27.4% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RGR 7
111
10 5 RGR 7

RESULT 19
US-09-792-480-11
1 Sequence 11: Application US/09792480
2 Patent No. US20020127198A1
3 GENERAL INFORMATION:
4 APPLICANT: Rothbard, Jonathan B.
5 APPLICANT: Wendel, Paul A.
6 APPLICANT: McGrane, P. Leo
7 APPLICANT: Sista, Lalitha V.S.
8 APPLICANT: Kirschberg, Thorsten A.
9 APPLICANT: Celigate, Inc.
10 TITLE OF INVENTION: Compositions and Methods for Enhanced Gene Delivery
11 FILE REFERENCE: 019801-000230US
12 CURRENT APPLICATION NUMBER: US/09/792-480
13 CURRENT FILING DATE: 2001-02-23
14 PRIOR APPLICATION NUMBER: US 09/548,420
15 PRIOR FILING DATE: 2000-08-24
16 PRIOR APPLICATION NUMBER: US 60/150,510
17 PRIOR FILING DATE: 1999-08-24
18 NUMBER OF SEQ ID NOS: 57
19 SOFTWARE: PatentIn Ver. 2.1
20 SEQ ID NO 11
21 LENGTH: 8
22 TYPE: PRT
23 ORGANISM: Artificial Sequence
24 FEATURE:
25 OTHER INFORMATION: Description of Artificial Sequence: tat-49-57
26 OTHER INFORMATION: truncated analog of HIV-1 tat protein basic region
27 NAME/KEY: MOD_RES
28 LOCATION: (1)
29 OTHER INFORMATION: Xaa = fluorosulfon linked to amino group of
30 OTHER INFORMATION: aminohexanoic acid (F1 aux) attached to the
31 OTHER INFORMATION: N-terminal amino group of Lys
32 US-09-792-480-11

Query Match 27.4% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RGR 7
111
10 4 RGR 6

RESULT 20
US-09-813-448-2
1 Sequence 2: Application US/09813448
2 Patent No. US20020142346A1
3 GENERAL INFORMATION:
4 APPLICANT: Nestor, John
5 APPLICANT: Wilcox, Carol
6 TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compoun
7 FILE REFERENCE: CNS-006
8 CURRENT APPLICATION NUMBER: US/09/813,448
9 CURRENT FILING DATE: 2001-03-20
10 PRIOR APPLICATION NUMBER: US 60/190,946
11 PRIOR FILING DATE: 2000-03-21
12 PRIOR APPLICATION NUMBER: US 60/190,996
13 PRIOR FILING DATE: 2000-03-21
14 PRIOR APPLICATION NUMBER: US 60/191,299
15 PRIOR FILING DATE: 2000-03-21
16 NUMBER OF SEQ ID NOS: 8
17 SOFTWARE: PatentIn version 3.0
18 SEQ ID NO 2
19 LENGTH: 8
20 TYPE: PRT
21 ORGANISM: Artificial Sequence
22 FEATURE:
23 OTHER INFORMATION: preferred amino acids for PDZ binding domain
24 US-09-813-448-2

Query Match 27.4% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
111
10 3 KKE 5

RESULT 21
US-09-943-123-19
1 Sequence 19: Application US/09943123
2 Publication No. US20020182701A1
3 GENERAL INFORMATION:
4 APPLICANT: CHANG, Y-H
5 APPLICANT: VETRO, J.A.
6 APPLICANT: MICKA, W.S.
7 TITLE OF INVENTION: Dominant Negative Variants of Methionine Aminopeptidase
8 FILE REFERENCE: 16153-9007
9 CURRENT APPLICATION NUMBER: US/09/943,123
10 CURRENT FILING DATE: 2001-08-30
11 NUMBER OF SEQ ID NOS: 26
12 SOFTWARE: PatentIn Ver. 2.0
13 SEQ ID NO 19
14 LENGTH: 8
15 TYPE: PRT
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 OTHER INFORMATION: Description of Artificial Sequence: synthetic
19 OTHER INFORMATION: transit peptide
20 US-09-943-123-19

Query Match 27.4% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RGR 7
111
10 5 RGR 6

RESULT 22
US-09-727-416-03

Sequence 67, Application: US/9726470A
 Publication No. US20030036628A1
 GENERAL INFORMATION:
 APPLICANT: Zheleva, Daniela J
 APPLICANT: Fischer, Peter M
 APPLICANT: McIntosh, Campbell
 APPLICANT: Andrews, Martin J
 APPLICANT: Chan, Weig C
 APPLICANT: Atkinson, Gail F
 TITLE OF INVENTION: p21 Peptides
 FILE REFERENCE: CCI-014
 CURRENT APPLICATION NUMBER: US/9726470A
 PRIOR FILING DATE: 2000-11-29
 PRIOR APPLICATION NUMBER: GB 96283236
 PRIOR FILING DATE: 1999-11-30
 NUMBER OF SEQ ID NOS: 275
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 67
 LENGTH: 8
 TYPE: PPT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: not derived
 FEATURE:
 OTHER INFORMATION: Synthesised with free amino terminus and as the
 OTHER INFORMATION: C-terminal carboxamide
 US-09-726-470A-67

Query Match 27.4%, Score 31, DB 11, Length 8;
 Best Local Similarity 100.0%, Pred. No. 5e-05;
 Matches 3, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

CY 1 AKK 4
 II
 DB 2 AKK 4

RESULT 24
 US-09-765-555-69
 Sequence 69, Application: US/976555
 Publication No. US20030037459A1
 GENERAL INFORMATION:
 APPLICANT: The Scripps Research Institute
 TITLE OF INVENTION: Methods and compositions to treat
 TITLE OF INVENTION: expression in p21-5
 FILE REFERENCE: 2780-25014-46
 CURRENT APPLICATION NUMBER: US/976555
 PRIOR FILING DATE: 2002-05-24
 PRIOR APPLICATION NUMBER: US 97620499
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: US 67/777,436
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 75
 SOFTWARE: FastSeq for Windows Version 3.1
 SEQ ID NO: 60
 LENGTH: 8
 TYPE: PPT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: ZFP domain
 US-09-765-555-69

Query Match 27.4%, Score 31, DB 11, Length 8;
 Best Local Similarity 100.0%, Pred. No. 5e-05;
 Matches 3, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

CY 7 RKO 9
 II
 DB 2 RKO 4

RESULT 24

US-09-880-748-2779
 Sequence 2779, Application: US/9880748
 Publication No. US2003005997A1
 GENERAL INFORMATION:
 APPLICANT: Rubin et al.
 TITLE OF INVENTION: Antibodies that immunospecifically bind Blys
 FILE REFERENCE: PFS25
 CURRENT APPLICATION NUMBER: US/09/880,748
 CURRENT FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/212,210
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/211,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 NUMBER OF SEQ ID NOS: 3239
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 2779
 LENGTH: 8
 TYPE: PPT
 ORGANISM: Homo sapiens
 US-09-880-748-2779

Query Match 27.4%, Score 31, DB 11, Length 8;
 Best Local Similarity 100.0%, Pred. No. 5e-05;
 Matches 3, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

CY 6 RKK 8
 III
 DB 2 RKK 4

RESULT 25
 US-09-876-904A-317
 Sequence 317, Application: US/9876904A
 Publication No. US20030027994A1
 GENERAL INFORMATION:
 APPLICANT: KODOLIKAS, TONY
 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES IM) AND THERAPEUTIC
 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 FILE REFERENCE: T6 2002-09
 CURRENT APPLICATION NUMBER: US/09/876,904A
 CURRENT FILING DATE: 2001-06-08
 PRIOR APPLICATION NUMBER: US 60/210,925
 PRIOR FILING DATE: 2000-06-09
 NUMBER OF SEQ ID NOS: 629
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 317
 LENGTH: 6
 TYPE: PPT
 ORGANISM: Saccharomyces cerevisiae
 FEATURE:
 OTHER INFORMATION: Recombination repair protein
 US-09-876-904A-317

Query Match 27.4%, Score 31, DB 11, Length 8;
 Best Local Similarity 100.0%, Pred. No. 5e-05;
 Matches 3, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

CY 7 RKO 9
 II
 DB 6 RKO 8

RESULT 24
 US-09-876-904A-352
 Sequence 352, Application: US/9880748
 Publication No. US20030027994A1

GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 352
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Human ATF-1, its basic region/leucine zipper.
US-09-876-904A-352

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
DB 6 KKE 8

RESULT 27
US-09-876-904A-393
Sequence 393, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 393
LENGTH: 8
TYPE: PRT
ORGANISM: Drosophila sp.
FEATURE:
OTHER INFORMATION: Drosophila BDF-2 (related to DREF/ATF)
US-09-876-904A-393

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
DB 6 KKE 8

RESULT 28
US-09-876-904A-394
Sequence 394, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A

CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 394
LENGTH: 8
TYPE: PRT
ORGANISM: Xenopus sp.
FEATURE:
OTHER INFORMATION: Xenopus KAR (retinoic acid receptor)
US-09-876-904A-394

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
DB 6 KKE 8

RESULT 29
US-09-876-904A-493
Sequence 493, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 493
LENGTH: 8
TYPE: PRT
ORGANISM: Rattus sp.
FEATURE:
OTHER INFORMATION: Rat JRP a protein factor that binds to the D site
US-09-876-904A-493

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKE 5
DB 4 KKE 6

RESULT 30
US-09-876-904A-502
Sequence 502, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 502

```

: LENGTH: 8
: TYPE: PRT
: ORGANISM: Mus sp.
: FEATURE:
: OTHER INFORMATION: Mouse ACP/EBP.
US-09-876-904A-502

Query Match      27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
   III
Db 5 AKK 7

RESULT 31
US-09-876-904A-505
: Sequence 505, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 505
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Rattus sp.
: FEATURE:
: OTHER INFORMATION: Rat LAP, a 32-kD liver-enriched transcriptional
: OTHER INFORMATION: activator, also present in lung, with 71% sequence
: OTHER INFORMATION: similarity to C/EBP.
US-09-876-904A-505

Query Match      27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
   III
Db 5 AKK 7

RESULT 32
US-09-876-904A-515
: Sequence 515, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 515
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Rattus sp.
: FEATURE:
: OTHER INFORMATION: Rat IL-60BP interacting with interleukin-6
US-09-876-904A-515

Query Match      27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
   III
Db 5 AKK 7

RESULT 33
US-09-876-904A-516
: Sequence 516, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 516
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Mus sp.
: FEATURE:
: OTHER INFORMATION: Mouse H 2RBP.
US-09-876-904A-516

Query Match      27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQR 7
   III
Db 3 RQR 5

RESULT 34
US-09-876-904A-517
: Sequence 517, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 517
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Gallus sp.
: FEATURE:
: OTHER INFORMATION: Chicken RXR.
US-09-876-904A-517

Query Match      27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 5 QQR 7
DB 3 QQR 5

RESULT 35

US-09-876-904A-518
; Sequence 518, Application US/09876904A
; Publication No. US20030072794A1

GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 518

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Human NF-116 (345 aa)

US-09-876-904A-518

Query Match 27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 5 AKK 7

RESULT 36

US-09-876-904A-537
; Sequence 537, Application US/09876904A
; Publication No. US20030072794A1

GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 537

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Xenopus laevis

; FEATURE:

; OTHER INFORMATION: Xenopus laevis 11 ribosomal protein (homologous to

; OTHER INFORMATION: yeast 12).

US-09-876-904A-537

Query Match 27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 5 AKK 7

RESULT 37

US-09-876-904A-599

; Sequence 599, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

US-09-876-904A-549

; Sequence 549, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 549

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

; FEATURE:

; OTHER INFORMATION: Yeast S10 ribosomal protein (homologous to human

; OTHER INFORMATION: S6).

US-09-876-904A-549

Query Match 27.4%; Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QQR 8

DB 4 QQR 6

RESULT 38

US-09-876-904A-595

; Sequence 595, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 595

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Parachinus angulosus

; FEATURE:

; OTHER INFORMATION: Sea urchin Parachinus angulosus sperm H1 (248 aa).

US-09-876-904A-595

Query Match 27.3%; Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3

DB 3 AKK 5

RESULT 39

US-09-876-904A-599

; Sequence 599, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

1 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
2
3 FILE REFERENCE: TB-2002.00
4
5 CURRENT APPLICATION NUMBER: US/09/876,904A
6
7 PRIOR FILING DATE: 2001-06-08
8
9 PRIOR FILING DATE: 2000-06-04
10
11 NUMBER OF SEQ ID NOS: 629
12
13 SOFTWARE: Patent In Ver. 2.1
14
15 SEQ ID NO 599
16
17 LENGTH: 8
18
19 TYPE: PRT
20
21 ORGANISM: *Parachinus angulosus*
22
23 FEATURE:
24
25 OTHER INFORMATION: Sea urchin *Parachinus angulosus* sperm HI (248 aa)
26
27 US-09 876-904A-599

Query Match 27.3% Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 4
DB 5 AKK 7

RESULT 40
US-10-014-322A-62
1 Sequence 62, Application US/10031422A
2 Publication No. US20030138914A1
3 GENERAL INFORMATION:
4 APPLICANT: Klecanthous, Harold
5 APPLICANT: Lissolo, Ling
6 APPLICANT: Tomb, Jean-Francois
7 APPLICANT: Miller, Charles
8 APPLICANT: Al-Gardawi, Amal
9
10 TITLE OF INVENTION: Helicobacter GHPs 100 and GHPs 750
11
12 FILE REFERENCE: 061327037002
13
14 CURRENT APPLICATION NUMBER: US/10/014,146A
15
16 PRIOR FILING DATE: 2002-12-15
17
18 PRIOR APPLICATION NUMBER: US-08/941,410
19
20 PRIOR FILING DATE: 1997-04-01
21
22 NUMBER OF SEQ ID NOS: 18
23
24 SOFTWARE: FastSeq for Windows Version 4.0
25
26 SEQ ID NO 13
27
28 LENGTH: 8
29
30 TYPE: PRT
31
32 ORGANISM: *Helicobacter pylori*
33
34 US-10-014-322A-62

Query Match 27.3% Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 4
DB 5 AKK 5

RESULT 41
US-10-014-322A-62
1 Sequence 79, Application US/10031422A
2 Publication No. US20030138914A1
3 GENERAL INFORMATION:
4 APPLICANT: Himmelspach, Michael
5 APPLICANT: Pfeleiderer, Michael
6 APPLICANT: Falkner, Falko-Guenther
7 APPLICANT: Eibl, Johann
8 APPLICANT: Dornier, Friedrich
9 APPLICANT: Schlokat, Uwe
10
11 TITLE OF INVENTION: Factor X Deficient Mutants
12 and Analogues Thereof
13
14 US-09 876-904A-599

1 NUMBER OF SEQUENCES: 145
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Townsend and Townsend and Crew LLP
4 STREET: Two Embarcadero Center, Eighth Floor
5 CITY: San Francisco
6 STATE: CA
7 COUNTRY: USA
8 ZIP: 94111-3834
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Diskette
12 COMPUTER: IBM Compatible
13 OPERATING SYSTEM: DOS
14
15 SOFTWARE: FastSeq for Windows Version 2.0
16
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/10/348,504
19 FILING DATE: 29-Jan-2003
20 CLASSIFICATION: <Unknown>
21
22 PRIOR APPLICATION NUMBER:
23 FILING DATE: 10-Nov-99 US/0030138914A1-1999
24 APPLICATION NUMBER: AT A 336/97
25 FILING DATE: 27-FEB-1997
26 APPLICATION NUMBER: WO PCT/AT98/00046
27 FILING DATE: 27-FEB-1998
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Auschelus, Scott L.
30 REGISTRATION NUMBER: 42,271
31 REFERENCE/DOCKET NUMBER: 20695D-0009000US
32
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 415-576-0200
35 TELEFAX: 415-576-0400
36
37 TELEX: <Unknown>
38
39 INFORMATION FOR SEQ ID NO: 78:
40
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 8 amino acids
43 TYPE: amino acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46
47 MOLECULE TYPE: peptide
48
49 SEQUENCE DESCRIPTION: SEQ ID NO: 78:
50 US-10-348-504-78

Query Match 27.3% Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KER 5
DB 2 KER 4

RESULT 42
US-10-014-322A-62
1 Sequence 62, Application US/10031422A
2 Publication No. US20030167129A1
3 GENERAL INFORMATION:
4 APPLICANT: Nestor, Jr., John
5 APPLICANT: Wilson, Carol
6 APPLICANT: Ian Hehir, Christina
7 APPLICANT: Kates, Steven
8 APPLICANT: Krstenansky, John
9
10 TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
11
12 FILE REFERENCE: CNS-008
13
14 CURRENT APPLICATION NUMBER: US/10/014,322A
15
16 CURRENT FILING DATE: 2002-07-08
17
18 PRIOR APPLICATION NUMBER: US 60/243,587
19
20 PRIOR FILING DATE: 2000-10-27
21
22 PRIOR APPLICATION NUMBER: US 09/813,651
23
24 PRIOR FILING DATE: 2001-03-20
25
26 PRIOR APPLICATION NUMBER: US 09/813,653
27
28 PRIOR FILING DATE: 2001-03-20
29
30 PRIOR APPLICATION NUMBER: US 09/813,448
31
32 PRIOR FILING DATE: 2001-03-20

```

: NUMBER OF SEQ ID NOS: 126
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 62
:   LENGTH: 8
:   TYPE: PRI
:   ORGANISM: Artificial sequence
:   FEATURE:
: OTHER INFORMATION: Preferred pep'ide for HIV binding domain
US-10-014-322A-62

Query Match      27.3%: Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KKE 4
DB      1
      3 KKE 5

RESULT 43
US-10-293-580-4;
: Sequence 41, Application US/10293580
: Publication No. US20030170767A1
: GENERAL INFORMATION:
: APPLICANT: Aurora Biosciences Corporation
: APPLICANT: Cubitt, Andrew B.
: TITLE OF INVENTION: Fluorescent protein sensors of post-translational modifications
: FILE REFERENCE: AURO1270 (08306/031301)
: CURRENT APPLICATION NUMBER: US/10/293-580
: PRIOR FILING DATE: 2002-11-12
: PRIOR APPLICATION NUMBER: US/09/129,112
: PRIOR FILING DATE: 1998-07-24
: NUMBER OF SEQ ID NOS: 74
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 41
:   LENGTH: 8
:   TYPE: PRI
:   ORGANISM: Artificial sequence
:   FEATURE:
: OTHER INFORMATION: Adenovirus endopeptidase
US-10-293-580-41

Query Match      27.3%: Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 3
DB      1
      5 AKK 7

RESULT 44
US-10-024-945-19
: Sequence 19, Application US/10024445
: Publication No. US20020142965A2
: GENERAL INFORMATION:
: APPLICANT: Kenneth Walter Ball
: APPLICANT: Ningnan Pan Chen
: APPLICANT: Timothy Michael Ramsey
: APPLICANT: Michael Lloyd Sabio
: APPLICANT: Sushill Kumar Sharma
: TITLE OF INVENTION: Inhibitors of L16 for L177-116
: FILE REFERENCE: 4-31664PI/Prov
: CURRENT APPLICATION NUMBER: US/10/024-945
: CURRENT FILING DATE: 2001-12-19
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: FastSeq for Windows version 4.0
: SEQ ID NO 19
:   LENGTH: 8
:   TYPE: PRI
:   ORGANISM: Artificial sequence
:   FEATURE:
: OTHER INFORMATION:
US-10-024-945-19
```

```

: OTHER INFORMATION: Synthetic protein
US-10-024-945-19

Query Match      27.3%: Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 4
DB      1
      2 AKK 4

RESULT 45
US-10-040-572-8
: Sequence 8, Application US/10040572
: Publication No. US20020155183A1
: GENERAL INFORMATION:
: APPLICANT: Sky High, LLC
: APPLICANT: Bathurst, Ian G.
: APPLICANT: Foster, Matthew
: TITLE OF INVENTION: AQUEOUS ANTI-APOPTOTIC COMPOSITIONS
: FILE REFERENCE: 4147-23-1
: CURRENT APPLICATION NUMBER: US/10/040-572
: CURRENT FILING DATE: 2002-03-12
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 8
:   LENGTH: 8
:   TYPE: PRI
:   ORGANISM: Glycine max
: OTHER INFORMATION:
US-10-040-572-8

Query Match      27.3%: Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KKE 4
DB      1
      4 KKE 5

RESULT 46
US-10-057-505-7
: Sequence 7, Application US/10057505
: Publication No. US20020164674A1
: GENERAL INFORMATION:
: APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
: APPLICANT: AUREA BIOSCIENCES CORPORATION
: APPLICANT: ISEN, Roger
: APPLICANT: HEZM, Roger
: APPLICANT: CURTIS, Andrew
: TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
: FILE REFERENCE: PEGEN260-3
: CURRENT APPLICATION NUMBER: US/10/057-505
: CURRENT FILING DATE: 2002-01-25
: PRIOR APPLICATION NUMBER: US-08/792,553
: PRIOR FILING DATE: 1997-01-31
: PRIOR APPLICATION NUMBER: US-09/196,003
: PRIOR FILING DATE: 1999-09-13
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 7
:   LENGTH: 8
:   TYPE: PRI
:   ORGANISM: Artificial sequence
:   FEATURE:
: OTHER INFORMATION: Linker moiety
US-10-057-505-7

Query Match      27.3%: Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AKK 3
DB 5 AKK 7

RESULT 47

US-10-080-100-9
Sequence 9, Application US/1006100
Publication No. US20020165356A1
GENERAL INFORMATION:
APPLICANT: Paribas, Carlos
TITLE OF INVENTION: Zinc Finger Binding Domains
FILE REFERENCE: TSRI 760.0
CURRENT APPLICATION NUMBER: US/10/060-100
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US/09/791-106
NUMBER OF SEQ ID NOS: 113
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthesized
US-10-080-100-5

Query Match 27.3%; Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKK 5
DB 3 KKK 5

RESULT 48

US-10-061-395-65
Sequence 20, Application US/10061395
Publication No. US20020165356A1
GENERAL INFORMATION:
APPLICANT: Paribas, Carlos
TITLE OF INVENTION: Zinc Finger Binding Domains
FILE REFERENCE: TSRI 760.0
CURRENT APPLICATION NUMBER: US/10/061-395
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US/09/791-106
NUMBER OF SEQ ID NOS: 113
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthesized
US-10-061-395-65

Query Match 27.3%; Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKK 9
DB 2 KKK 4

RESULT 49

US-10-014-485A-48

Sequence 48, Application US/1001485A
Publication No. US20020166684A1
GENERAL INFORMATION:
APPLICANT: Cell Signaling Technology, Inc.
APPLICANT: ZHANG, Hui
APPLICANT: ZHANG, Yi
TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES
FILE REFERENCE: US/10/014-485A
CURRENT APPLICATION NUMBER: US/10/014-485A
PRIOR FILING DATE: 2002-03-16
PRIOR APPLICATION NUMBER: US 09/148,712
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: US 09/545,364
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patent In version 4.1
SEQ ID NO 48
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)...(6)
OTHER INFORMATION: PHOSPHORYLATION: serine at position 6 is phosphorylated
US-10-014-485A-48

Query Match 27.3%; Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKK 7
DB 3 KKK 3

RESULT 50

US-10-061-395-65
Sequence 65, Application US/10061395
Publication No. US20020166684A1
GENERAL INFORMATION:
APPLICANT: Zardner, Maurice
APPLICANT: Smith, Ernest S.
TITLE OF INVENTION: Methods of Identifying Regulator Molecules
FILE REFERENCE: 1821.0080004
CURRENT APPLICATION NUMBER: US/10/061.395
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/271,423
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 65/265,440
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 65/265,589
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patent In version 4.1
SEQ ID NO 65
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Myristoylation signal sequence from cAMP-dependent kinase
US-10-061-395-65

Query Match 27.3%; Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 5 AKK 8

Search completed: September 30, 2003, 10:32:51
Job time : 25.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode.

Run on: September 30, 2003, 10:07:04 : Search time: 41.0844 Seconds
(without alignment)

Title: US-09-787-443-2
Perfect score: 11
Sequence: AKKERQRKDTQ 11

Scoring table: OLICO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 15672613 residues

Word size : 0

Total number of hits satisfying chosen parameters: 274822

Minimum DB seq length: 8
Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

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- 3: /SIDSI/qcgdata/geneseq/qnosesq_emb1/AA1942.DAT:
- 4: /SIDSI/qcgdata/geneseq/qnosesq_emb1/AA1943.DAT:
- 5: /SIDSI/qcgdata/geneseq/qnosesq_emb1/AA1944.DAT:
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Proj. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	21	NCAM Igl binding p
2	11	100.0	11	21	NCAM Igl binding p
3	11	100.0	11	23	Human neural cell
4	5	45.5	9	24	HLA protein 121P2A
5	5	45.5	9	24	HLA protein 121P2A
6	5	45.5	9	24	HLA protein 121P2A
7	5	45.5	9	24	HLA protein 121P2A
8	5	45.5	9	24	HLA protein 121P2A
9	5	45.5	9	24	HLA protein 121P2A

10	5	45.5	9	24	ABP84044	HLA protein 121P2A
11	5	45.5	9	24	ABP84046	HLA protein 121P2A
12	5	45.5	9	24	ABP84047	HLA protein 121P2A
13	5	45.5	9	24	ABP84051	HLA protein 121P2A
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15	5	45.5	9	24	ABP84341	HLA protein 121P2A
16	5	45.5	9	24	ABP84343	HLA protein 121P2A
17	5	45.5	9	24	ABP84346	HLA protein 121P2A
18	5	45.5	9	24	ABP84348	HLA protein 121P2A
19	5	45.5	9	24	ABP84628	HLA protein 121P2A
20	5	45.5	9	24	ABP84630	HLA protein 121P2A
21	5	45.5	9	24	ABP84631	HLA protein 121P2A
22	5	45.5	9	24	ABP84635	HLA protein 121P2A
23	5	45.5	9	24	ABP84636	HLA protein 121P2A
24	5	45.5	9	24	ABP84925	HLA protein 121P2A
25	5	45.5	9	24	ABP84926	HLA protein 121P2A
26	5	45.5	9	24	ABP84929	HLA protein 121P2A
27	5	45.5	9	24	ABP84931	HLA protein 121P2A
28	5	45.5	9	24	ABP84932	HLA protein 121P2A
29	5	45.5	9	24	ABP85222	HLA protein 121P2A
30	5	45.5	9	24	ABP85223	HLA protein 121P2A
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33	5	45.5	9	24	ABP85230	HLA protein 121P2A
34	5	45.5	9	24	ABP85519	HLA protein 121P2A
35	5	45.5	9	24	ABP85520	HLA protein 121P2A
36	5	45.5	9	24	ABP85523	HLA protein 121P2A
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38	5	45.5	9	24	ABP85527	HLA protein 121P2A
39	5	45.5	9	24	ABP86092	HLA protein 121P2A
40	5	45.5	9	24	ABP86093	HLA protein 121P2A
41	5	45.5	9	24	ABP86094	HLA protein 121P2A
42	5	45.5	9	24	ABP86096	HLA protein 121P2A
43	5	45.5	9	24	ABP86098	HLA protein 121P2A
44	5	45.5	9	24	ABP86576	HLA protein 121P2A
45	5	45.5	9	24	ABP86577	HLA protein 121P2A
46	5	45.5	9	24	ABP86580	HLA protein 121P2A
47	5	45.5	9	24	ABP86581	HLA protein 121P2A
48	5	45.5	9	24	ABP87064	HLA protein 121P2A
49	5	45.5	9	24	ABP87065	HLA protein 121P2A
50	5	45.5	9	24	ABP87067	HLA protein 121P2A
51	5	45.5	9	24	ABP87069	HLA protein 121P2A
52	5	45.5	9	24	ABP87072	HLA protein 121P2A
53	5	45.5	9	24	ABP87552	HLA protein 121P2A
54	5	45.5	9	24	ABP87554	HLA protein 121P2A
55	5	45.5	9	24	ABP87555	HLA protein 121P2A
56	5	45.5	9	24	ABP87556	HLA protein 121P2A
57	5	45.5	9	24	ABP87557	HLA protein 121P2A
58	5	45.5	9	24	ABP87999	HLA protein 121P2A
59	5	45.5	9	24	ABP88000	HLA protein 121P2A
60	5	45.5	9	24	ABP88003	HLA protein 121P2A
61	5	45.5	9	24	ABP88004	HLA protein 121P2A
62	5	45.5	9	24	ABP88006	HLA protein 121P2A
63	5	45.5	9	24	ABP88440	HLA protein 121P2A
64	5	45.5	9	24	ABP88441	HLA protein 121P2A
65	5	45.5	9	24	ABP88442	HLA protein 121P2A
66	5	45.5	9	24	ABP88892	HLA protein 121P2A
67	5	45.5	9	24	ABP88893	HLA protein 121P2A
68	5	45.5	9	24	ABP88895	HLA protein 121P2A
69	5	45.5	9	24	ABP88897	HLA protein 121P2A
70	5	45.5	9	24	ABP88898	HLA protein 121P2A
71	5	45.5	9	24	ABP89388	HLA protein 121P2A
72	5	45.5	9	24	ABP89390	HLA protein 121P2A
73	5	45.5	9	24	ABP89391	HLA protein 121P2A
74	5	45.5	9	24	ABP89392	HLA protein 121P2A
75	5	45.5	9	24	ABP89394	HLA protein 121P2A
76	5	45.5	9	24	ABP89820	HLA protein 121P2A
77	5	45.5	9	24	ABP89821	HLA protein 121P2A
78	5	45.5	9	24	ABP89823	HLA protein 121P2A
79	5	45.5	9	24	ABP89825	HLA protein 121P2A
80	5	45.5	9	24	ABP89826	HLA protein 121P2A
81	5	45.5	9	24	ABP89826	HLA protein 121P2A
82	5	45.5	9	24	ABP89826	HLA protein 121P2A

83	5	45.5	9	24	ABP42365	HLA protein 121P2A	156	5	45.5	15	24	ABP94131	HLA protein 121P2A
84	5	45.5	9	24	ABP53306	HLA protein 121P2A	157	5	45.5	15	24	ABP94132	HLA protein 121P2A
85	5	45.5	9	24	ABP94308	HLA protein 121P2A	158	5	45.5	15	24	ABP94133	HLA protein 121P2A
86	5	45.5	9	24	ABP40309	HLA protein 121P2A	159	5	45.5	15	24	ABP94134	HLA protein 121P2A
87	5	45.5	9	24	ABP94310	HLA protein 121P2A	160	5	45.5	15	24	ABP94135	HLA protein 121P2A
88	5	45.5	10	24	ABP43891	HLA protein 121P2A	161	5	45.5	15	24	ABP94137	HLA protein 121P2A
89	5	45.5	10	24	ABP43892	HLA protein 121P2A	162	5	45.5	15	24	ABP94138	HLA protein 121P2A
90	5	45.5	10	24	ABP43893	HLA protein 121P2A	163	5	45.5	15	24	ABP94140	HLA protein 121P2A
91	5	45.5	10	24	ABP43894	HLA protein 121P2A	164	5	45.5	15	24	ABP94142	HLA protein 121P2A
92	5	45.5	10	24	ABP43900	HLA protein 121P2A	165	5	45.5	15	24	ABP94143	HLA protein 121P2A
93	5	45.5	10	24	ABP43901	HLA protein 121P2A	166	5	45.5	15	24	ABP94144	HLA protein 121P2A
94	5	45.5	10	24	ABP43908	HLA protein 121P2A	167	5	45.5	15	24	ABP94639	HLA protein 121P2A
95	5	45.5	10	24	ABP44190	HLA protein 121P2A	168	5	45.5	15	24	ABP94641	HLA protein 121P2A
96	5	45.5	10	24	ABP44191	HLA protein 121P2A	169	5	45.5	15	24	ABP94642	HLA protein 121P2A
97	5	45.5	10	24	ABP44194	HLA protein 121P2A	170	5	45.5	15	24	ABP94645	HLA protein 121P2A
98	5	45.5	10	24	ABP44198	HLA protein 121P2A	171	5	45.5	15	24	ABP94646	HLA protein 121P2A
99	5	45.5	10	24	ABP44199	HLA protein 121P2A	172	5	45.5	15	24	ABP94647	HLA protein 121P2A
100	5	45.5	10	24	ABP44471	HLA protein 121P2A	173	5	45.5	15	24	ABP94648	HLA protein 121P2A
101	5	45.5	10	24	ABP44472	HLA protein 121P2A	174	5	45.5	15	24	ABP94649	HLA protein 121P2A
102	5	45.5	10	24	ABP44473	HLA protein 121P2A	175	5	45.5	15	24	ABP94650	HLA protein 121P2A
103	5	45.5	10	24	ABP44481	HLA protein 121P2A	176	5	45.5	15	24	ABP94652	HLA protein 121P2A
104	5	45.5	10	24	ABP44482	HLA protein 121P2A	177	5	45.5	15	24	ABP95141	HLA protein 121P2A
105	5	45.5	10	24	ABP44486	HLA protein 121P2A	178	5	45.5	15	24	ABP95142	HLA protein 121P2A
106	5	45.5	10	24	ABP44774	HLA protein 121P2A	179	5	45.5	15	24	ABP95143	HLA protein 121P2A
107	5	45.5	10	24	ABP44775	HLA protein 121P2A	180	5	45.5	15	24	ABP95147	HLA protein 121P2A
108	5	45.5	10	24	ABP44777	HLA protein 121P2A	181	5	45.5	15	24	ABP95148	HLA protein 121P2A
109	5	45.5	10	24	ABP44779	HLA protein 121P2A	182	5	45.5	15	24	ABP95149	HLA protein 121P2A
110	5	45.5	10	24	ABP44779	HLA protein 121P2A	183	5	45.5	15	24	ABP95150	HLA protein 121P2A
111	5	45.5	10	24	ABP44782	HLA protein 121P2A	184	5	45.5	15	24	ABP95151	HLA protein 121P2A
112	5	45.5	10	24	ABP45070	HLA protein 121P2A	185	5	45.5	15	24	ABP95152	HLA protein 121P2A
113	5	45.5	10	24	ABP45071	HLA protein 121P2A	186	5	45.5	15	24	ABP95153	HLA protein 121P2A
114	5	45.5	10	24	ABP45073	HLA protein 121P2A	187	5	45.5	15	24	ABP95154	HLA protein 121P2A
115	5	45.5	10	24	ABP45078	HLA protein 121P2A	188	5	45.5	15	24	ABP95568	HLA protein 121P2A
116	5	45.5	10	24	ABP45079	HLA protein 121P2A	189	5	45.5	15	24	ABP95570	HLA protein 121P2A
117	5	45.5	10	24	ABP45080	HLA protein 121P2A	190	5	45.5	15	24	ABP95572	HLA protein 121P2A
118	5	45.5	10	24	ABP45087	HLA protein 121P2A	191	5	45.5	15	24	ABP95573	HLA protein 121P2A
119	5	45.5	10	24	ABP45369	HLA protein 121P2A	192	5	45.5	15	24	ABP95574	HLA protein 121P2A
120	5	45.5	10	24	ABP45370	HLA protein 121P2A	193	5	45.5	15	24	ABP95575	HLA protein 121P2A
121	5	45.5	10	24	ABP45374	HLA protein 121P2A	194	5	45.5	15	24	ABP95576	HLA protein 121P2A
122	5	45.5	10	24	ABP45375	HLA protein 121P2A	195	5	45.5	15	24	ABP95578	HLA protein 121P2A
123	5	45.5	10	24	ABP45376	HLA protein 121P2A	196	5	45.5	15	24	ABP95579	HLA protein 121P2A
124	5	45.5	10	24	ABP45664	HLA protein 121P2A	197	5	45.5	15	24	ABP95580	HLA protein 121P2A
125	5	45.5	10	24	ABP45664	HLA protein 121P2A	198	4	36.4	8	16	AAK73354	Human TSH receptor
126	5	45.5	10	24	ABP45667	HLA protein 121P2A	199	4	36.4	8	16	AAK73355	Human TSH receptor
127	5	45.5	10	24	ABP45671	HLA protein 121P2A	200	4	36.4	8	22	ABP14230	HIV A02 super moti
128	5	45.5	10	24	ABP45672	HLA protein 121P2A	201	4	36.4	8	22	ABP14231	HIV A02 super moti
129	5	45.5	10	24	ABP45672	HLA protein 121P2A	202	4	36.4	8	22	ABP16592	HIV A24 super moti
130	5	45.5	10	24	ABP45672	HLA protein 121P2A	203	4	36.4	8	22	ABP17494	HIV B27 super moti
131	5	45.5	10	24	ABP45672	HLA protein 121P2A	204	4	36.4	8	22	ABP19685	HIV B62 super moti
132	5	45.5	10	24	ABP45672	HLA protein 121P2A	205	4	36.4	8	23	ABP74662	Transcription fact
133	5	45.5	10	24	ABP45672	HLA protein 121P2A	206	4	36.4	8	23	ABP74664	Transcription fact
134	5	45.5	10	24	ABP45672	HLA protein 121P2A	207	4	36.4	8	23	ABP74675	Transcription fact
135	5	45.5	10	24	ABP45672	HLA protein 121P2A	208	4	36.4	9	15	AAK61061	Dynorphin-like pol
136	5	45.5	10	24	ABP45672	HLA protein 121P2A	209	4	36.4	9	22	ABP14242	HIV A02 super moti
137	5	45.5	10	24	ABP45672	HLA protein 121P2A	210	4	36.4	9	22	ABP16400	HIV A24 super moti
138	5	45.5	10	24	ABP45672	HLA protein 121P2A	211	4	36.4	9	22	ABP17593	HIV B27 super moti
139	5	45.5	10	24	ABP45672	HLA protein 121P2A	212	4	36.4	9	22	ABP17594	HIV B27 super moti
140	5	45.5	10	24	ABP45672	HLA protein 121P2A	213	4	36.4	9	22	ABP19687	HIV B62 super moti
141	5	45.5	10	24	ABP45672	HLA protein 121P2A	214	4	36.4	9	22	ABP22276	HIV A03 motif vpu
142	5	45.5	10	24	ABP45672	HLA protein 121P2A	215	4	36.4	9	22	ABP24033	HIV A11 motif vpu
143	5	45.5	10	24	ABP45672	HLA protein 121P2A	216	4	36.4	9	22	ABP24326	HIV A24 motif rev
144	5	45.5	10	24	ABP45672	HLA protein 121P2A	217	4	36.4	9	24	ABP20464	Human cancer-relat
145	5	45.5	10	24	ABP45672	HLA protein 121P2A	218	4	36.4	9	24	ABP20829	Human cancer-relat
146	5	45.5	10	24	ABP45672	HLA protein 121P2A	219	4	36.4	9	24	ABP21852	Human cancer-relat
147	5	45.5	10	24	ABP45672	HLA protein 121P2A	220	4	36.4	9	24	ABP22054	Human cancer-relat
148	5	45.5	10	24	ABP45672	HLA protein 121P2A	221	4	36.4	9	24	ABP22064	Human cancer-relat
149	5	45.5	10	24	ABP45672	HLA protein 121P2A	222	4	36.4	9	24	ABP22225	Human cancer-relat
150	5	45.5	10	24	ABP45672	HLA protein 121P2A	223	4	36.4	9	24	ABP23265	Human cancer-relat
151	5	45.5	10	24	ABP45672	HLA protein 121P2A	224	4	36.4	9	24	ABP23630	Human cancer-relat
152	5	45.5	10	24	ABP45672	HLA protein 121P2A	225	4	36.4	9	24	ABP23752	HLA protein 121P2A
153	5	45.5	10	24	ABP45672	HLA protein 121P2A	226	4	36.4	9	24	ABP23754	HLA protein 121P2A
154	5	45.5	10	24	ABP45672	HLA protein 121P2A	227	4	36.4	9	24	ABP44048	HLA protein 121P2A
155	5	45.5	13	23	ABP45672	DNA ref-3 protein	228	4	36.4	9	24	ABP44050	HLA protein 121P2A

229	4	36.4	9	24	ABP84345	HLA protein 121P2A	302	4	36.4	11	22	ABP16617	HIV A24 super moti
230	4	36.4	9	24	ABP84347	HLA protein 121P2A	303	4	36.4	11	22	ABP16618	HIV A24 super moti
231	4	36.4	9	24	ABP84348	HLA protein 121P2A	304	4	36.4	11	22	ABP17507	HIV B27 super moti
232	4	36.4	9	24	ABP84349	HLA protein 121P2A	305	4	36.4	11	22	ABP19679	HIV B62 super moti
233	4	36.4	9	24	ABP84350	HLA protein 121P2A	306	4	36.4	11	22	ABP24378	HIV A24 motif vpu
234	4	36.4	9	24	ABP84351	HLA protein 121P2A	307	4	36.4	11	23	ABG59345	Human neural cell
235	4	36.4	9	24	ABP84352	HLA protein 121P2A	308	4	36.4	11	23	ABG59345	Human neural cell
236	4	36.4	9	24	ABP84353	HLA protein 121P2A	309	4	36.4	11	23	AAO18039	Human immunoglobul
237	4	36.4	9	24	ABP84354	HLA protein 121P2A	310	4	36.4	12	23	AAO18039	Sequence of peptid
238	4	36.4	9	24	ABP84355	HLA protein 121P2A	311	4	36.4	12	17	AAW96957	Multi-drug resista
239	4	36.4	9	24	ABP84356	HLA protein 121P2A	312	4	36.4	12	18	AAW25309	Peptide clone Laci
240	4	36.4	9	24	ABP84357	HLA protein 121P2A	313	4	36.4	12	21	AAH03584	Immunogenic peptid
241	4	36.4	9	24	ABP84358	HLA protein 121P2A	314	4	36.4	12	21	AAH03584	Immunogenic peptid
242	4	36.4	9	24	ABP84359	HLA protein 121P2A	315	4	36.4	12	23	ABO42999	Yeast Ume-3 RXXL m
243	4	36.4	9	24	ABP84360	HLA protein 121P2A	316	4	36.4	12	23	ABO42999	DNA repair protein
244	4	36.4	9	24	ABP84361	HLA protein 121P2A	317	4	36.4	13	14	AAH30447	Synthetic sequence
245	4	36.4	9	24	ABP84362	HLA protein 121P2A	318	4	36.4	13	18	AAW04620	Thymopoietin II 29
246	4	36.4	9	24	ABP84363	HLA protein 121P2A	319	4	36.4	13	20	AAW31028	Non-crosslinked pr
247	4	36.4	9	24	ABP84364	HLA protein 121P2A	320	4	36.4	13	21	AAH79338	Equine infectious
248	4	36.4	9	24	ABP84365	HLA protein 121P2A	321	4	36.4	13	21	AAH79338	Equine infectious
249	4	36.4	9	24	ABP84366	HLA protein 121P2A	322	4	36.4	13	22	AAU06104	RNA binding peptid
250	4	36.4	9	24	ABP84367	HLA protein 121P2A	323	4	36.4	13	22	AAU06104	RNA binding peptid
251	4	36.4	9	24	ABP84368	HLA protein 121P2A	324	4	36.4	13	22	AAH91755	Thymic peptide SEQ
252	4	36.4	9	24	ABP84369	HLA protein 121P2A	325	4	36.4	13	23	AAE27460	Human keratinocyte
253	4	36.4	9	24	ABP84370	HLA protein 121P2A	326	4	36.4	13	23	AAE27460	Human keratinocyte
254	4	36.4	9	24	ABP84371	HLA protein 121P2A	327	4	36.4	13	23	ABG79737	Human keratinocyte
255	4	36.4	9	24	ABP84372	HLA protein 121P2A	328	4	36.4	13	23	ABG79737	Human keratinocyte
256	4	36.4	9	24	ABP84373	HLA protein 121P2A	329	4	36.4	13	23	AAO18034	Human immunoglobul
257	4	36.4	9	24	ABP84374	HLA protein 121P2A	330	4	36.4	13	24	ABJ00535	Human IgE cyclic i
258	4	36.4	10	22	ABP14254	HLA protein 121P2A	331	4	36.4	14	12	AAH15705	Bioactive syntheti
259	4	36.4	10	22	ABP14255	HLA protein 121P2A	332	4	36.4	14	14	AAH30442	Rev HIV-lbru 37-50
260	4	36.4	10	22	ABP16609	HLA protein 121P2A	333	4	36.4	14	14	AAH30442	Synthetic sequence
261	4	36.4	10	22	ABP17504	HLA protein 121P2A	334	4	36.4	14	14	AAH30442	Synthetic sequence
262	4	36.4	10	22	ABP17505	HLA protein 121P2A	335	4	36.4	14	14	AAH30442	Synthetic sequence
263	4	36.4	10	22	ABP17506	HLA protein 121P2A	336	4	36.4	14	19	AAW68346	Human glycoalbumin
264	4	36.4	10	22	ABP22277	HLA protein 121P2A	337	4	36.4	14	19	AAW68346	MHC binding peptid
265	4	36.4	10	22	ABP22278	HLA protein 121P2A	338	4	36.4	14	21	AAH52877	Human immunodefici
266	4	36.4	10	22	ABP22279	HLA protein 121P2A	339	4	36.4	14	21	AAH52877	Altered MHC determ
267	4	36.4	10	22	ABP22280	HLA protein 121P2A	340	4	36.4	14	22	ABH56784	Altered MHC determ
268	4	36.4	10	22	ABP22281	HLA protein 121P2A	341	4	36.4	14	22	ABH56784	Human SNP related
269	4	36.4	10	22	ABP22282	HLA protein 121P2A	342	4	36.4	14	22	AAH56875	Human peptide #150
270	4	36.4	10	22	ABP22283	HLA protein 121P2A	343	4	36.4	14	22	AAH56875	Human peptide #151
271	4	36.4	10	22	ABP22284	HLA protein 121P2A	344	4	36.4	14	22	AAH56875	Human peptide #677
272	4	36.4	10	22	ABP22285	HLA protein 121P2A	345	4	36.4	14	22	AAH56875	Human peptide #678
273	4	36.4	10	22	ABP22286	HLA protein 121P2A	346	4	36.4	14	22	AAH56875	Human peptide #193
274	4	36.4	10	22	ABP22287	HLA protein 121P2A	347	4	36.4	14	22	AAH56875	Human peptide #193
275	4	36.4	10	22	ABP22288	HLA protein 121P2A	348	4	36.4	14	22	AAH56875	Human protease fra
276	4	36.4	10	22	ABP22289	HLA protein 121P2A	349	4	36.4	14	22	AAH56875	Altered MHC determ
277	4	36.4	10	22	ABP22290	HLA protein 121P2A	350	4	36.4	14	22	AAH56875	Antigenic peptide
278	4	36.4	10	22	ABP22291	HLA protein 121P2A	351	4	36.4	14	22	AAH56875	Proposed Supertant
279	4	36.4	10	22	ABP22292	HLA protein 121P2A	352	4	36.4	14	22	AAH56875	T-cell receptor pe
280	4	36.4	10	22	ABP22293	HLA protein 121P2A	353	4	36.4	14	22	AAH56875	Helper T-cell clas
281	4	36.4	10	22	ABP22294	HLA protein 121P2A	354	4	36.4	14	22	AAH56875	DP-1 transcription
282	4	36.4	10	22	ABP22295	HLA protein 121P2A	355	4	36.4	14	22	AAH56875	HIV-derived MHC cl
283	4	36.4	10	22	ABP22296	HLA protein 121P2A	356	4	36.4	14	22	AAH56875	BRCAL-associated R
284	4	36.4	10	22	ABP22297	HLA protein 121P2A	357	4	36.4	14	22	AAH56875	Solid phase synthe
285	4	36.4	10	22	ABP22298	HLA protein 121P2A	358	4	36.4	14	22	AAH56875	HIV DR super motif
286	4	36.4	10	22	ABP22299	HLA protein 121P2A	359	4	36.4	14	22	AAH56875	HIV DR super motif
287	4	36.4	10	22	ABP22300	HLA protein 121P2A	360	4	36.4	14	22	AAH56875	HIV DR super motif
288	4	36.4	10	22	ABP22301	HLA protein 121P2A	361	4	36.4	14	22	AAH56875	HIV DR 3b motif vp
289	4	36.4	10	22	ABP22302	HLA protein 121P2A	362	4	36.4	14	22	AAH56875	DR3 binding peptid
290	4	36.4	10	22	ABP22303	HLA protein 121P2A	363	4	36.4	14	22	AAH56875	HTL candidate epit
291	4	36.4	10	22	ABP22304	HLA protein 121P2A	364	4	36.4	14	22	AAH56875	HIV-1 epitope #49
292	4	36.4	10	22	ABP22305	HLA protein 121P2A	365	4	36.4	14	22	AAH56875	Human DNA mismatch
293	4	36.4	10	22	ABP22306	HLA protein 121P2A	366	4	36.4	14	22	AAH56875	Interleukin-2 rece
294	4	36.4	10	22	ABP22307	HLA protein 121P2A	367	4	36.4	14	22	AAH56875	Human casein Kinas
295	4	36.4	10	22	ABP22308	HLA protein 121P2A	368	4	36.4	14	22	AAH56875	Antigen binding si
296	4	36.4	10	22	ABP22309	HLA protein 121P2A	369	4	36.4	14	22	AAH56875	HLA-DR2 molecule b
297	4	36.4	10	22	ABP22310	HLA protein 121P2A	370	4	36.4	14	22	AAH56875	HLA-DR2 molecule b
298	4	36.4	10	22	ABP22311	HLA protein 121P2A	371	4	36.4	14	22	AAH56875	Human SPAT protein
299	4	36.4	10	22	ABP22312	HLA protein 121P2A	372	4	36.4	14	22	AAH56875	Human cancer-relat
300	4	36.4	10	22	ABP22313	HLA protein 121P2A	373	4	36.4	14	22	AAH56875	Human cancer-relat
301	4	36.4	10	22	ABP22314	HLA protein 121P2A	374	4	36.4	14	22	AAH56875	Human cancer-relat

475	4	36.4	15	24	ABR36319	Human cancer relat	448	3	27.3	8	21	AA808328	Epitope derived fr
476	4	36.4	15	24	ABR36319	Human cancer relat	449	3	27.3	8	21	AA93161	Peptide motif #2 a
477	4	36.4	15	24	ABR36340	Human cancer relat	450	3	27.3	8	21	AA959137	Human PAK65 kinase
478	4	36.4	15	24	ABR36444	Human cancer relat	451	3	27.3	8	21	AA966392	HLA-B8-binding HIV
479	4	36.4	15	24	ABR36445	Human cancer relat	452	3	27.3	8	21	AA963610	Desmoglein cell ad
480	4	36.4	15	24	ABR36670	Human cancer relat	453	3	27.3	8	21	AA963612	Desmoglein cell ad
481	4	36.4	15	24	ABR36671	Human cancer relat	454	3	27.3	8	21	AA963649	Desmoglein cell ad
482	4	36.4	15	24	ABR37111	Human cancer relat	455	3	27.3	8	21	AA963651	Desmoglein cell ad
483	4	36.4	15	24	ABR37237	Human cancer relat	456	3	27.3	8	21	AA963694	Desmoglein cell ad
484	4	36.4	15	24	ABR37340	Human cancer relat	457	3	27.3	8	21	AA963696	Desmoglein cell ad
485	4	36.4	15	24	ABR37432	Human cancer relat	458	3	27.3	8	21	AA963739	Desmoglein cell ad
486	4	36.4	15	24	ABR37433	Human cancer relat	459	3	27.3	8	21	AA963741	Desmoglein cell ad
487	4	36.4	15	24	ABR37647	Human cancer relat	460	3	27.3	8	21	AA963784	Desmoglein cell ad
488	4	36.4	15	24	ABR37648	Human cancer relat	461	3	27.3	8	21	AA963786	Desmoglein cell ad
489	4	36.4	15	24	ABP94146	HLA protein 121P2A	462	3	27.3	8	21	AA963829	Desmoglein cell ad
490	4	36.4	15	24	ABP94141	HLA protein 121P2A	463	3	27.3	8	21	AA963831	Desmoglein cell ad
491	4	36.4	15	24	ABP94543	HLA protein 121P2A	464	3	27.3	8	21	AA963871	Desmoglein cell ad
492	4	36.4	15	24	ABP94541	HLA protein 121P2A	465	3	27.3	8	21	AA963873	Desmoglein cell ad
493	4	36.4	15	24	ABP95144	HLA protein 121P2A	466	3	27.3	8	21	AA963885	Desmoglein cell ad
494	4	36.4	15	24	ABP95146	HLA protein 121P2A	467	3	27.3	8	21	AA963887	Desmoglein cell ad
495	4	36.4	15	24	ABP95577	HLA protein 121P2A	468	3	27.3	8	21	AA963920	Desmocollin cell a
496	3	27.3	8	11	AA802190	Peptide which bind	469	3	27.3	8	21	AA963922	Desmocollin cell a
497	3	27.3	8	11	AA805924	Low toxicity immun	470	3	27.3	8	21	AA963962	Desmocollin cell a
498	3	27.3	8	11	AA805925	Low toxicity immun	471	3	27.3	8	21	AA963964	Desmocollin cell a
499	3	27.3	8	13	AA829309	Nerve growth stimu	472	3	27.3	8	21	AA964004	Desmocollin cell a
500	3	27.3	8	14	AA848895	YK tryptic peptide	473	3	27.3	8	21	AA964006	Desmocollin cell a
501	3	27.3	8	14	AA848895	Sm B/B' epitope 83	474	3	27.3	8	21	AA964046	Desmocollin cell a
502	3	27.3	8	15	AA848895	Sm B/B' epitope 88	475	3	27.3	8	21	AA964048	Desmocollin cell a
503	3	27.3	8	15	AA852631	Newcastle Disease	476	3	27.3	8	21	AA964088	Desmocollin cell a
504	3	27.3	8	15	AA848277	cAMP-dependent kin	477	3	27.3	8	21	AA964090	Desmocollin cell a
505	3	27.3	8	16	AA860441	Antiproliferative	478	3	27.3	8	21	AA964133	Desmocollin cell a
506	3	27.3	8	16	AA862139	Plasminogen activa	479	3	27.3	8	21	AA964135	Desmocollin cell a
507	3	27.3	8	16	AA873509	Human TSH receptor	480	3	27.3	8	21	AA943646	Fragment of a huma
508	3	27.3	8	16	AA873507	Human TSH receptor	481	3	27.3	8	22	ABP11642	HIV A01 super moti
509	3	27.3	8	16	AA873518	Human TSH receptor	482	3	27.3	8	22	ABP11748	HIV A01 super moti
510	3	27.3	8	16	AA873533	Human TSH receptor	483	3	27.3	8	22	ABP12549	HIV A02 super moti
511	3	27.3	8	16	AA873556	Human TSH receptor	484	3	27.3	8	22	ABP12550	HIV A02 super moti
512	3	27.3	8	16	AA873717	Bovine glial cell	485	3	27.3	8	22	ABP12582	HIV A02 super moti
513	3	27.3	8	16	AA891050	Amino acids 152-15	486	3	27.3	8	22	ABP12584	HIV A02 super moti
514	3	27.3	8	17	AA801570	Compacting peptide	487	3	27.3	8	22	ABP13244	HIV A02 super moti
515	3	27.3	8	17	AA808502	CD8 alpha chain re	488	3	27.3	8	22	ABP14446	HIV A03 super moti
516	3	27.3	8	17	AA805582	Freundynin peptide	489	3	27.3	8	22	ABP14968	HIV A03 super moti
517	3	27.3	8	17	AA807405	Streptococcal M pr	490	3	27.3	8	22	ABP15086	HIV A03 super moti
518	3	27.3	8	17	AA807405	Streptococcal M pr	491	3	27.3	8	22	ABP15109	HIV A03 super moti
519	3	27.3	8	17	AA802223	Small nuclear ribo	492	3	27.3	8	22	ABP15560	HIV A24 super moti
520	3	27.3	8	17	AA808643	GF1 tryptic pept	493	3	27.3	8	22	ABP15903	HIV A24 super moti
521	3	27.3	8	18	AA842237	Peptide repeat mot	494	3	27.3	8	22	ABP17131	HIV B27 super moti
522	3	27.3	8	18	AA842237	Strum immunoregula	495	3	27.3	8	22	ABP17132	HIV B27 super moti
523	3	27.3	8	19	AA921599	Human neuroendocr	496	3	27.3	8	22	ABP17309	HIV B27 super moti
524	3	27.3	8	19	AA944014	Human CYP19A4 spec	497	3	27.3	8	22	ABP17493	HIV B27 super moti
525	3	27.3	8	19	AA944014	Endobacteri color	498	3	27.3	8	22	ABP17591	HIV B27 super moti
526	3	27.3	8	19	AA944014	Mouse mast cell pr	499	3	27.3	8	22	ABP17958	HIV B58 super moti
527	3	27.3	8	19	AA944014	Peptide motif: fo	500	3	27.3	8	22	ABP18859	HIV B62 super moti
528	3	27.3	8	19	AA944014	Partial sequence o							
529	3	27.3	8	19	AA944014	Human toxin peptide							
530	3	27.3	8	19	AA944014	Human toxin peptide							
531	3	27.3	8	20	AA944014	RNA binding peptide							
532	3	27.3	8	20	AA944014	Peptide motif #2 1							
533	3	27.3	8	20	AA944014	Peptide motif #2 1							
534	3	27.3	8	20	AA944014	Dehydrogenase pept							
535	3	27.3	8	20	AA944014	Fragment of human							
536	3	27.3	8	20	AA944014	V beta 6 clone for							
537	3	27.3	8	20	AA944014	V beta 6 clone for							
538	3	27.3	8	20	AA944014	Thrombophilus therm							
539	3	27.3	8	20	AA944014	Localisation signa							
540	3	27.3	8	20	AA944014	Bifidobacterium bi							
541	3	27.3	8	20	AA944014	Timeless gene prot							
542	3	27.3	8	20	AA944014	T cell epitope/MHC							
543	3	27.3	8	20	AA944014	Peptide motif of a							
544	3	27.3	8	21	AA944014	cAMP-dependent kin							
545	3	27.3	8	21	AA944014	cAMP-dependent pro							
546	3	27.3	8	21	AA944014	Peptide modulating							
547	3	27.3	8	21	AA944014	Peptide modulating							

ALIGNMENTS

RESULT 1

AA98528
 ID AA98528 standard: peptide: 11 AA.

XX
 AC AA98528:

XX
 DT 07-AUG-2000 (first entry)

XX
 DE NCAM Igl binding peptide D3.

XX
 KW NCAM; neural cell adhesion molecule; Igl: immunoglobulin domain 1;
 neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
 impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
 Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
 treatment; prosthetic nerve guide; treatment; nervous system.


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XX OS Synthetic.
XX AC
XX PN W0200018801-A2.
XX PD 06-APR-2000.
XX PF 23-SEP-1999; 99WO-DK00500.
XX PR 29-SEP-1998; 98DK-0001232.
XX PR 29-APR-1999; 99DK-0000592.
XX PA (RONN/) RONN L C B.
XX PA (ROCK/) ROCK E.
XX PA (HOLM/) HOLM A.
XX PA (OLSE/) OLSEN M.
XX PA (JENS/) JENSEN P H.
XX PA (POUL/) POULSEN F M.
XX PA (SORO/) SOROKA V.
XX PA (RALE/) RALETS I.
XX PA (BERE/) BEREZIN V.
XX PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
XX PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX DR WPI: 2000-293111/25.
XX PT Compositions that bind neural cell adhesion molecules useful for
XX PT treating disorders of the nervous system and muscles e.g. Alzheimer's
XX PT and Parkinson's diseases
XX PS Claim 20; Page 82; 119pp: English.
XX CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
XX CC NCAM is found in three forms, two of which are transmembrane forms, while
XX CC the third is attached via a lipid anchor to the cell membrane. All three
XX CC NCAM forms have an extracellular structure consisting of five immunoglobulin
XX CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX CC N-terminal. The present sequence represents a peptide which binds to the
XX CC NCAM-Ig1 domain, and is capable of stimulating or promoting neurite
XX CC outgrowth from NCAM presenting cells, and is also capable of promoting
XX CC the proliferation of NCAM presenting cells. The compound may be used in
XX CC the treatment of normal, degenerated or damaged NCAM presenting cells.
XX CC The compound may in particular be used to treat diseases of the central
XX CC and peripheral nervous systems such as post operative nerve damage,
XX CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
XX CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
XX CC dementia, sclerosis, nerve degeneration associated with diabetes,
XX CC mellitus, disorders affecting the circadian clock or neuro-muscular
XX CC transmission and schizophrenia. Conditions affecting the muscles may also
XX CC be treated with the compound, such as conditions associated with impaired
XX CC function of neuromuscular connections (e.g. genetic or traumatic shock or
XX CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX CC liver and bowel may also be treated using the compound. The compound is
XX CC used in a prosthetic nerve guide, and also to stimulate the ability to
XX CC learn, and to stimulate the memory of a subject.
XX SQ Sequence 11 AA:
XX Query Match 100.0%; Score 11; DB 21; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-04;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 AKKERQKDTQ 11
XX DB 1 AKKERQKDTQ 11
XX RESULT 2
XX AAY88561

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ID AAY88561 standard; peptide; 11 AA.
XX AC
XX XX AAY88561;
XX DT 07-AUG-2000 (first entry)
XX DE
XX DE NCAM Ig1 binding peptide D3 used as a control peptide.
XX KW NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;
XX KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
XX KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
XX KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
XX KW treatment; prosthetic nerve guide; treatment; nervous system.
XX OS Synthetic.
XX PN W0200018801-A2.
XX PD 06-APR-2000.
XX PF 23-SEP-1999; 99WO-DK00500.
XX PR 29-SEP-1998; 98DK-0001232.
XX PR 29-APR-1999; 99DK-0000592.
XX PA (RONN/) RONN L C B.
XX PA (ROCK/) ROCK E.
XX PA (HOLM/) HOLM A.
XX PA (OLSE/) OLSEN M.
XX PA (OSTE/) OSTERGAARD S.
XX PA (JENS/) JENSEN P H.
XX PA (POUL/) POULSEN F M.
XX PA (SORO/) SOROKA V.
XX PA (RALE/) RALETS I.
XX PA (BERE/) BEREZIN V.
XX PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
XX PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX DR WPI: 2000-293111/25.
XX PT Compositions that bind neural cell adhesion molecules useful for
XX PT treating disorders of the nervous system and muscles e.g. Alzheimer's
XX PT and Parkinson's diseases
XX PS Example 5; Fig 7; 119pp: English.
XX CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
XX CC NCAM is found in three forms, two of which are transmembrane forms, while
XX CC the third is attached via a lipid anchor to the cell membrane. All three
XX CC NCAM forms have an extracellular structure consisting of five immunoglobulin
XX CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX CC N-terminal. The invention relates to a compound containing a peptide
XX CC which binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2
XX CC domains, and is capable of stimulating or promoting neurite outgrowth
XX CC from NCAM presenting cells, and is also capable of promoting the
XX CC proliferation of NCAM presenting cells. The present sequence represents a
XX CC control peptide used in the identification of those binding peptides
XX CC which can be used in the compound. The compound may be used in the
XX CC treatment of normal, degenerated or damaged NCAM presenting cells. The
XX CC compound may in particular be used to treat diseases of the central and
XX CC peripheral nervous systems such as post operative nerve damage, traumatic
XX CC nerve damage, impaired myelination of nerve fibres, conditions resulting
XX CC from a stroke, Parkinson's disease, Alzheimer's disease, dementia,
XX CC sclerosis, nerve degeneration associated with diabetes mellitus,
XX CC disorders affecting the circadian clock or neuro-muscular transmission
XX CC and schizophrenia. Conditions affecting the muscles may also be treated
XX CC with the compound, such as conditions associated with impaired function
XX CC of neuromuscular connections (e.g. genetic or traumatic shock or
XX CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX CC liver and bowel may also be treated using the compound. The compound is
XX CC used in a prosthetic nerve guide, and also to stimulate the ability to
XX CC learn, and to stimulate the memory of a subject.

```

CC learn, and to stimulate the memory of a subject.

XX Sequence 11 AA;

SQ Query Match 100.0%; Score 11; DB 21; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKKERQKDTQ 11

DB 1 AKKERQKDTQ 11

RESULT 4

ABP83746

ID ABP83746 standard; Peptide: 11 AA;

AC ABP83746;

DT 21 OCT-2002 (first entry)

DE Human neural cell adhesion molecule (NCAM) peptide #2.

XX Human neural cell adhesion molecule; NCAM; heart muscle cell survival;
KW acute myocardial infarction; central nervous system disorder; stroke;
KW peripheral nervous system disorder; postoperative nerve damage;
KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;
KW postischaemic damage; multifactorial dementia; multiple sclerosis;
KW nerve degeneration; diabetes mellitus; neuro muscular degeneration;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW atrophic muscle disorder; focal degeneration; nephrosis.

XX Homo sapiens.

XX WO200247719-A2.

PN 20 JUN-2002.

XX 12-DEC-2001; 2001WO-DK00822.

XX 12 DEC-2000; 2000DK-0001863.

PR (ENKA) ENKAM PHARM AS.

PA Bock E, Berezin V, Kohler LB;

PI WPI: 2002-593473/62.

XX Use of a compound comprising a peptide of neural cell adhesion

PT molecule, in the preparation of medicament for preventing death of

PI cells presenting NCAM or NCAM ligand and treated ventral nervous

PT system diseases -

XX Claim 26: Page 39; 57pp; English.

XX The invention relates to use of a compound (I) comprising a peptide
CC which comprises at least 5 contiguous amino acid residues of a sequence
CC of the neural cell adhesion molecule (NCAM), its fragment, variant or its
CC mimic, for the preparation of a medicament for preventing death of cells
CC presenting the NCAM or an NCAM ligand (I) is useful in the preparation
CC of a medicament for preventing death of cells presenting the NCAM or an
CC NCAM ligand. The medicament is for the stimulation of the survival of
CC heart muscle cells, such as survival after acute myocardial infarction.
CC The medicament is for the treatment of diseases or conditions of the
CC central and peripheral nervous system, such as postoperative nerve
CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
CC impaired myelination of nerve fibres, post-ischaemic damage, e.g.
CC resulting from a stroke, multifactorial dementia, multiple sclerosis, nerve
CC degeneration associated with diabetes mellitus, neuro-muscular
CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease
CC and Huntington's disease. The medicament is for the treatment of diseases
CC or conditions of the muscles including conditions with impaired function
CC of neuro-muscular connections, such as genetic or traumatic atrophic

CC muscle disorders, and for the treatment of diseases of conditions of
CC various organs, such as degenerative conditions of the gonads, pancreas
CC (e.g. diabetes mellitus type I and II) and kidney (e.g. nephrosis).
CC ABC69429-ABC69452 represent human NCAM peptides of the invention.

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AKKERQKDTQ 11

DB 1 AKKERQKDTQ 11

RESULT 4

ABP83746

ID ABP83746 standard; Peptide: 9 AA;

AC ABP83746;

DT 28-MAR-2003 (first entry)

DE HLA protein 121P2A3 peptide #101.

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

KW humoral immune response; cellular immune response;

KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

XX WO200283068-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002WO-US11359.

XX 10-APR-2001; 2001US-242739P.

XX 25-APR-2001; 2001US-286640P.

XX 22 JUN-2001; 2001US-300373P.

XX (AGEN-) AGENSYS INC.

XX Challita-eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;

PI Afar DEH, Saifran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPI: 2003-092956/C8.

XX New composition comprising a substance that modulates the status of

PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune

PT responses or in assessing the status of 121P2A3 gene products in normal

PT versus cancerous tissues -

XX Claim 13: Page 130; 362pp; English.

XX The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cytostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterising cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene
CC products in normal versus cancerous tissues. The proteins are useful
CC for generating and characterising domain-specific antibodies, for
CC identifying agents or cellular factors that bind to 121P2A3 or a
CC particular structure domain, and in various therapeutic and diagnostic
CC contexts, including cancer vaccines. The antibodies or T cells reactive
CC with the product are useful in passive or active immunisation, and in
CC imaging methodologies for the management of cancer. The sequences shown
CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of

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CC the invention.
XX
SQ Sequence 9 AA;
Query Match 45.5%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KERQR 7
DB 4 KERQR 8
RESULT 5
ABP83747
ID ABP83747 standard; peptide: 9 AA.
XX
AC ABP83747;
XX
DT 28 MAR-2003 (first entry)
XX
CE HLA protein L21P2A3 peptide #102.
XX
KW Human; L21P2A3; cytostatic; immunostimulant; vaccine; SSH;
KW humoral immune response; cellular immune response;
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
CS Homo sapiens.
XX
PN W0200283068-A2.
XX
PD 24 OCT-2002.
XX
PF 09-APR-2002; 2002MO-US11359.
XX
PR 10-APR-2001; 2001US-282739P.
XX
PR 25-APR-2001; 2001US-286630P.
XX
PR 22 JUN-2001; 2001US-300373P.
XX
PA (AGEN) AGENSYS INC.
XX
PI Chaitana-eid PM, Raitano AH, Faris M, Hubert RS, Mitchell SC;
PI Afar DEH, Saittan D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX
WPI: 2003-092956/08.
XX
New composition comprising a substance that modulates the status of
L21P2A3 polypeptides, useful for eliciting humoral or cellular immune
responses or in assessing the status of L21P2A3 gene products in normal
versus cancerous tissues -
Claim 13: Page 130; 362pp; English.
XX
The invention relates to a novel composition comprising a substance that
modulates the status of a protein, L21P2A3. The composition of the
invention has cytostatic and immunostimulant activity, and is useful as a
vaccine. The L21P2A3 proteins and polynucleotides are useful for
eliciting humoral or cellular immune response. The polynucleotides are
useful for characterising cytogenetic abnormalities of this chromosomal
locus, as tools that can be used to delineate cytogenetic abnormalities
in the chromosomal region that encodes L21P2A3 that may contribute to
malignant phenotype, and in assessing the status of L21P2A3 gene
products in normal versus cancerous tissues. The proteins are useful
for generating and characterising domain-specific antibodies, for
identifying agents or cellular factors that bind to L21P2A3 or a
particular structure domain, and in various therapeutic and diagnostic
contexts, including cancer vaccines. The antibodies or T cells reactive
with the product are useful in passive or active immunisation, and in
imaging methodologies for the management of cancer. The sequences shown
in ABP83646 - ABP95595 represent peptides from the L21P2A3 variants of
the invention.
XX
SQ Sequence 9 AA;
Query Match 45.5%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;

```

Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 3 KERQR 7
 IIII
 DB 1 KERQR 5

 RESULT 7
 ABP83753 Standard; peptide: 9 AA.
 XX AC ABP83753
 XX AC ABP83753
 XX 26-MAR-2004 (first entry)
 XX DE HLA protein L21P2A3 peptide #105.
 XX DE HLA protein L21P2A3; cytostatic immunostimulant; vaccine; SSH;
 XX KW humoral immune response; cellular immune response;
 XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX OS Homo sapiens.
 XX PN W0200283068-A2.
 XX PN W1200283068-A2.
 XX PD 24-OCT-2002.
 XX PF 09-APR-2002; 2002W0-US11359.
 XX PF 10-APR-2001; 2001US-282739P.
 XX PR 25-APR-2001; 2001US-286630P.
 XX PR 22-JUN-2001; 2001US-300473P.
 XX XX
 XX PA (AGEN-) AGENSYS INC.
 XX XX
 XX PI Chaitin eid PM, Raitano AB, Farris M, Hubert RS, Mitchell SC;
 XX PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX XX
 XX DR WPI: 2003-092956/08.
 XX XX
 XX PT New composition comprising a substance that modulates the status of
 XX PT L21P2A3 polypeptides, useful for eliciting humoral or cellular immune
 XX PT responses or in assessing the status of L21P2A3 gene products in normal
 XX PT versus cancerous tissues.
 XX PS Claim 13: Page 130: 362pp: English.
 XX XX
 XX CC The invention relates to a novel composition comprising a substance that
 XX CC modulates the status of a protein, L21P2A3. The composition of the
 XX CC invention has cytostatic and immunostimulant activity, and is useful as a
 XX CC vaccine. The L21P2A3 proteins and polynucleotides are useful for
 XX CC eliciting humoral or cellular immune response. The polynucleotides are
 XX CC useful for characterising cytogenetic abnormalities of this chromosomal
 XX CC locus, as tools that can be used to delineate cytogenetic abnormalities
 XX CC in the chromosomal region that encodes L21P2A3 that may contribute to
 XX CC malignant phenotype, and in assessing the status of L21P2A3 gene
 XX CC products in normal versus cancerous tissues. The proteins are useful
 XX CC for generating and characterising domain-specific antibodies, for
 XX CC identifying agents or cellular factors that bind to L21P2A3 or a
 XX CC particular structure domain, and in various therapeutic and diagnostic
 XX CC contexts, including cancer vaccines. The antibodies or T cells reactive
 XX CC with the product are useful in passive or active immunisation, and in
 XX CC imaging methodologies for the management of cancer. The sequences shown
 XX CC in ABP83646 - ABP95595 represent peptides from the L21P2A3 variants of
 XX CC the invention.
 XX SQ Sequence 9 AA:

 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 3 KERQR 7
 IIII
 DB 3 KERQR 7

IIII
 2 KERQR 6

 RESULT 8
 ABP83754
 XX ABP83753 Standard; peptide: 9 AA.
 XX AC ABP83753
 XX AC ABP83753
 XX 26-MAR-2004 (first entry)
 XX DE HLA protein L21P2A3 peptide #106.
 XX DE HLA protein L21P2A3; cytostatic immunostimulant; vaccine; SSH;
 XX KW humoral immune response; cellular immune response;
 XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX OS Homo sapiens.
 XX PN W0200283068-A2.
 XX PN W1200283068-A2.
 XX PD 24-OCT-2002.
 XX PF 09-APR-2002; 2002W0-US11359.
 XX PF 10-APR-2001; 2001US-282739P.
 XX PR 25-APR-2001; 2001US-286630P.
 XX PR 22-JUN-2001; 2001US-300473P.
 XX XX
 XX PA (AGEN-) AGENSYS INC.
 XX XX
 XX PI Chaitin eid PM, Raitano AB, Farris M, Hubert RS, Mitchell SC;
 XX PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX XX
 XX DR WPI: 2003-092956/08.
 XX XX
 XX PT New composition comprising a substance that modulates the status of
 XX PT L21P2A3 polypeptides, useful for eliciting humoral or cellular immune
 XX PT responses or in assessing the status of L21P2A3 gene products in normal
 XX PT versus cancerous tissues.
 XX PS Claim 13: Page 130: 424pp: English.
 XX XX
 XX CC The invention relates to a novel composition comprising a substance that
 XX CC modulates the status of a protein, L21P2A3. The composition of the
 XX CC invention has cytostatic and immunostimulant activity, and is useful as a
 XX CC vaccine. The L21P2A3 proteins and polynucleotides are useful for
 XX CC eliciting humoral or cellular immune response. The polynucleotides are
 XX CC useful for characterising cytogenetic abnormalities of this chromosomal
 XX CC locus, as tools that can be used to delineate cytogenetic abnormalities
 XX CC in the chromosomal region that encodes L21P2A3 that may contribute to
 XX CC malignant phenotype, and in assessing the status of L21P2A3 gene
 XX CC products in normal versus cancerous tissues. The proteins are useful
 XX CC for generating and characterising domain-specific antibodies, for
 XX CC identifying agents or cellular factors that bind to L21P2A3 or a
 XX CC particular structure domain, and in various therapeutic and diagnostic
 XX CC contexts, including cancer vaccines. The antibodies or T cells reactive
 XX CC with the product are useful in passive or active immunisation, and in
 XX CC imaging methodologies for the management of cancer. The sequences shown
 XX CC in ABP83646 - ABP95595 represent peptides from the L21P2A3 variants of
 XX CC the invention.
 XX SQ Sequence 9 AA:

 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 3 KERQR 7
 IIII
 DB 3 KERQR 7

KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283068-A2.
 PN 24 OCT-2002.
 PD 24 OCT-2002.
 PP C9-APR-2002; 2002WO-US11359.
 XX 10-APR-2001; 2001US-282739P.
 PR 25-APR-2001; 2001US-286630P.
 PR 22-JUN-2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 PA Chaita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 PI WPI; 2003-092956/08.
 DR New composition comprising a substance that modulates the status of
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX Claim 13; Page 136; 362pp; English.
 PS The invention relates to a novel composition comprising a substance that
 XX modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP8340 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA:
 SQ Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DB 11111
 2 KERQR 6
 RESULT 14
 ABP84340
 ID ABP84340 standard; peptide: 9 AA.
 XX AC ABP84340;
 XX 28-MAR-2003 (first entry)
 DE HLA protein 121P2A3 peptide #695.
 XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 OS Homo sapiens.
 PN WO200283068-A2.

OS Homo sapiens.
 XX WO200283068-A2.
 PN 24 OCT-2002.
 PD 24 OCT-2002.
 PP C9-APR-2002; 2002WO-US11359.
 XX 10-APR-2001; 2001US-282739P.
 PR 25-APR-2001; 2001US-286630P.
 PR 22-JUN-2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 PA Chaita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 PI WPI; 2003-092956/08.
 DR New composition comprising a substance that modulates the status of
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX Claim 13; Page 142; 362pp; English.
 PS The invention relates to a novel composition comprising a substance that
 XX modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA:
 SQ Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DB 11111
 5 KERQR 9
 RESULT 15
 ABP84341
 ID ABP84341 standard; peptide: 9 AA.
 XX AC ABP84341;
 XX 28-MAR-2003 (first entry)
 DE HLA protein 121P2A3 peptide #696.
 XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 OS Homo sapiens.
 PN WO200283068-A2.

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XX PD 24-OCT-2002.
XX PR 09 APR-2002; 2002WO-US11359.
XX PR 10 APR-2001; 2001US-282739P.
XX PR 25-APR-2001; 2001US-286630P.
XX PR 22-JUN-2001; 2001US-300373P.
XX PA (AGEN-) AGENSYS INC.
XX PI Chailita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX PI Atar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX WPI: 2003-092956/08.
XX PR New composition comprising a substance that modulates the status of
XX PI 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX PI responses or in assessing the status of 121P2A3 gene products in normal
XX PI versus cancerous tissues.
XX PS Claim 13; Page 142; 362pp; English.
XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a protein, 121P2A3. The composition of the
XX CC invention has cytostatic and immunostimulant activity, and is useful as a
XX CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
XX CC eliciting humoral or cellular immune response. The polynucleotides are
XX CC useful for characterising cytogenetic abnormalities of this chromosomal
XX CC locus, as tools that can be used to delineate cytogenetic abnormalities
XX CC in the chromosomal region that encodes 121P2A3 that may contribute to
XX CC malignant phenotype, and in assessing the status of 121P2A3 gene
XX CC products in normal versus cancerous tissues. The proteins are useful
XX CC for generating and characterising domain-specific antibodies, for
XX CC identifying agents or cellular factors that bind to 121P2A3 or a
XX CC particular structure domain, and in various therapeutic and diagnostic
XX CC contexts, including cancer vaccines. The antibodies or T cells reactive
XX CC with the product are useful in passive or active immunisation, and in
XX CC imaging methodologies for the management of cancer. The sequences shown
XX CC in ABP84646 - ABP95595 represent peptides from the 121P2A3 variants of
XX CC the invention.
XX SQ Sequence 9 AA:
Query Match: 45.5%; Score 5; DP 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9, 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 4 KERQR 7
DB 1 KERQR 5
RESULT 16
ABP84343
ID ABP84343 standard; peptide: 9 AA.
XX AC ABP84343;
XX UT 28-MAR-2003 (first entry)
XX DE HLA protein 121P2A3 peptide #598.
XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX KW humoral immune response; cellular immune response;
XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX OS Homo sapiens.
XX PN W0200283068-A2.
XX PD 24-OCT-2002.
XX PR 09-APR-2002; 2002WO-US11359.
XX PR 10 APR-2001; 2001US-282739P.

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XX PR 09-APR-2002; 2002WO-US11359.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 25-APR-2001; 2001US-286630P.
XX PR 22-JUN-2001; 2001US-300373P.
XX PA (AGEN-) AGENSYS INC.
XX PI Chailita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX PI Atar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX WPI: 2003-092956/08.
XX PR New composition comprising a substance that modulates the status of
XX PI 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX PI responses or in assessing the status of 121P2A3 gene products in normal
XX PI versus cancerous tissues.
XX PS Claim 13; Page 142; 362pp; English.
XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a protein, 121P2A3. The composition of the
XX CC invention has cytostatic and immunostimulant activity, and is useful as a
XX CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
XX CC eliciting humoral or cellular immune response. The polynucleotides are
XX CC useful for characterising cytogenetic abnormalities of this chromosomal
XX CC locus, as tools that can be used to delineate cytogenetic abnormalities
XX CC in the chromosomal region that encodes 121P2A3 that may contribute to
XX CC malignant phenotype, and in assessing the status of 121P2A3 gene
XX CC products in normal versus cancerous tissues. The proteins are useful
XX CC for generating and characterising domain-specific antibodies, for
XX CC identifying agents or cellular factors that bind to 121P2A3 or a
XX CC particular structure domain, and in various therapeutic and diagnostic
XX CC contexts, including cancer vaccines. The antibodies or T cells reactive
XX CC with the product are useful in passive or active immunisation, and in
XX CC imaging methodologies for the management of cancer. The sequences shown
XX CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
XX CC the invention.
XX SQ Sequence 9 AA:
Query Match: 45.5%; Score 5; DP 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9, 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 4 KERQR 7
DB 4 KERQR 8
RESULT 17
ABP84346
ID ABP84346 standard; peptide: 9 AA.
XX AC ABP84346;
XX UT 28-MAR-2003 (first entry)
XX DE HLA protein 121P2A3 peptide #761.
XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX KW humoral immune response; cellular immune response;
XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX OS Homo sapiens.
XX PN W0200283068-A2.
XX PD 24-OCT-2002.
XX PR 09-APR-2002; 2002WO-US11359.
XX PR 10 APR-2001; 2001US-282739P.

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PR 25 APR-2001; 2001US-286630P.
 XX 22 JUN-2001; 2001US-300373P.
 PA (AGEN-) AGENSYS INC.
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC,
 PI Afar DEH, Safran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 DR New composition comprising a substance that modulates the status of
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PI versus cancerous tissues
 XX Claim 14; Page 142; 362pp; English.
 PS The invention relates to a novel composition comprising a substance that
 XX modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA;
 SQ Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Prod. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DB 3 KERQR 7
 AC
 AC ABP8448 standard; peptide; 9 AA.
 XX
 XX 28-MAR-2003 (first entry)
 DT HLA protein 121P2A3 peptide #703.
 DE Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 XX humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 CS WO200283068-A2.
 XX 24-OCT-2002.
 PD 09-APR-2002; 2002WO-US11359.
 XX 10-APR-2001; 2001US-282739P.
 PR 25-APR-2001; 2001US-286630P.
 PR 22-JUN-2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 PA Challita eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI

PA (AGEN-) AGENSYS INC.
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Safran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 DR New composition comprising a substance that modulates the status of
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PI versus cancerous tissues
 XX Claim 14; Page 142; 362pp; English.
 PS The invention relates to a novel composition comprising a substance that
 XX modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA;
 SQ Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Prod. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DB 2 KERQR 5
 AC
 AC ABP84628 standard; peptide; 9 AA.
 XX
 XX 28-MAR-2003 (first entry)
 DT HLA protein 121P2A3 peptide #983.
 DE Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 CS WO200283068-A2.
 XX 24-OCT-2002.
 PD 09-APR-2002; 2002WO-US11359.
 XX 10-APR-2001; 2001US-282739P.
 PR 25-APR-2001; 2001US-286630P.
 PR 22-JUN-2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 PA Challita eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI

PI Atar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX
 PS Claim 13; Page 147; 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP84646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA:
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DE 1 KERQR 5
 RESULT 20
 ABP84646
 ID ABP84646 standard; peptide: 9 AA.
 AC ABP84646;
 DE 28-MAR-2003 (first entry)
 DE HLA protein 121P2A3 peptide #986.
 DE Human 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression; subtractive hybridisation; HLA; human leukocyte antigen.
 KW Homo sapiens.
 US W0200283068-A2.
 PN 24-OCT-2002.
 PD 09-APR-2002; 2002WO-US11359.
 PF 10-APR-2001; 2001US-282739P.
 PR 25-APR-2001; 2001US-286630P.
 PR 22-JUN-2001; 2001US-300374P.
 XX
 PA (AGEN) AGENSYS INC.
 XX
 PI Chailita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Atar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune

XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues
 XX
 PS Claim 13; Page 147; 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP84646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA:
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DE 1 KERQR 5
 RESULT 21
 ABP84646
 ID ABP84646 standard; peptide: 9 AA.
 AC ABP84646;
 DE 28-MAR-2003 (first entry)
 DE HLA protein 121P2A3 peptide #986.
 DE Human 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression; subtractive hybridisation; HLA; human leukocyte antigen.
 KW Homo sapiens.
 US W0200283068-A2.
 PN 24-OCT-2002.
 PD 09-APR-2002; 2002WO-US11359.
 PF 10-APR-2001; 2001US-282739P.
 PR 25-APR-2001; 2001US-286630P.
 PR 22-JUN-2001; 2001US-300374P.
 XX
 PA (AGEN) AGENSYS INC.
 XX
 PI Chailita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Atar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune

PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues .
 XX
 PS Claim 13; Page 147; 362pp; English.
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 45.5%; Score 5; LH 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DB 4 KERQR 8
 II III
 RESULT 22
 ABP84635
 ID ABP84635 standard; peptide: 9 AA.
 XX
 AC ABP84635;
 XX
 BI 28-MAR-2004 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #990.
 XX
 DE Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS
 XX WO200283068-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 09-APR-2002; 2002WO-US11359.
 PF
 XX 10-APR-2001; 2001US-282739P.
 PR
 XX 25-APR-2001; 2001US-286630P.
 PR
 XX 22-JUN-2001; 2001US-300373P.
 XX
 XX (AGEN-) AGENSYS INC.
 PA
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 P1 Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 DR
 XX New composition comprising a substance that modulates the status of:
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues .
 XX
 XX

PS Claim 13; Page 147; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DB 3 KERQR 7
 II III
 RESULT 23
 ABP84636
 ID ABP84636 standard; peptide: 9 AA.
 XX
 AC ABP84636;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #991.
 XX
 KW Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS
 XX WO200283068-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 09-APR-2002; 2002WO-US11359.
 PF
 XX 10-APR-2001; 2001US-282739P.
 PR
 XX 25-APR-2001; 2001US-286630P.
 PR
 XX 22-JUN-2001; 2001US-300373P.
 XX
 XX (AGEN-) AGENSYS INC.
 PA
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 P1 Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 DR
 XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues .
 XX
 PS Claim 13; Page 147; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that

CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX Sequence 9 AA:
 SQ Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 DI 2 KERQR 6

RESULT 24
 ABP84925
 ID ABP84925 standard; peptide: 9 AA.
 AC ABP84925;
 DT 26-MAR-2003 (first entry)
 DE HLA protein 121P2A3 peptide #1280.
 KW Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

OS Homo sapiens.
 PN W0200283068-A2.
 PD 24 OCT 2002.
 PF 09-APR-2002: 2002WO-US11359.
 PR 10-APR-2001: 2001US-282739P.
 PR 25-APR-2001: 2001US-286630P.
 PR 22-JUN-2001: 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 PA Challita-eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.

XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.

PS Claim 13; Page 153; 362pp; English.
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities

CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX Sequence 9 AA:
 SQ Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 DI 4 KERQR 8

RESULT 25
 ABP84926
 ID ABP84926 standard; peptide: 9 AA.
 AC ABP84926;
 DT 28-MAR-2003 (first entry)

DE HLA protein 121P2A3 peptide #1281.
 KW Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

OS Homo sapiens.
 PN W0200283068-A2.
 PD 24 OCT 2002.
 PF 09-APR-2002: 2002WO-US11359.
 PR 10-APR-2001: 2001US-282739P.
 PR 25-APR-2001: 2001US-286630P.
 PR 22-JUN-2001: 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 PA Challita-eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.

XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.

PS Claim 13; Page 153; 362pp; English.

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities

CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83546 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX Sequence 9 AA;
 SQ

Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 I I I I I
 Db 3 KERQR 7

RESULT: 26

ABP84929
 ID ABP84929 standard; peptide: 9 AA.

XX AC

XX AC

XX 28 MAR-2003 (first entry)

XX HLA protein 121P2A3 peptide #1284.

XX Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

XX WO200283068-A2.

XX 24 OCT-2002.

XX 09-APR-2002; 2002WO-US11359.

XX 10-APR-2001; 2001US-282739P.

XX 25-APR-2001; 2001US-286630P.

XX 22-JUN-2001; 2001US-300373P.

XX (AGEN) AGENSYS INC.

XX Chailita-oid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

XX Afar DEH, Safran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPT: 2003-092956/08.

XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 XX Claim 13; Page 153; 362pp; English.

XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful

CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83546 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX Sequence 9 AA;

Query Match 45.5%; Score 5; DB 24; Length 9;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7

I I I I I

Db 5 KERQR 9

RESULT 27

ABP84931

ID ABP84931 standard; peptide: 9 AA.

XX AC

XX AC

XX 28-MAR-2003 (first entry)

XX HLA protein 121P2A3 peptide #1286.

XX Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.

XX WO200283068-A2.

XX 24-OCT-2002.

XX 09-APR-2002; 2002WO-US11359.

XX 10-APR-2001; 2001US-282739P.

XX 25-APR-2001; 2001US-286630P.

XX 22-JUN-2001; 2001US-300373P.

XX (AGEN) AGENSYS INC.

XX Chailita-oid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

XX Afar DEH, Safran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPT: 2003-092956/08.

XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 XX Claim 13; Page 153; 362pp; English.

XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic

CC contexts, including cancer vaccines. The antibodies or T cells reactive
CC with the product are useful in passive or active immunisation, and in
CC imaging methodologies for the management of cancer. The sequences shown
CC in ABP846 - ABP95595 represent peptides from the 121P2A3 variants of
CC the invention.
XX
SQ Sequence 9 AA:
Query Match 45.5% Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9; 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KERQR 7
ID 1 KERQR 5
DE
RESULT 28
ABP84932
ID ABP84932 standard; peptide: 9 AA:
XX
AC ABP84932:
XX
DI 28 MAR-2003 (first entry)
XX
DE HLA protein 121P2A3 peptide #1287.
XX
KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
KW humoral immune response; cellular immune response;
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
CS Homo sapiens.
XX
FN W0200283068-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US11359.
XX
PR 10-APR-2001; 2001US-282739P.
XX
PR 25-APR-2001; 2001US-286630P.
XX
PR 22-JUN-2001; 2001US-300373P.
XX
PA (AGEN) AGENSYS INC.
XX
FI Chaitin-aid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
FI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX
UR WPI: 2003-092956/08.
XX
PT New composition comprising a substance that modulates the status of
PI 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PI responses or in assessing the status of 121P2A3 gene products in normal
PI versus cancerous tissues.
XX
PS Claim 13; Page 153; 362pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cytostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterising cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene
CC products in normal versus cancerous tissues. The proteins are useful
CC for generating and characterising domain-specific antibodies, for
CC identifying agents or cellular factors that bind to 121P2A3 or a
CC particular structure domain, and in various therapeutic and diagnostic
CC contexts, including cancer vaccines. The antibodies or T cells reactive
CC with the product are useful in passive or active immunisation, and in
CC imaging methodologies for the management of cancer. The sequences shown

CC in ABP846 - ABP95595 represent peptides from the 121P2A3 variants of
CC the invention.
XX
SQ Sequence 9 AA:
Query Match 45.5% Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9; 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KERQR 7
ID 2 KERQR 5
DE
RESULT 29
ABP85222
ID ABP85222 standard; peptide: 9 AA:
XX
AC ABP85222:
XX
DI 28 MAR-2003 (first entry)
XX
DE HLA protein 121P2A3 peptide #1577.
XX
KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
KW humoral immune response; cellular immune response;
KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
CS Homo sapiens.
XX
FN W0200283068-A2.
XX
PD 24-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US11359.
XX
PR 10-APR-2001; 2001US-282739P.
XX
PR 25-APR-2001; 2001US-286630P.
XX
PR 22-JUN-2001; 2001US-300373P.
XX
PA (AGEN) AGENSYS INC.
XX
FI Chaitin-aid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
FI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX
UR WPI: 2003-092956/08.
XX
PT New composition comprising a substance that modulates the status of
PI 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PI responses or in assessing the status of 121P2A3 gene products in normal
PI versus cancerous tissues.
XX
PS Claim 13; Page 159; 362pp; English.
XX
CC The invention relates to a novel composition comprising a substance that
CC modulates the status of a protein, 121P2A3. The composition of the
CC invention has cytostatic and immunostimulant activity, and is useful as a
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC eliciting humoral or cellular immune response. The polynucleotides are
CC useful for characterising cytogenetic abnormalities of this chromosomal
CC locus, as tools that can be used to delineate cytogenetic abnormalities
CC in the chromosomal region that encodes 121P2A3 that may contribute to
CC malignant phenotype, and in assessing the status of 121P2A3 gene
CC products in normal versus cancerous tissues. The proteins are useful
CC for generating and characterising domain-specific antibodies, for
CC identifying agents or cellular factors that bind to 121P2A3 or a
CC particular structure domain, and in various therapeutic and diagnostic
CC contexts, including cancer vaccines. The antibodies or T cells reactive
CC with the product are useful in passive or active immunisation, and in
CC imaging methodologies for the management of cancer. The sequences shown
CC in ABP846 - ABP95595 represent peptides from the 121P2A3 variants of
CC the invention.

SQ Sequence 9 AA;
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 I I I I I
 Db 3 KERQR 7

RESULT 31
 ABP85227
 ID ABP85227 standard; peptide: 9 AA.
 XX AC ABP85227;
 XX DI 28-MAR-2003 (first entry)
 XX DE HLA protein 121P2A3 peptide #1582.
 XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX QS Homo sapiens.
 XX PN W0200283066 A2.
 XX PD 24-OCT-2002.
 XX PF 09 APR 2001; 2002WO-US11359.
 XX PR 10-APR-2001; 2001US-282739P.
 XX PR 25-APR-2001; 2001US-286630P.
 XX PR 22-JUN-2001; 2001US-300473P.
 XX PA (AGEN) AGENSYS INC.
 XX PI Challita-eld PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEB, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 XX New composition comprising a substance that modulates the status of
 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 responses or in assessing the status of 121P2A3 gene products in normal
 versus cancerous tissues -
 PS Claim 13; Page 159; 362pp; English.
 CC The invention relates to a novel composition comprising a substance that
 modulates the status of a protein, 121P2A3. The composition of the
 invention has cytostatic and immunostimulant activity, and is useful as a
 vaccine. The 121P2A3 proteins and polynucleotides are useful for
 eliciting humoral or cellular immune response. The polynucleotides are
 useful for characterising cytogenetic abnormalities of this chromosomal
 locus, as tools that can be used to delineate cytogenetic abnormalities
 in the chromosomal region that encodes 121P2A3 that may contribute to
 malignant phenotype, and in assessing the status of 121P2A3 gene
 products in normal versus cancerous tissues. The proteins are useful
 for generating and characterising domain-specific antibodies, for
 identifying agents or cellular factors that bind to 121P2A3 or a
 particular structure domain, and in various therapeutic and diagnostic
 contexts, including cancer vaccines. The antibodies or T cells reactive
 with the product are useful in passive or active immunisation, and in
 imaging methodologies for the management of cancer. The sequences shown
 in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 the invention.
 SQ Sequence 9 AA;
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 9 AA;
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 I I I I I
 DB 5 KERQR 9

RESULT 42

ABP85228
 ID ABP85228 standard: peptide; 9 AA.

XX AC
 XX XX
 XX 28-MAR-2003 (first entry)

XX DE HLA protein 121P2A3 peptide #1584.

XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

XX KW humoral immune response; cellular immune response;

XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX OS Homo sapiens.

XX PN W0200283068-A2.

XX PD 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US11359.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 25-APR-2001; 2001US-286630P.

XX PR 22-JUN-2001; 2001US-300373P.

XX PA (AGEN-) AGENSYS INC.

XX PI Chailita eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;

XX PI Atar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX PR WPI; 2003-092956/08.

XX PT New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal versus cancerous tissues.

XX PS Claim 13; Page 159; 362pp; English.

XX CC The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune responses. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP8546 - ABP95595 represent peptides from the 121P2A3 variants of the invention.

XX CC Query Match 45.5%; Score 6; LB 4; Length 9;

XX CC Best Local Similarity 100.0%; Pref. No. 9.4e-05;

XX CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7

I I I I I

DB 1 KERQR 5

RESULT 33

ABP85230
 ID ABP85230 standard: peptide; 9 AA.

XX AC
 XX XX
 XX 28-MAR-2003 (first entry)

XX DE HLA protein 121P2A3 peptide #1585.

XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

XX KW humoral immune response; cellular immune response;

XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX OS Homo sapiens.

XX PN W0200283068-A2.

XX PD 24-OCT-2002.

XX PF 09-APR-2002; 2002WO-US11359.

XX PR 10-APR-2001; 2001US-282739P.

XX PR 25-APR-2001; 2001US-286630P.

XX PR 22-JUN-2001; 2001US-300373P.

XX PA (AGEN-) AGENSYS INC.

XX PI Chailita eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;

XX PI Atar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX PR WPI; 2003-092956/08.

XX PT New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal versus cancerous tissues.

XX PS Claim 13; Page 159; 362pp; English.

XX CC The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune responses. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP8546 - ABP95595 represent peptides from the 121P2A3 variants of the invention.

XX CC Query Match 45.5%; Score 5; DB 24; Length 9;

XX CC Best Local Similarity 100.0%; Pref. No. 9.3e+05;

XX CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7

I I I I I

DB 2 KERQR 6

RESULT 34


```

XX OS Homo sapiens.
XX
XX PN W0200283068-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 09-APR-2002; 2002WO-US11359.
XX
XX PR 10-APR-2001; 2001US-282739P.
XX
XX PR 25-APR-2001; 2001US-286630P.
XX
XX PR 22-JUN-2001; 2001US-300373P.
XX
XX PA (AGEN-) AGENSYS INC.
XX
XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX PI Alar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX
XX DR WPI: 2003-092956/08.
XX
XX PT New composition comprising a substance that modulates the status of
XX PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX PT responses or in assessing the status of 121P2A3 gene products in normal
XX PT versus cancerous tissues.
XX
XX PS Claim 13: Page 165; 362pp; English.
XX
XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a protein, 121P2A3. The composition of the
XX CC vaccine has cytostatic and immunostimulant activity, and is useful as a
XX CC eliciting humoral or cellular immune response. The polynucleotides are
XX CC useful for characterising cytogenetic abnormalities of this chromosomal
XX CC locus, as tools that can be used to delineate cytogenetic abnormalities
XX CC in the chromosomal region that encodes 121P2A3 that may contribute to
XX CC malignant phenotype, and in assessing the status of 121P2A3 gene
XX CC products in normal versus cancerous tissues. The proteins are useful
XX CC for generating and characterising domain-specific antibodies, for
XX CC identifying agents or cellular factors that bind to 121P2A3 or a
XX CC particular structure domain, and in various therapeutic and diagnostic
XX CC contexts, including cancer vaccines. The antibodies or T cells reactive
XX CC with the product are useful in passive or active immunisation, and in
XX CC imaging methodologies for the management of cancer. The sequences shown
XX CC in ABP81646 - ABP95595 represent peptides from the 121P2A3 variants of
XX CC the invention.
XX
XX SQ Sequence 9 AA;
XX
XX Query Match: 45.5%; Score 5; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 KERQR 7
XX I I I I
XX DB 2 KERQR 6
XX
XX RESULT 49
XX ABP86092
XX ID ABP86092 standard; peptide: 9 AA.
XX
XX AC ABP86092;
XX
XX CT 28-MAR-2003 (first entry)
XX
XX DE HLA protein 121P2A3 peptide #2447.
XX
XX DI Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX DE humoral immune response; cellular immune response;
XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
XX OS Homo sapiens.
XX
XX PN W0200283068-A2.
XX
XX PD 24-OCT-2002.

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PN W0200283068-A2.
XX
XX PD 24-OCT-2002.
XX
XX PF 09-APR-2002; 2002WO-US11359.
XX
XX PR 10-APR-2001; 2001US-282739P.
XX
XX PR 25-APR-2001; 2001US-286630P.
XX
XX PR 22-JUN-2001; 2001US-300373P.
XX
XX PA (AGEN-) AGENSYS INC.
XX
XX PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX PI Alar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX
XX DR WPI: 2003-092956/08.
XX
XX PT New composition comprising a substance that modulates the status of
XX PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX PT responses or in assessing the status of 121P2A3 gene products in normal
XX PT versus cancerous tissues.
XX
XX PS Claim 13: Page 177; 362pp; English.
XX
XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a protein, 121P2A3. The composition of the
XX CC vaccine has cytostatic and immunostimulant activity, and is useful as a
XX CC eliciting humoral or cellular immune response. The polynucleotides are
XX CC useful for characterising cytogenetic abnormalities of this chromosomal
XX CC locus, as tools that can be used to delineate cytogenetic abnormalities
XX CC in the chromosomal region that encodes 121P2A3 that may contribute to
XX CC malignant phenotype, and in assessing the status of 121P2A3 gene
XX CC products in normal versus cancerous tissues. The proteins are useful
XX CC for generating and characterising domain-specific antibodies, for
XX CC identifying agents or cellular factors that bind to 121P2A3 or a
XX CC particular structure domain, and in various therapeutic and diagnostic
XX CC contexts, including cancer vaccines. The antibodies or T cells reactive
XX CC with the product are useful in passive or active immunisation, and in
XX CC imaging methodologies for the management of cancer. The sequences shown
XX CC in ABP81646 - ABP95595 represent peptides from the 121P2A3 variants of
XX CC the invention.
XX
XX SQ Sequence 9 AA;
XX
XX Query Match: 45.5%; Score 5; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 KERQR 7
XX I I I I
XX DB 2 KERQR 6
XX
XX RESULT 49
XX ABP86093
XX ID ABP86093 standard; peptide: 9 AA.
XX
XX AC ABP86093;
XX
XX CT 28-MAR-2003 (first entry)
XX
XX DE HLA protein 121P2A3 peptide #2448.
XX
XX DI Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX KW humoral immune response; cellular immune response;
XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
XX OS Homo sapiens.
XX
XX PN W0200283068-A2.
XX
XX PD 24-OCT-2002.

```

09-APR-2002; 2004WO-US11359.
10-APR-2001; 2001US-284739P.
25-APR-2001; 2001US-286630P.
22-JUN-2001; 2001US-300374P.
(AGEN-) AGENSYS INC.
Chattanooga TN, Reitano AP, Ellis M, Poffert RS, McInnes, SC,
Alar DEH, Salfrán D, Morrison K, Morris J JR, Orr W, Jakubowski A;
WPI; 2003 092956/06.
New composition comprising a substance that mediates the status of
121P2A3 polypeptides, useful for eliciting humoral or cellular immune
responses or in assessing the status of 121P2A3 gene products in normal
versus cancerous tissues -
Claim 13; Page 177; 362pp; English.
The invention relates to a novel composition comprising a substance that
modulates the status of a protein, 121P2A3. The composition of the
invention has cytostatic and immunostimulant activity, and is useful as a
vaccine, the 121P2A3 proteins and polynucleotides are useful for
eliciting humoral or cellular immune response. The polynucleotides are
useful for characterizing cytogenetic abnormalities of this chromosomal
locus, as tools that can be used to delineate cytogenetic abnormalities
in the chromosomal region that encodes 121P2A3 that may contribute to
malignant phenotype, and in assessing the status of 121P2A3 gene
products in normal versus cancerous tissues. The proteins are useful
for generating and characterising domain-specific antibodies, for
identifying agents or cellular factors that bind to 121P2A3 or a
particular structure domain, and in various therapeutic and diagnostic
contexts, including cancer vaccines. The antibodies of T cells reactive
with the product are useful in passive or active immunisation, and in
imaging methodologies for the management of cancer. The sequences shown
in APP8646 - ABP95595 represent peptides from the 121P2A3 variants of
the invention.
Sequence 5 AA:

Query Match: 45.5%; Score 6; E=24; Length 9
Best local Similarity 100.0%, Prod Seq 9 aa=60
Matches 5; Conservative 0; M.Similarities 0; Indels 0; Gaps
07 3 KERQR 7
ID 11111
ID 4 KERQR 8
RESIDUE 4:
APP8646
ID APP8646 standard; peptide 9 AA.
XX AC APP86094;
XX
DT 28-MAR-2003 (first entry)
DE HLA protein 121P2A3 peptide #244.
XX
KW Human; 121P2A3; cytototoxic lymphocyte-mediated SSH.
KW Immune response; cellular immune response;
KW Suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX OS Homo sapiens.
XX PS W2002H4066-A2.
XX
PD 24 OCT-2002.
XX
XX 09-APR-2002; 2004WO-US11359.

XX (AGEN-) AGENSYS INC.
 XX
 PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 DR WP1: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX
 PS Claim 13; Page 177; 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP8646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DE IIIII
 3 KERQR 7
 RESULT 4;
 ID ABP86096
 AC ABP86096 standard; peptide: 9 AA.
 AC ABP86096;
 XX
 DT 28-MAR-2004 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #2451.
 XX
 DE Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN W0200283068-A2.
 XX
 DT 24-OCT-2002.
 XX
 PF 09-APR-2002; 2002MO-US11359.
 XX
 PF 10-APR-2001; 2001US-282739P.
 XX
 PF 25-APR-2001; 2001US-286630P.
 XX
 PF 22-JUN-2001; 2001US-300373P.
 XX
 FA (AGEN-) AGENSYS INC.
 XX
 PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX

PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 DR WP1: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX
 PS Claim 13; Page 177; 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP8646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DE IIIII
 5 KERQR 9
 RESULT 44
 ID ABP86576
 AC ABP86576 standard; peptide: 9 AA.
 AC ABP86576;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #2931.
 XX
 DE Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN W0200283068-A2.
 XX
 DT 24-OCT-2002.
 XX
 PF 09-APR-2002; 2002MO-US11359.
 XX
 PF 10-APR-2001; 2001US-282739P.
 XX
 PF 25-APR-2001; 2001US-286630P.
 XX
 PF 22-JUN-2001; 2001US-300373P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX

DR WP1: 2003-092956/08.
 XX
 XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 XX
 XX Claim 13: Page 181: 362pp; English.
 XX
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 XX Sequence 9 AA:
 SQ

Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 DB 4 KERQR 8
 IIII
 IIII

RESULT 45
 ABP86577
 ID ABP86577 standard; peptide: 9 AA.
 AC
 AC ABP86577;
 DI 28-MAR 2003 (first entry)
 XX
 XX HLA protein 121P2A3 peptide #2932.
 DE
 XX Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX
 XX Homo sapiens.
 CS
 XX WO200283068-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 04-APR 2002; 2002WO-US11359.
 PF
 XX 10-APR-2001; 2001US-282739P.
 PR
 XX 25-APR-2001; 2001US-286630P.
 PR
 XX 22 JUN-2001; 2001US-300373P.
 XX
 XX (AGEN-) AGENSYS INC.
 PA
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 XX WP1: 2003-092956/08.
 XX
 XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 PT

PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 XX
 XX Claim 13: Page 182: 362pp; English.
 XX
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 XX Sequence 9 AA:
 SQ

Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 DB 4 KERQR 8
 IIII
 IIII

RESULT 46
 ABP86580
 ID ABP86580 standard; peptide: 9 AA.
 AC
 AC ABP86580;
 XX
 XX 28-MAR 2003 (first entry)
 DI
 XX HLA protein 121P2A3 peptide #2935.
 DE
 XX Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX
 XX Homo sapiens.
 CS
 XX WO200283068-A2
 PN
 XX 24-OCT-2002.
 PD
 XX 09-APR-2002; 2002WO-US11359.
 PF
 XX 10-APR-2001; 2001US-282739P.
 PR
 XX 25-APR-2001; 2001US-286630P.
 PR
 XX 22-JUN-2001; 2001US-300373P.
 XX
 XX (AGEN-) AGENSYS INC.
 PA
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 XX WP1: 2003-092956/08.
 XX
 XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 PT

XX Claim 13; Page 182; 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3, the composition of the
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 45.5%; Score 5; EB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 Db 1111
 3 KERQR 7
 RESULT 47
 ABP86581
 ID ABP86581 standard; peptide; 9 AA.
 XX
 AC ABP86581;
 DT 28-MAR-2003 (first entry)
 DE HLA protein 121P2A3 peptide #2936.
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WC200283068-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-US11359.
 XX
 PR 10-APR-2001; 2001US-282739P.
 XX
 PR 25-APR-2001; 2001US-286630P.
 XX
 PR 22-JUN-2001; 2001US-300373P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Chailita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 WP1: 2003-092956/08.
 XX
 CC New composition comprising a substance that modulates the status of
 CC 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 CC responses or in assessing the status of 121P2A3 gene products in normal
 CC versus cancerous tissues -
 XX
 PS Claim 13; Page 182; 362pp; English.
 XX

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 Db 1111
 1 KERQR 5
 RESULT 48
 ABP86583
 ID ABP86583 standard; peptide; 9 AA.
 XX
 AC ABP86583;
 DT 28-MAR-2003 (first entry)
 DE HLA protein 121P2A3 peptide #2938.
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WC200283068-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-US11359.
 XX
 PR 10-APR-2001; 2001US-282739P.
 XX
 PR 25-APR-2001; 2001US-286630P.
 XX
 PR 22-JUN-2001; 2001US-300373P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Chailita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 WP1: 2003-092956/08.
 XX
 CC New composition comprising a substance that modulates the status of
 CC 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 CC responses or in assessing the status of 121P2A3 gene products in normal
 CC versus cancerous tissues -
 XX
 PS Claim 13; Page 182; 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC vaccine has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP81646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX
 XX
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Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pied. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KEROR 7
 IIII
 DB 5 KEROR 9

RESULT 50
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 ID ABP87065 standard; peptide: 9 AA.
 XX
 AC ABP87065;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #3420.
 XX
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 OS Homo sapiens.
 XX
 FN WO200283068-A2.
 XX
 PD 24 OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-US11359.
 XX
 PE 10-APR-2001; 2001US-282739P.
 XX
 PR 25-APR-2001; 2001US-286630P.
 XX
 PR 22-JUN-2001; 2001US-300373P.
 XX
 PA (AGEN) AGENSYS INC.
 XX
 PI Chellita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 DR WPI: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 PS
 XX Claim 13; Page 186; 362pp; English.

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene

CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP81646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX
 XX
 SQ Sequence 9 AA;

Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pied. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KEROR 7
 IIII
 DB 5 KEROR 9

RESULT 50
 ABP87065
 ID ABP87065 standard; peptide: 9 AA.
 XX
 AC ABP87065;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #3420.
 XX
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 OS Homo sapiens.
 XX
 FN WO200283068-A2.
 XX
 PD 24 OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-US11359.
 XX
 PE 10-APR-2001; 2001US-282739P.
 XX
 PR 25-APR-2001; 2001US-286630P.
 XX
 PR 22-JUN-2001; 2001US-300373P.
 XX
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 PI Chellita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 DR WPI: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 PS
 XX Claim 13; Page 186; 362pp; English.

CC The invention relates to a novel composition comprising a substance that
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 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
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CC products in normal versus cancerous tissues. The proteins are useful
CC for generating and characterising domain specific antibodies, for
CC identifying agents or cellular factors that bind to 121P2A3 or a
CC particular structure domain, and in various therapeutic and diagnostic
CC contexts, including cancer vaccines. The antibodies or T cells reactive
CC with the product are useful in passive or active immunisation, and in
CC imaging methodologies for the management of cancer. The sequences shown
CC in AB983646 - AB95595 represent peptides from the 121P2A3 variants of
CC the invention.
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Query Match: 45.5%; Score 5; Pos 24; Length 9.
Best local Similarity 100.0%; Pred. No. 9; 30-60%
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0

QY 3 KERQR 7
DB 1 KERQR 5

Search Completed: September 30, 2003, 11:24:18
Job Time : 47.1657 secs

GenCore version 5.1.6
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OM protein protein search, using sw model

Run on: September 30, 2003, 10:07:04 ; Search time 41.0833 Seconds
(without alignments)
42.499 Million cell updates/sec

Title: US-09-787-443-3

Perfect score: 11

Sequence: 1 ARALNMGAKPK 11

Scoring table: OLICO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 273822

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Maximum DB Seq length: 15

Post-processing: Listing first 500 summaries

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- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	ID	Description
1	11	100.0	11	21	AA188529	NCAM Igl binding p
2	11	100.0	11	21	AA188563	NCAM Igl binding p
3	11	100.0	11	23	ABG69331	Human neural cell
4	4	36.4	8	19	AAW75820	Mouse mast cell pr
5	4	36.4	8	22	AAJ01170	Hepatitis C virus
6	4	36.4	8	22	AAJ02158	Hepatitis C virus
7	4	36.4	8	22	AAJ02181	Hepatitis C virus
8	4	36.4	8	22	AAJ02671	Hepatitis C virus
9	4	36.4	8	23	AB884505	Encephalomyocardit

4	36.4	8	23	AAG79508	C. trachomatis epi
10	36.4	8	23	ABM45443	Desmoglein-1 CAR p
11	36.4	8	23	ABM45444	Desmoglein-1 CAR p
12	36.4	8	23	ABM45448	Desmoglein-1 CAR p
13	36.4	8	23	ABM45449	Desmoglein-1 CAR p
14	36.4	8	23	ABM45455	Desmoglein-1 CAR p
15	36.4	8	23	ABM45456	Desmoglein-1 CAR p
16	36.4	8	23	ABM45489	Desmoglein-1 CAR p
17	36.4	8	23	ABM45490	Desmoglein-3 CAR p
18	36.4	8	23	ABM45494	Desmoglein-3 CAR p
19	36.4	8	23	ABM45495	Desmoglein-3 CAR p
20	36.4	8	23	ABM45500	Desmoglein-3 CAR p
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23	36.4	8	23	ABM46181	Desmoglein-1 CAR s
24	36.4	8	23	ABM46187	Desmoglein-1 CAR s
25	36.4	8	23	ABM46194	Desmoglein-1 CAR s
26	36.4	8	23	ABM46203	Desmoglein-1 CAR s
27	36.4	8	23	ABM46204	Desmoglein-1 CAR s
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29	36.4	8	23	ABM46212	Desmoglein-1 CAR s
30	36.4	8	23	ABM46215	Desmoglein-1 CAR s
31	36.4	8	23	ABM46222	Desmoglein-1 CAR s
32	36.4	8	23	ABM46231	Desmoglein-1 CAR s
33	36.4	8	23	ABM46232	Desmoglein-1 CAR s
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49	36.4	8	23	ABM46326	Desmoglein-1 CAR s
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55	36.4	8	23	ABM46459	Desmoglein-3 CAR s
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58	36.4	8	23	ABM46480	Desmoglein-3 CAR s
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79	36.4	9	15	AA195221	E. tenella EtMIC4/
80	36.4	9	17	AAW49326	Peptide fragment (
81	36.4	9	21	AAW95893	Human leucocyte an
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					HER2/NEU DR superm

83	4	36.4	9	22	AAJ00170	Hepatitis C virus	156	4	36.4	9	23	ABR46520	Desmoglein-3 CAR S
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85	4	36.4	9	22	AAJ00984	Hepatitis C virus	158	4	36.4	9	23	ABR46530	Desmoglein-3 CAR S
86	4	36.4	9	22	AAJ01387	Hepatitis C virus	159	4	36.4	9	23	ABR46532	Desmoglein-3 CAR S
87	4	36.4	9	22	AAJ01799	Hepatitis C virus	160	4	36.4	9	23	ABR46533	Desmoglein-3 CAR S
88	4	36.4	9	22	AAJ02182	Hepatitis C virus	161	4	36.4	9	23	ABR46538	Desmoglein-3 CAR S
89	4	36.4	9	22	AAJ02315	Hepatitis C virus	162	4	36.4	9	23	ABR46544	Desmoglein-3 CAR S
90	4	36.4	9	22	AAJ02679	Hepatitis C virus	163	4	36.4	9	23	ABR46553	Desmoglein-3 CAR S
91	4	36.4	9	23	AHG65476	Selective targetin	164	4	36.4	9	23	ABR46554	Desmoglein-3 CAR S
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93	4	36.4	9	23	ABG34118	Antigenic peptide	166	4	36.4	9	23	ABR46557	Desmoglein-3 CAR S
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101	4	36.4	9	23	ABR45496	Desmoglein-3 CAR P	174	4	36.4	10	16	AAJ79780	Rabbit testis sper
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107	4	36.4	9	23	ABR46182	Desmoglein-1 CAR S	180	4	36.4	10	18	AAW32745	Human platelet gly
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131	4	36.4	9	23	ABR46294	Desmoglein-1 CAR S	204	4	36.4	10	23	AAJ099409	Human ECSM4 peptid
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138	4	36.4	9	23	ABR46336	Desmoglein-1 CAR S	211	4	36.4	10	23	ABR46189	Desmoglein-1 CAR S
139	4	36.4	9	23	ABR46347	Desmoglein-3 CAR S	212	4	36.4	10	23	ABR46190	Desmoglein-1 CAR S
140	4	36.4	9	23	ABR46458	Desmoglein-3 CAR S	213	4	36.4	10	23	ABR46196	Desmoglein-1 CAR S
141	4	36.4	9	23	ABR46460	Desmoglein-3 CAR S	214	4	36.4	10	23	ABR46197	Desmoglein-1 CAR S
142	4	36.4	9	23	ABR46461	Desmoglein-3 CAR S	215	4	36.4	10	23	ABR46212	Desmoglein-1 CAR S
143	4	36.4	9	23	ABR46466	Desmoglein-3 CAR S	216	4	36.4	10	23	ABR46213	Desmoglein-1 CAR S
144	4	36.4	9	23	ABR46472	Desmoglein-3 CAR S	217	4	36.4	10	23	ABR46217	Desmoglein-1 CAR S
145	4	36.4	9	23	ABR46481	Desmoglein-3 CAR S	218	4	36.4	10	23	ABR46218	Desmoglein-1 CAR S
146	4	36.4	9	23	ABR46482	Desmoglein-3 CAR S	219	4	36.4	10	23	ABR46224	Desmoglein-1 CAR S
147	4	36.4	9	23	ABR46484	Desmoglein-3 CAR S	220	4	36.4	10	23	ABR46225	Desmoglein-1 CAR S
148	4	36.4	9	23	ABR46485	Desmoglein-3 CAR S	221	4	36.4	10	23	ABR46240	Desmoglein-1 CAR S
149	4	36.4	9	23	ABR46490	Desmoglein-3 CAR S	222	4	36.4	10	23	ABR46241	Desmoglein-1 CAR S
150	4	36.4	9	23	ABR46496	Desmoglein-3 CAR S	223	4	36.4	10	23	ABR46245	Desmoglein-1 CAR S
151	4	36.4	9	23	ABR46505	Desmoglein-3 CAR S	224	4	36.4	10	23	ABR46246	Desmoglein-1 CAR S
152	4	36.4	9	23	ABR46506	Desmoglein-3 CAR S	225	4	36.4	10	23	ABR46252	Desmoglein-1 CAR S
153	4	36.4	9	23	ABR46508	Desmoglein-3 CAR S	226	4	36.4	10	23	ABR46253	Desmoglein-1 CAR S
154	4	36.4	9	23	ABR46509	Desmoglein-3 CAR S	227	4	36.4	10	23	ABR46268	Desmoglein-1 CAR S
155	4	36.4	9	23	ABR46514	Desmoglein-3 CAR S	228	4	36.4	10	23	ABR46269	Desmoglein-1 CAR S

224	4	36.4	10	23	ABB46273	Desmoglein-1 CAR S	302	4	36.4	11	23	ABB46475	Desmoglein-3 CAR S
230	4	36.4	10	23	ABB46274	Desmoglein-1 CAR S	303	4	36.4	11	23	ABB46493	Desmoglein-3 CAR S
231	4	36.4	10	23	ABB46280	Desmoglein-1 CAR S	304	4	36.4	11	23	ABB46498	Desmoglein-3 CAR S
232	4	36.4	10	23	ABB46281	Desmoglein-1 CAR S	305	4	36.4	11	23	ABB46499	Desmoglein-3 CAR S
233	4	36.4	10	23	ABB46296	Desmoglein-1 CAR S	306	4	36.4	11	23	ABB46498	Desmoglein-3 CAR S
234	4	36.4	10	23	ABB46297	Desmoglein-1 CAR S	307	4	36.4	11	23	ABB46517	Desmoglein-3 CAR S
235	4	36.4	10	23	ABB46307	Desmoglein-1 CAR S	308	4	36.4	11	23	ABB46518	Desmoglein-3 CAR S
236	4	36.4	10	23	ABB46302	Desmoglein-1 CAR S	309	4	36.4	11	23	ABB46522	Desmoglein-3 CAR S
237	4	36.4	10	23	ABB46308	Desmoglein-1 CAR S	310	4	36.4	11	23	ABB46523	Desmoglein-3 CAR S
238	4	36.4	10	23	ABB46309	Desmoglein-1 CAR S	311	4	36.4	11	23	ABB46541	Desmoglein-3 CAR S
239	4	36.4	10	23	ABB46462	Desmoglein-3 CAR S	312	4	36.4	11	23	ABB46542	Desmoglein-3 CAR S
240	4	36.4	10	23	ABB46463	Desmoglein-3 CAR S	313	4	36.4	11	23	ABB46546	Desmoglein-3 CAR S
241	4	36.4	10	23	ABB46467	Desmoglein-3 CAR S	314	4	36.4	11	23	ABB46547	Desmoglein-3 CAR S
242	4	36.4	10	23	ABB46468	Desmoglein-3 CAR S	315	4	36.4	11	23	ABB46565	Desmoglein-3 CAR S
243	4	36.4	10	23	ABB46473	Desmoglein-3 CAR S	316	4	36.4	11	23	ABB46566	Desmoglein-3 CAR S
244	4	36.4	10	23	ABB46486	Desmoglein-3 CAR S	317	4	36.4	11	23	ABB46570	Desmoglein-3 CAR S
245	4	36.4	10	23	ABB46487	Desmoglein-3 CAR S	318	4	36.4	11	23	ABB46571	Desmoglein-3 CAR S
246	4	36.4	10	23	ABB46491	Desmoglein-3 CAR S	319	4	36.4	11	24	ABP60263	Synthetic peptide
247	4	36.4	10	23	ABB46492	Desmoglein-3 CAR S	320	4	36.4	12	20	AAW90055	Rhodococcus sp. M4
248	4	36.4	10	23	ABB46497	Desmoglein-3 CAR S	321	4	36.4	12	22	AAW65549	N-terminal modifie
249	4	36.4	10	23	ABB46510	Desmoglein-3 CAR S	322	4	36.4	12	23	AAW51191	HGF/SF antibody-b1
250	4	36.4	10	23	ABB46511	Desmoglein-3 CAR S	323	4	36.4	12	23	ABB46476	Desmoglein-3 CAR S
251	4	36.4	10	23	ABB46515	Desmoglein-3 CAR S	324	4	36.4	12	23	ABB46477	Desmoglein-3 CAR S
252	4	36.4	10	23	ABB46516	Desmoglein-3 CAR S	325	4	36.4	12	23	ABB46500	Desmoglein-3 CAR S
253	4	36.4	10	23	ABB46521	Desmoglein-3 CAR S	326	4	36.4	12	23	ABB46501	Desmoglein-3 CAR S
254	4	36.4	10	23	ABB46534	Desmoglein-3 CAR S	327	4	36.4	12	23	ABB46524	Desmoglein-3 CAR S
255	4	36.4	10	23	ABB46535	Desmoglein-3 CAR S	328	4	36.4	12	23	ABB46525	Desmoglein-3 CAR S
256	4	36.4	10	23	ABB46539	Desmoglein-3 CAR S	329	4	36.4	12	23	ABB46548	Desmoglein-3 CAR S
257	4	36.4	10	23	ABB46540	Desmoglein-3 CAR S	330	4	36.4	12	23	ABB46549	Desmoglein-3 CAR S
258	4	36.4	10	23	ABB46545	Desmoglein-3 CAR S	331	4	36.4	12	23	ABB46572	Desmoglein-3 CAR S
259	4	36.4	10	23	ABB46558	Desmoglein-3 CAR S	332	4	36.4	12	23	ABB46573	Desmoglein-3 CAR S
260	4	36.4	10	23	ABB46559	Desmoglein-3 CAR S	333	4	36.4	12	24	ABP60227	Synthetic peptide
261	4	36.4	10	23	ABB46563	Desmoglein-3 CAR S	334	4	36.4	13	20	AAV34065	Histone H1 isoform
262	4	36.4	10	23	ABB46564	Desmoglein-3 CAR S	335	4	36.4	13	21	AAV57363	Human histone H1.5
263	4	36.4	10	23	ABB46565	Desmoglein-3 CAR S	336	4	36.4	13	22	AAU04989	N-terminal peptide
264	4	36.4	10	23	ABB46567	Desmoglein-3 CAR S	337	4	36.4	13	22	AAU74179	BCL2 Bhl domain mu
265	4	36.4	10	23	ABB46568	Desmoglein-3 CAR S	338	4	36.4	13	23	AAU86049	Human glucocerebro
266	4	36.4	11	15	AAW55834	Meningococcal OMP	339	4	36.4	14	14	AAW32965	Mastoparan analogu
267	4	36.4	11	18	AAW34126	LiFA-1 beta subunit	340	4	36.4	14	14	AAW32978	Mastoparan analogu
268	4	36.4	11	18	AAW34129	LiFA-1 beta subunit	341	4	36.4	14	14	AAW32960	Mastoparan analogu
269	4	36.4	11	20	AAW74420	HJ loop peptide KU	342	4	36.4	14	18	AAW32306	Leishmania immunog
270	4	36.4	11	20	AAW84054	Human V3 loop HIV	343	4	36.4	14	20	AAV55119	ATCC HB 11646 mono
271	4	36.4	11	22	AAJ00171	Hepatitis C virus	344	4	36.4	14	21	AAW26724	ATM kinase substra
272	4	36.4	11	22	AAJ00737	Hepatitis C virus	345	4	36.4	14	21	AAW86865	Human haematopoiet
273	4	36.4	11	22	AAJ02486	Hepatitis C virus	346	4	36.4	14	22	AAW98716	Human peptide #199
274	4	36.4	11	22	AAJ01538	Hepatitis C virus	347	4	36.4	14	22	AAW00343	Human protein frag
275	4	36.4	11	22	AAJ02159	Hepatitis C virus	348	4	36.4	14	22	ABP60225	Synthetic peptide
276	4	36.4	11	22	AAJ02474	Hepatitis C virus	349	4	36.4	14	24	ABP60225	peptide #1 derived
277	4	36.4	11	22	AAJ02672	Hepatitis C virus	350	4	36.4	15	18	AAW29480	peptide #2 derived
278	4	36.4	11	22	AAJ02807	Hepatitis C virus	351	4	36.4	15	18	AAW29481	Peptide #7 derived
279	4	36.4	11	23	AAW46191	Desmoglein-1 CAR S	352	4	36.4	15	18	AAW29486	Peptide #9 derived
280	4	36.4	11	23	AAW46192	Desmoglein-1 CAR S	353	4	36.4	15	18	AAW29488	Peptide resembling
281	4	36.4	11	23	AAW46198	Desmoglein-1 CAR S	354	4	36.4	15	18	AAW38936	Histone HIS-3 deri
282	4	36.4	11	23	AAW46199	Desmoglein-1 CAR S	355	4	36.4	15	20	AAV34043	Histone HIS-3 deri
283	4	36.4	11	23	AAW46219	Desmoglein-1 CAR S	356	4	36.4	15	20	AAV34044	Histone HIS-3 deri
284	4	36.4	11	23	AAW46220	Desmoglein-1 CAR S	357	4	36.4	15	20	AAV34050	Histone HIS-3 deri
285	4	36.4	11	23	AAW46225	Desmoglein-1 CAR S	358	4	36.4	15	20	AAV34052	Histone HIS-3 deri
286	4	36.4	11	23	AAW46227	Desmoglein-1 CAR S	359	4	36.4	15	20	AAV34063	Histone H1 isoform
287	4	36.4	11	23	AAW46247	Desmoglein-1 CAR S	360	4	36.4	15	20	AAV34064	Histone H1 isoform
288	4	36.4	11	23	AAW46248	Desmoglein-1 CAR S	361	4	36.4	15	20	AAW73962	Antigenic fragment
289	4	36.4	11	23	AAW46254	Desmoglein-1 CAR S	362	4	36.4	15	21	AAV98869	HLA class II bindi
290	4	36.4	11	23	AAW46255	Desmoglein-1 CAR S	363	4	36.4	15	21	AAV98870	HLA class II bindi
291	4	36.4	11	23	AAW46276	Desmoglein-1 CAR S	364	4	36.4	15	21	AAV57341	Human histone H1 p
292	4	36.4	11	23	AAW46276	Desmoglein-1 CAR S	365	4	36.4	15	21	AAV57342	Human histone H1 p
293	4	36.4	11	23	AAW46282	Desmoglein-1 CAR S	366	4	36.4	15	21	AAV57348	Human histone H1 p
294	4	36.4	11	23	AAW46283	Desmoglein-1 CAR S	367	4	36.4	15	21	AAV57350	Human histone H1 p
295	4	36.4	11	23	AAW46303	Desmoglein-1 CAR S	368	4	36.4	15	21	AAV57361	Human histone H1.5
296	4	36.4	11	23	AAW46304	Desmoglein-1 CAR S	369	4	36.4	15	21	AAV57362	Human histone H1.5
297	4	36.4	11	23	AAW46310	Desmoglein-1 CAR S	370	4	36.4	15	22	AAW64552	Human sugar transp
298	4	36.4	11	23	AAW46311	Desmoglein-1 CAR S	371	4	36.4	15	22	AAW64608	Human X chromosome
299	4	36.4	11	23	AAW46319	Desmoglein-3 CAR S	372	4	36.4	15	22	AAW88656	HER2/NEU DR superm
300	4	36.4	11	23	AAW46470	Desmoglein-3 CAR S	373	4	36.4	15	22	AAW89039	Her2/neu DR superm
301	4	36.4	11	23	AAW46474	Desmoglein-3 CAR S	374	4	36.4	15	22	AAW89040	Her2/neu DR superm

375	4	36.4	15	22	AAG8906.4	HR2/neu DR super1
376	4	36.4	15	22	AAG89120	HR2/neu HLA class
377	4	36.4	15	23	ABP93140	Beta lactamase 11
378	4	36.4	15	23	ABP98559	Human cell cycle c
379	4	36.4	15	23	ABG71682	N-terminal peptide
380	4	36.4	15	23	ABG71682	Human SBS5-rGAL-12
381	4	36.4	15	23	ABF28205	CXC chemokine rece
382	4	36.4	15	23	ABF52537	7p15-21 polycytop
383	4	36.4	15	23	ABJ22104	Human interleukin
384	4	36.4	15	23	ABB44241	Cysteine-X-cysteine
385	4	36.4	15	23	AAO13921	Human alpha-galact
386	4	36.4	15	23	AAE19270	Human TP-2 or IFP-3
387	4	36.4	15	23	AAE15177	Human YSK1 protei
388	4	36.4	15	23	AAE26130	Maize Starch synth
389	4	27.3	8	5	ABH66564	Sequence of cyclic
390	3	27.3	8	7	AAR43574	Amino acid pendant
391	3	27.3	8	7	AAP61399	Sequence of thromb
392	3	27.3	8	9	AAP61975	Synthetic substrat
393	3	27.3	8	10	AAP91784	Synthetic SCM-acti
394	3	27.3	8	10	AAP91784	Synthetic SCM-acti
395	3	27.3	8	10	AAP90545	Synthetic SCM-acti
396	3	27.3	8	10	AAP90689	Synthetic SCM-acti
397	3	27.3	8	10	AAP90684	Synthetic SCM-acti
398	3	27.3	8	10	AAP91779	Synthetic SCM-acti
399	3	27.3	8	10	AAP91781	Synthetic SCM-acti
400	3	27.3	8	10	AAP91782	Synthetic SCM-acti
401	3	27.3	8	12	AAR11094	LHRH pseudopeptid
402	3	27.3	8	12	AAR12511	IL2 p-asmidium sur
403	3	27.3	8	13	AAR37876	First eight amino
404	3	27.3	8	14	AAR43404	Ca/SSA epitope 262
405	3	27.3	8	14	AAR43404	Ca/SSA epitope 145
406	3	27.3	8	14	AAR43404	Sc B/B' epitope 47
407	3	27.3	8	14	AAR43404	Sc B/B' epitope 76
408	3	27.3	8	14	AAR43404	Sc B/B' epitope 77
409	3	27.3	8	14	AAR43500	Sm B/B' epitope 78
410	3	27.3	8	14	AAR43501	Sm B/B' epitope 79
411	3	27.3	8	14	AAR43502	Sm B/B' epitope 80
412	3	27.3	8	14	AAR43245	Cytotoxic T lympho
413	3	27.3	8	15	AAR43270	Plasma membrane ic
414	3	27.3	8	15	AAR48279	Protein P60(SF) c
415	3	27.3	8	15	AAR60208	Synthetic SCM-act
416	3	27.3	8	15	AAR69968	Peptide signal seq
417	3	27.3	8	15	AAR69450	Antiproliferative
418	3	27.3	8	16	AAR78840	P. taeniatum circ
419	3	27.3	8	16	AAR73357	Human TSH receptor
420	3	27.3	8	16	AAR73358	Human TSH receptor
421	3	27.3	8	16	AAR73359	Human TSH receptor
422	3	27.3	8	16	AAR72689	Human TSH receptor
423	3	27.3	8	16	AAR67910	Act1 2 phenylloxaz
424	3	27.3	8	16	AAR67910	Act1 2 phenylloxaz
425	3	27.3	8	16	AAR67910	Myeloperoxidase
426	3	27.3	8	16	AAR73484	Primer annealing
427	3	27.3	8	16	AAR67910	Lactoferrin horon
428	3	27.3	8	17	AAW11100	Alaroselective pl
429	3	27.3	8	17	AAR67910	CSF clone A19 Vbet
430	3	27.3	8	17	AAP91949	Phytase intercal p
431	3	27.3	8	18	AAI15871	Helicobacter pylor
432	3	27.3	8	18	AAW12494	Helicobacter pylor
433	3	27.3	8	18	AAW12494	Helicobacter pylor
434	3	27.3	8	18	AAW12494	Helicobacter pylor
435	3	27.3	8	18	AAW12494	Helicobacter pylor
436	3	27.3	8	18	AAW12494	Helicobacter pylor
437	3	27.3	8	18	AAW12494	Helicobacter pylor
438	3	27.3	8	18	AAW12494	Helicobacter pylor
439	3	27.3	8	18	AAW12494	Helicobacter pylor
440	3	27.3	8	18	AAW12494	Helicobacter pylor
441	3	27.3	8	18	AAW12494	Helicobacter pylor
442	3	27.3	8	18	AAW12494	Helicobacter pylor
443	3	27.3	8	19	AAW12494	Helicobacter pylor
444	3	27.3	8	19	AAW12494	Helicobacter pylor
445	3	27.3	8	19	AAW12494	Helicobacter pylor
446	3	27.3	8	19	AAW12494	Helicobacter pylor
447	3	27.3	8	19	AAW12494	Helicobacter pylor

ALIGNMENTS

RESULT 1

AAI86529 AAY88529 standard: peptide; 11 AA.
 ID AAY88529 standard: peptide; 11 AA.
 XX
 AC AAY88529
 XX
 DT 07-AUG 2000 (first entry)
 XX
 DE NCAM Iq1 binding peptide 14.
 XX
 KW NCAM: neural cell adhesion molecule; Iq1: immunoglobulin domain 1;
 KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
 KW impaired myelination; strokes; Parkinson's disease; memory; schizophrenia;
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
 KW treatment; prosthetic nerve guide; treatment; nervous system.

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XX OS Synthetic.
XX AC WO2000:8801-A2.
XX XX C6 APR-2000.
XX XX 23 SEP-1999; 99WO-DK00500.
XX PR 29 SEP 1998; 98DK-0001232.
XX PR 29 APR-1999; 99DK-0000592.
XX XX (RONN/) RONN L C B.
XX PA (BOCK/) BOCK E.
XX PA (HOLM/) HOLM A.
XX PA (OLSE/) OLSEN M.
XX PA (OSTE/) OSTERGAARD S.
XX PA (JENS/) JENSEN P H.
XX PA (POUL/) POULSEN F M.
XX PA (SORO/) SOROKA V.
XX PA (RALE/) RALETS I.
XX PA (BERE/) BEREZIN V.
XX PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
XX PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX XX WPI: 2000-293111/25.
XX PT Compositions that bind neural cell adhesion molecules useful for
XX PT treating disorders of the nervous system and muscles e.g. Alzheimer's
XX PT and Parkinson's diseases.
XX PS Claim 20; page 82; 119pp; English.
XX CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
XX CC NCAM is found in three forms, two of which are transmembrane forms, while
XX CC the third is attached via a lipid anchor to the cell membrane. All three
XX CC NCAM forms have an extracellular structure consisting five immunoglobulin
XX CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX CC N-terminal. The present sequence represents a peptide which binds to the
XX CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
XX CC NCAM Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
XX CC outgrowth from NCAM presenting cells, and is also capable of promoting the
XX CC proliferation of NCAM presenting cells. The compound may be used in
XX CC the treatment of normal, degenerated or damaged NCAM presenting cells.
XX CC The compound may in particular be used to treat diseases of the central
XX CC and peripheral nervous systems such as post operative nerve damage,
XX CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
XX CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
XX CC dementias, sclerosis, nerve degeneration associated with diabetes
XX CC mellitus, disorders affecting the circadian clock or neuro-muscular
XX CC transmission and schizophrenia. Conditions affecting the muscles may also
XX CC be treated with the compound, such as conditions associated with impaired
XX CC function of neuromuscular connections (e.g. genetic or traumatic shock or
XX CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX CC liver and bowel may also be treated using the compound. The compound is
XX CC learn, and to stimulate the memory of a subject.
XX SC Sequence 11 AA:
Query Match 100.0%; Score 11; Lb 21; Length 11;
Best Local Similarity 100.0%; Fred. No. 1.4e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKALNWGAKPK 11
Db 1 AKALNWGAKPK 11
RESULT 2
AAY88563

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ID AAY88563 standard: peptide: 11 AA.
XX AC AAY88563;
XX DT 07-AUG-2000 (first entry)
XX XX NCAM Ig1 binding peptide D4 used as a control peptide.
XX DE NCAM: neural cell adhesion molecule; Ig1: immunoglobulin domain 1;
XX KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
XX KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
XX KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
XX KW treatment; prosthetic nerve guide; treatment; nervous system.
XX OS Synthetic.
XX PN WO2000:8801-A2.
XX XX C6-APR-2000.
XX PD 23-SEP-1999; 99WO-DK00500.
XX PF 29-SEP-1998; 98DK-0001232.
XX PR 29-APR-1999; 99DK-0000592.
XX XX (RONN/) RONN L C B.
XX PA (BOCK/) BOCK E.
XX PA (HOLM/) HOLM A.
XX PA (OLSE/) OLSEN M.
XX PA (OSTE/) OSTERGAARD S.
XX PA (JENS/) JENSEN P H.
XX PA (POUL/) POULSEN F M.
XX PA (SORO/) SOROKA V.
XX PA (RALE/) RALETS I.
XX PA (BERE/) BEREZIN V.
XX PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
XX PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX XX WPI: 2000-293111/25.
XX PT Compositions that bind neural cell adhesion molecules useful for
XX PT treating disorders of the nervous system and muscles e.g. Alzheimer's
XX PT and Parkinson's diseases.
XX PS Example 5; Fig 7; 119pp; English.
XX CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
XX CC NCAM is found in three forms, two of which are transmembrane forms, while
XX CC the third is attached via a lipid anchor to the cell membrane. All three
XX CC NCAM forms have an extracellular structure consisting five immunoglobulin
XX CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX CC N-terminal. The invention relates to a compound containing a peptide
XX CC which binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2
XX CC domains, and is capable of stimulating or promoting neurite outgrowth
XX CC from NCAM presenting cells, and is also capable of promoting the
XX CC proliferation of NCAM presenting cells. The present sequence represents a
XX CC control peptide used in the identification of those binding peptides
XX CC which can be used in the compound. The compound may be used in the
XX CC treatment of normal, degenerated or damaged NCAM presenting cells. The
XX CC compound may in particular be used to treat diseases of the central and
XX CC peripheral nervous systems such as post operative nerve damage, traumatic
XX CC nerve damage, impaired myelination of nerve fibres, conditions resulting
XX CC from a stroke, Parkinson's disease, Alzheimer's disease, dementias,
XX CC sclerosis, nerve degeneration associated with diabetes mellitus,
XX CC disorders affecting the circadian clock or neuro-muscular transmission
XX CC and schizophrenia. Conditions affecting the muscles may also be treated
XX CC with the compound, such as conditions associated with impaired function
XX CC of neuromuscular connections (e.g. genetic or traumatic shock or
XX CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX CC liver and bowel may also be treated using the compound. The compound is
XX CC used in a prosthetic nerve guide, and also to stimulate the ability to

```

CC learn, and to stimulate the memory of a subject.

XX Sequence 11 AA;
SQ Query Match 100.0%; Score 11; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAALNWGAKPK 11
IIII IIIII
DB 1 ARAALNWGAKPK 11

RESULT 4
AB659331
ID AB659331 standard; Peptide: 11 AA.

XX AC AB659331;

QY 21-OCT-2002 (first entry)

DE Human neural cell adhesion molecule (NCAM) peptide #3

XX Human neural cell adhesion molecule; NCAM; heart muscle cell survival;
KW acute myocardial infarction; central nervous system disorder; stroke;
KW peripheral nervous system disorder; postoperative nerve damage;
KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;
KW postischemic damage; multifactorial dementia; multiple sclerosis;
KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW atrophic muscle disorder; gonad degeneration; nephrosis.

XX OS Homo sapiens.

XX XX Homo sapiens.

PN WO200247719-A2.

XX 20 JUN-2002.

PP 12-DEC-2001; 2001WO-DK00822.

XX 12-DEC-2000; 2000DK-0001863.

PR (ENKA) ENKAM PHARM AS.

PA Roek E. Berezin V. Kohler LB;

XX WPI: 2002-583473/62.

XX Use of a compound comprising a peptide of neural cell adhesion molecule, in the preparation of a medicament for prevention death of cells presenting NCAM or NCAM ligand and related central nervous system diseases

PS Claim 26; page 39; 57pp; English.

XX The invention relates to use of a compound (I) comprising a peptide which comprises at least 5 contiguous amino acid residues of a sequence of the neural cell adhesion molecule (NCAM), its fragment, variant or its mimic, for the preparation of a medicament for preventing death of cells presenting the NCAM or an NCAM ligand (I) is useful in the preparation of a medicament for preventing death of cells presenting the NCAM or an NCAM ligand. The medicament is for the stimulation of the survival of heart muscle cells, such as survival after acute myocardial infarction. The medicament is for the treatment of diseases of conditions of the central and peripheral nervous system, such as postoperative nerve damage, traumatic nerve damage, etc. resulting from spinal cord injury. Impaired myelination of nerve fibres, postischemic damage, e.g. resulting from a stroke, multifactorial dementia, multiple sclerosis, nerve degeneration associated with diabetes mellitus, neuro-muscular degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and Huntington's disease. The medicament is for the treatment of diseases or conditions of the muscles including conditions with impaired function of neuro-muscular connections, such as genetic or traumatic atrophic

CC muscle disorders, and for the treatment of diseases of conditions of various organs, such as degenerative conditions of the gonads, pancreas (e.g. diabetes mellitus type I and II) and kidney (e.g. nephrosis).

CC AB659329-AB659352 represent human NCAM peptides of the invention.

XX SQ Sequence 11 AA;
Query Match 100.0%; Score 11; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAALNWGAKPK 11
IIII IIIII
DB 1 ARAALNWGAKPK 11

RESULT 4

AAW75820

XX ID AAW75820 standard; peptide: 8 AA.

XX AC AAW75820;

QY 27-OCT-1998 (first entry)

DE Mouse mast cell protease (mMCP-6) susceptible peptide 14.

XX Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;
KW tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;
KW antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
KW hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;
KW inflammatory skin condition.

XX CS Synthetic.

XX CS Mus SP.

PN WO9833812 A1.

XX 06-AUG-1998.

PP 30-JAN-1998; 98WO-US01865.

XX 05-FEB-1997; 97JS-CO07090.

PR (BGHM) BRIGHAM & WOMENS HOSPITAL.

PA Huang C. Stevens RL;

XX WPI: 1998-437390/37.

XX Tryptase 6 complex inhibitory peptides - used to treat mast cell-mediated inflammatory disorders e.g. asthma

PS Examples; Page 26; 69pp; English.

XX Sequences shown in AAW75807 to AAW75835 represent mouse mast cell protease (mMCP-6) susceptible peptides obtained in the absence of heparin. The invention provides sequences shown in AAW63160 to AAW63169 that are inhibitors of mMCP-6. These tryptase-6 complex inhibitor peptides can be used for treating a mast cell-mediated inflammatory disorder. The inhibitors can be used to treat inflammatory disorders including asthma, allergic rhinitis, urticaria and antioedema, eczematous dermatitis (atopic dermatitis), hyperproliferative skin disease, anaphylaxis, peptic ulcers, inflammatory bowel disorder, hyperresponsiveness and inflammatory skin conditions.

XX SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAAL 4
I.III

```

10 4 ARAL 7
11
12 RESULT 5
13 AAJ01170
14 ID AAJ01170 standard; Peptide; 8 AA.
15 AC AAJ01170.
16 XX
17 XX 02-JUL-2001 (first entry)
18 XX
19 XX Hepatitis C virus epitope #116.
20 XX
21 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA binding motif;
22 KW antiviral.
23 XX
24 XX Hepatitis C virus.
25 OS
26 XX
27 XX W0200121189-A1.
28 PN
29 XX
30 XX 29-MAR-2001.
31 PD
32 XX
33 XX 19-JUL-2000; 2000WO-US19774.
34 PF
35 XX
36 XX 19-JUL-1999; 99US-0357737.
37 PR
38 XX (EPIM ) EPIIMUNE INC.
39 PA
40 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
41 PI Baker DM, Cellis E, Kubo RT, Grey HM;
42 XX
43 XX WPI: 2001-308046/32.
44 DR
45 XX
46 XX A new composition useful as a vaccines against hepatitis C virus
47 PT
48 XX
49 XX Disclosure; Page 154; 214pp; English.
50 PS
51 XX The present invention describes a composition comprising a prepared
52 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
53 CC These are derived from HCV HLA-binding motifs. They are useful in
54 CC vaccines for the prevention and treatment of HCV infection in humans. The
55 CC present sequence is an epitope used in the disclosure of the invention.
56 XX
57 XX Sequence 8 AA;
58 SQ
59
60 Query Match 36.4%; Score 4; DB 22; Length 8;
61 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
62 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
63
64 QY 1 ARAL 4
65 DB 1111
66 3 ARAL 5
67
68 RESULT 7
69 AAJ02181
70 ID AAJ02181 standard; Peptide; 8 AA.
71 XX
72 XX AAJ02181;
73 AC
74 XX
75 XX 02-JUL-2001 (first entry)
76 DT
77 XX
78 XX Hepatitis C virus epitope #2172.
79 DE
80 XX
81 XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
82 KW antiviral.
83 KW
84 XX
85 XX Hepatitis C virus.
86 OS
87 XX
88 XX W0200121189-A1.
89 PN
90 XX
91 XX 29-MAR-2001.
92 PD
93 XX
94 XX 19-JUL-2000; 2000WO-US19774.
95 PF
96 XX
97 XX 19-JUL-1999; 99US-0357737.
98 PR
99 XX (EPIM-) EPIIMUNE INC.
100 PA
101 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
102 PI Baker DM, Cellis E, Kubo RT, Grey HM;
103 XX
104 XX WPI: 2001-308046/32.
105 DR
106 XX
107 XX A new composition useful as a vaccines against hepatitis C virus
108 PT
109 XX
110 XX Disclosure; Page 154; 214pp; English.
111 PS
112 XX The present invention describes a composition comprising a prepared
113 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
114 CC These are derived from HCV HLA-binding motifs. They are useful in
115 CC vaccines for the prevention and treatment of HCV infection in humans. The
116 CC present sequence is an epitope used in the disclosure of the invention.
117 XX
118 XX Sequence 8 AA;
119 SQ

```



```

Query Match          36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARAL 4
DB      4 ARAL 7

RESULT 8
AAJ02671
ID AAJ0267; standard; Peptide: 8 AA.
AC AAJ02671;
XX
XX
DT 02-JUL-2001 (first entry)
DE
DE Hepatitis C virus epitope #2662.
XX
XX Hepatitis C virus; HCV; epitope: vaccine; immunization; HLA binding motif;
XX antiviral.
XX
XX Hepatitis C virus.
XX
XX W020012189-A2.
XX
XX 29 MAR 2001.
XX
XX 19-JUL-2000; 2000WO-US19774.
XX
XX 19-JUL-1999; 99US-0357737.
XX
XX (EPIM- ) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BB, Chesnut R;
XX Baker DM, Cells E, Kubo RT, Grey HM;
XX
XX WPI: 2001-108046/32.
XX
XX A new composition useful as a vaccine against hepatitis C virus
XX
XX Disclosure: Page 166; 214pp; English.
XX
XX The present invention describes a composition comprising a prepared
XX hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
XX These are derived from HCV HLA-binding motifs. They are useful in
XX vaccines for the prevention and treatment of HCV infection in humans. The
XX present sequence is an epitope used in the disclosure of the invention.
XX
SQ Sequence 8 AA;

Query Match          36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARAL 4
DB      3 ARAL 6

RESULT 9
ABH84505
ID ABH84505 standard; Protein; 8 AA.
XX
XX ABH84505;
AC
XX
XX 09-JAN-2003 (first entry)
XX
XX Encephalomyocarditis virus autocatalytic peptide cleavage site #2.
DE
DE Replacon; structural region; vaccine; subgenomic replicon; gene therapy;
XX structural protein; C protein; PreM protein; E protein; immunisation.

```

```

XX Encephalomyocarditis virus.
OS
XX W0200272803-A2.
PN
XX 19-SEP-2002.
PD
XX
XX 21-FEB-2002; 2002WO-US06962.
PF
XX
XX 09-MAR-2001; 2001US-274584P.
PR
XX
XX (USSR ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Pang X, Dayton AI, Zhang M;
PI
XX
XX WPI: 2002-723344/78.
DR
XX
XX New subgenomic replicon of dengue virus origin comprising a deletion
PT for the sequence coding for C, PreM and/or E structural proteins.
PT useful as vaccines for immunization against dengue virus infection.
XX
XX Disclosure: Page 12; 66pp; English.
XX
XX This invention describes a novel subgenomic replicon of dengue virus
CC origin comprising a deletion for the sequence coding for C, PreM and E
CC (DeltaCME), for PreM and E (DeltaME), or for E (DeltaE) structural
CC proteins, and/or which is adapted to receive at least a nucleotide
CC sequence without disrupting its replication capabilities. The products
CC of the invention can be used for constructing (1) a vaccine or a
CC therapeutic comprising the subgenomic replicon and a carrier; (2) a
CC dengue virus-like particle comprising the subgenomic replicon, and
CC structural proteins of the homologous dengue virus, which encapsulates
CC the subgenomic replicon; and (3) methods of immunisation and treatment
CC comprising administering to the individual the subgenomic replicon or
CC the dengue virus like particle cited above. The subgenomic replicons are
CC useful in gene therapy as vaccines for immunisation against dengue virus
CC infection. This sequence represents an Encephalomyocarditis virus strain
CC B autocatalytic peptide cleavage site which can be added to the
CC subgenomic replicon of the invention to optimise expression of desired
CC foreign proteins.
XX
XX Sequence 8 AA;

Query Match          36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 AKPK 11
DB      4 AKPK 7

RESULT 10
AAG79508
ID AAG79508 standard; peptide: 8 AA.
AC
XX
XX AAG79508;
AC
XX
XX 29-NOV-2002 (first entry)
DT
XX
XX C. trachomatis epitopic peptide #1.
DE
XX
XX Epitope: Chlamydia trachomatis; serovar; medicine; infection; human.
XX
XX Chlamydia trachomatis.
XX
XX W0200265129-A2.
XX
XX 22-AUG-2002.
PD
XX
XX 12-FEB-2002; 2002WO-GB000600.
PF
XX
XX 12-FEB-2001; 2001GB-0003387.
PR

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XX (YABA-) YABA LTD.
 XX Jones GE;
 XX WPI: 2002-667025/71.
 XX
 XX Epitopic sequences useful in the diagnosis, prognosis and treatment of
 PT infections, which bind specifically to human antibodies against
 PT Chlamydia trachomatis -
 PS
 PS Example 1: Page 28; 39pp; English.
 XX
 CC The sequences given in AAC79508-21 are epitopic peptides which were
 CC tested for binding specificity using rabbit serum rather than human
 CC serum. These peptides bind specifically to human antibodies against
 CC Chlamydia trachomatis. The epitopic sequences of the invention are
 CC able to distinguish between infections with the different serovars of
 CC Chlamydia trachomatis (including species-specific and/or serovar-specific
 CC and/or chlamydial hsp60-specific antibody) in a biological sample derived
 CC from the subject, and are also able to identify chronic forms of
 CC infection, compared to the prior art methods. The epitopic peptides may
 CC be used in medicine, for use in diagnosis of infection of a human subject
 CC by C. trachomatis using a biological sample (e.g. blood, saliva, mucus
 CC or other body fluid, or tissue or any other solubilisable sample which
 CC might contain antibodies to C. trachomatis) derived from the subject,
 CC for determining the susceptibility of a subject to develop a chronic
 CC C. trachomatis infection with reference to the presence or absence of
 CC at least one specific serovar in the subject, and for the detection of
 CC an antibody against C. trachomatis in a biological sample.
 XX
 SQ Sequence 8 AA:
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GAKP 10
 DE i i i
 2 GAKP 5
 RESULT 11
 ABB45444
 ID ABB45444 standard; Peptide: 8 AA.
 XX
 XX ABB45444:
 XX
 XX 30 JAN-2002 (first entry)
 XX Desmoglein-1 CAR peptide SEQ ID NO 163
 DE
 DE Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW Cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis.
 XX
 XX Synthetic.
 XX W0200172956-A2.
 XX 04 OCT-2001.
 XX 27-MAR-2001; 2001WO-1601400.
 XX 27-MAR-2000; 2000US-0535852.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk GW, Symonds JM, Gouri HC;
 XX WPI: 2002-025778/03.
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 XX Claim 15; Page 95; 127pp; English.
 XX
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB4544-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA:
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RAIN 5
 DE i i i
 2 RAIN 5
 RESULT 12
 ABB45444
 ID ABB45444 standard; Peptide: 8 AA.
 XX
 XX ABB45444:
 XX
 XX 30 JAN-2002 (first entry)
 XX Desmoglein-1 CAR peptide SEQ ID NO 163.
 DE
 DE Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW Cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis.
 XX
 XX Synthetic.
 XX W0200172956-A2.
 XX 04 OCT-2001.
 XX 27-MAR-2001; 2001WO-1601400.
 XX 27-MAR-2000; 2000US-0535852.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk GW, Symonds JM, Gouri HC;
 XX WPI: 2002-025778/03.
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 XX Claim 15; Page 95; 127pp; English.
 XX
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB4544-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment

CC that specifically binds a desmosomal cadherin CAR sequence and/or a
CC polynucleotide encoding a polypeptide that comprises a desmosomal
CC cadherin CAR sequence or analogue. The modulating agents have
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC facilitate wound healing and/or reduce scar tissue, for enhancing
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC treating an autoimmune blistering disorder and to treat cancer
CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
XX

SQ Sequence: 8 AA:

Query Match: 36.4%; Score: 4; ID: 24; Length: 10
Best Local Similarity: 100.0%; Pred. X-axis: 0.00
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0

QY 2 KALN 5
Gd 2 KALN 5

RESULTS

ABB45448
ID ABB45448 standard; Peptide: 8 AA.
XX
AC ABB45448;
XX
DI 10 JAN-2002 (first entry)
XX
DE Desmoglein 1 CAR peptide SEQ ID No 167.
XX
KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytoskeletal; antiapoptotic; wound healing; reduce scar tissue;
KW skin grafts; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis.
XX
OS Synthesized.
XX
PN WU200172953-AZ.
XX
ID 14-OCT-2001.
XX
XX 27-MAR-2001: 2001WO-1801400.
XX
XX 27-MAR-2000: 2000US-0535952.
XX
XX (ADDEX) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuk CW, Symonds JM, Gour RJ:
XX WPI: 2002-025776/03.
XX
XX Modulating agents for inhibiting or enhancing desmosomal cadherin
XX mediated cell adhesion, useful for facilitating wound healing and/or
XX reducing scar tissue, treating cancer and inducing apoptosis
XX
XX Claim 15; Page 95; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing
XX desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX comprising a desmosomal cadherin cell adhesion domain CAR sequence
XX (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
XX sequence, a substance such as an antibody or antigen binding fragment
XX that specifically binds a desmosomal cadherin CAR sequence and/or a
XX polynucleotide encoding a polypeptide that comprises a desmosomal
XX cadherin CAR sequence or analogue. The modulating agents have
XX immunosuppressive, cytostatic and antiapoptotic activity and are used to
XX facilitate wound healing and/or reduce scar tissue, for enhancing
XX adhesion of foreign tissue implants (e.g. skin graft or organ implant),
XX treating an autoimmune blistering disorder and to treat cancer
XX (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
XX

XX SQ Sequence: 8 AA:

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ID  ABB45455 standard; Peptide: 8 AA.
XX
AC  ABB45455;
XX
DE  10 JAN-2002 (first entry)
XX
XY  Desmoglein-1 CAR peptide SEQ ID NO 174.
XX
KW  Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW  cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW  skin graft; organ implant; autoimmune blistering disorder; cancer;
KW  apoptosis.
XX
OS  Synthetic.
XX
XX  WO200172956-A2.
XX
PC  04-OCT-2001.
XX
PF  27-MAR-2001; 2001WO-1B01400.
XX
PR  27-MAR-2000; 2000US-0535852.
XX
PA  (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI  Blaschuk CM, Symonds JM, Gout BJ;
XX  WPI: 2002-025778/03.
XX
PT  Modulating agents for inhibiting or enhancing desmosomal cadherin
PT  mediated cell adhesion, useful for facilitating wound healing and/or
PT  reducing scar tissue, treating cancer and inducing apoptosis.
XX
PS  Claim 15; Page 95; 127pp; English.
XX
CC  The invention relates to modulating agents for inhibiting or enhancing
CC  desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC  comprising a desmosomal cadherin cell adhesion recognition CAR sequence
CC  (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
CC  sequence, a substance such as an antibody or antigen-binding fragment
CC  that specifically binds a desmosomal cadherin CAR sequence and/or a
CC  polynucleotide encoding a polypeptide that comprises a desmosomal
CC  cadherin CAR sequence or analogue. The modulating agents have
CC  immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC  facilitate wound healing and/or reduce scar tissue, for enhancing
CC  adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC  treating an autoimmune blistering disorder and to treat cancer
CC  (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX
SQ  Sequence 8 AA:

Query Match 36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
DB 1111
3 RALN 6

RESULT 17
APR45489
ID  APR45489 standard; Peptide: 8 AA.
XX
AC  APR45489;
XX
DE  30-JAN-2002 (first entry)
XX
DE  Desmoglein-3 CAR peptide SEQ ID NO 208.
XX
KW  Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW  cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW  skin graft; organ implant; autoimmune blistering disorder; cancer;
KW  apoptosis.
XX
OS  Synthetic.
XX
XX  WO200172956-A2.
XX
PC  04-OCT-2001.
XX
PF  27-MAR-2001; 2001WO-1B01400.
XX
PR  27-MAR-2000; 2000US-0535852.
XX

```

XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Symonds JM, Gour BJ;
 XX WPI: 2002-025778/03.
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 XX Claim 15; Page 96; 127pp; English.
 XX
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 XX Sequence 8 AA;
 XX
 XX Query Match 36.4%; Score 4; DB 23; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 RALN 5
 XX IIII
 XX Db 2 RALN 5
 XX
 XX RESULT 18
 XX ABB45490
 XX ID ABB45490 standard; Peptide: 8 AA;
 XX AC ABB45490;
 XX DT 30-JAN-2002 (first entry)
 XX DE Desmoglein-3 CAR peptide SEQ ID NO 205;
 XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis.
 XX OS Synthetic.
 XX PN W0200172956-A2.
 XX PD 04-OCT-2001.
 XX PF 27-MAR-2001; 2001WO-1B01400.
 XX PR 27-MAR-2000; 2000US-0535852.
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX PI Blaschuk OW, Symonds JM, Gour BJ;
 XX WPI: 2002-025778/03.
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX

PS Claim 15; Page 96; 127pp; English.
 XX
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 XX Sequence 8 AA;
 XX
 XX Query Match 36.4%; Score 4; DB 23; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 RALN 5
 XX IIII
 XX Db 2 RALN 5
 XX
 XX RESULT 19
 XX ABB45494
 XX ID ABB45494 standard; Peptide: 8 AA;
 XX AC ABB45494;
 XX DT 30-JAN-2002 (first entry)
 XX DE Desmoglein-3 CAR peptide SEQ ID NO 213.
 XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis.
 XX OS Synthetic.
 XX PN W0200172956-A2.
 XX PD 04-OCT-2001.
 XX PF 27-MAR-2001; 2001WO-1B01400.
 XX PR 27-MAR-2000; 2000US-0535852.
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX PI Blaschuk OW, Symonds JM, Gour BJ;
 XX WPI: 2002-025778/03.
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 XX Claim 15; Page 96; 127pp; English.
 XX
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to

CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA;

Query Match

Best Local Similarity 36.4%; Score 4; DB 23; Length 8;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 3 RALN 6

RESULT 20

ABB45495

ID ABB45495 standard; Peptide: 8 AA.

XX ABB45495;

AC (first entry)

DE Desmoqlein-3 CAR peptide SEQ ID NO: 214

XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytotatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis.

XX Synthetic.

OS WO200172956-A2.

PN 04-OCT-2001.

XX 27-MAR-2001; 2001WO-IB01400.

XX 27-MAR-2000; 2000US-0535852.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Symonds JM, Gour BJ.

XX WPI; 2002-025778/03.

XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PI mediated cell adhesion, useful for facilitating wound healing and/or
 PI reducing scar tissue, treating cancer and inducing apoptosis -

XX Claim 15; Page 96; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX

Sequence 8 AA:

Query Match

Best Local Similarity 36.4%; Score 4; DB 23; Length 8;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 3 RALN 6

RESULT 21

ABB45500

ID ABB45500 standard; Peptide: 8 AA.

XX ABB45500;

DE 30-JAN-2002 (first entry)

DE Desmoqlein-3 CAR peptide SEQ ID NO: 219.

XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytotatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis.

XX Synthetic.

OS WO200172956-A2.

PN 04-OCT-2001.

XX 27-MAR-2001; 2001WO-IB01400.

XX 27-MAR-2000; 2000US-0535852.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Symonds JM, Gour BJ.

XX WPI; 2002-025778/03.

XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PI mediated cell adhesion, useful for facilitating wound healing and/or
 PI reducing scar tissue, treating cancer and inducing apoptosis -

XX Claim 15; Page 96; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX

Sequence 8 AA:

Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 4 RALN 7

RESULT 22

ABB46175

ID ABB46175 standard; Peptide: 8 AA.

XX ABB46175;

XX

```

DT 30-JAN-2002 (first entry)
DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 919.
XX
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW skin graft; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis; cyclic.
XX
XX Synthetic.
XX
XX WO200172956-A2.
XX
XX PD 04-OCT-2001.
XX
XX PF 27-MAR-2001; 2001WO-1B01400.
XX
XX PR 27-MAR-2000; 2000US-0535852.
XX
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX PI Blaschuk OW, Symonds JM, Gour BJ.
XX
XX PR 27-MAR-2000; 2000US-0535852.
XX
XX PS Claim 18; Page 100; 127pp; English.
XX
XX The invention relates to modulating agents for inhibiting or enhancing
XX desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX comprising a desmosomal cadherin cell adhesion recognition CAR sequence
XX (AB45341-AB47262), a non-peptide mimetic of a desmosomal cadherin CAR
XX sequence, a substance such as an antibody or antigen-binding fragment
XX that specifically binds a desmosomal cadherin CAR sequence and/or a
XX polynucleotide encoding a polypeptide that comprises a desmosomal
XX cadherin CAR sequence or analogue. The modulating agents have
XX immunosuppressive, cytostatic and antiapoptotic activity and are used to
XX facilitate wound healing and/or reduce scar tissue, for enhancing
XX adhesion of foreign tissue implants (e.g. skin graft or organ implant),
XX treating an autoimmune blistering disorder and to treat cancer
XX (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX
XX Sequence 8 AA:
XX
XX Query Match 36.4%; Score 4; DR 23; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 RAIN 5
XX
XX DB 2 RAIN 5
XX
XX
XX
XX RESULT 24
XX AB46176
XX ID AB46176 standard; Peptide: 8 AA.
XX
XX AC A5H46176;
XX
XX DT 30 JAN-2002 (first entry)
XX
XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 920.
XX
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW skin graft; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis; cyclic.
XX
XX OS Synthetic.
XX
XX PN WO200172956-A2.
XX
XX PD 04-OCT-2001.
XX
XX PF 27-MAR-2001; 2001WO-1B01400.
XX
XX PR 27-MAR-2000; 2000US-0535852.
XX
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX PI Blaschuk OW, Symonds JM, Gour BJ.

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XX WPI: 2002-025778/03.
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer, and inducing apoptosis.
 XX Claim 18: Page 100; 127pp; English.
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX Sequence 8 AA:
 SQ
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Prod. No. 9.3e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RALN 5
 ID IIII
 DB 3 RALN 6
 Desmoqlein-1 CAR sequence cyclic peptide SEQ ID NO 931.
 Desmosomal cadherin: cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX Synthetic.
 XX WO200172956-A2.
 XX 04-OCT-2001.
 XX 27-MAR-2001; 2001WO-1B01400.
 XX 27-MAR-2000; 2000US-0535852.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Symonds JM, Gour BJ;
 WPI: 2002-025778/03.
 Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer, and inducing apoptosis.
 XX Claim 18: Page 100; 127pp; English.
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX Sequence 8 AA:
 SQ
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Prod. No. 9.3e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RALN 5
 ID IIII
 DB 3 RALN 6
 Desmoqlein-1 CAR sequence cyclic peptide SEQ ID NO 931.
 Desmosomal cadherin: cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX Synthetic.
 XX WO200172956-A2.
 XX 04-OCT-2001.
 XX 27-MAR-2001; 2001WO-1B01400.
 XX 27-MAR-2000; 2000US-0535852.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Symonds JM, Gour BJ;
 WPI: 2002-025778/03.
 Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer, and inducing apoptosis.
 XX Claim 18: Page 100; 127pp; English.
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX Sequence 8 AA:
 SQ

CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX Sequence 9 AA:
 SQ
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Prod. No. 9.3e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RALN 5
 ID IIII
 DB 4 RALN 7
 Desmoqlein-1 CAR sequence cyclic peptide SEQ ID NO 938.
 Desmosomal cadherin: cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX Synthetic.
 XX WO200172956-A2.
 XX 04-OCT-2001.
 XX 27-MAR-2001; 2001WO-1B01400.
 XX 27-MAR-2000; 2000US-0535852.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Symonds JM, Gour BJ;
 WPI: 2002-025778/03.
 Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis.
 XX Claim 18: Page 100; 127pp; English.
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX Sequence 9 AA:
 SQ


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XX SQ Sequence 8 AA:
Query Match 36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
DB 4 RALN 7

RESULT 27
ABB46203
ID ABB46203 standard; Peptide: 8 AA.
XX AC ABB46203;
XX DT 30-JAN-2002 (first entry)
XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 947.
XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
XX KW cytosstatic; antiapoptotic; wound healing; reduce scar tissue;
XX KW skin graft; organ implant; autoimmune blistering disorder; cancer;
XX KW apoptosis; cyclic.
XX OS Synthetic.
XX PN WO200172956-A2.
XX PD 04-OCT 2001.
XX PF 27-MAR-2001; 2001WO-1B01400.
XX PR 27-MAR-2000; 2000US-0535852.
XX PA (ADHEX) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuk OW, Symonds JM, Gaur RJ;
XX DR WPI: 2002-025778/03.
XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin
PT mediated cell adhesion, useful for facilitating wound healing and/or
PT reducing scar tissue, treating cancer and inducing apoptosis.
XX PS Claim 13; Page 100; 127pp; English.
XX CC The invention relates to modulating agents for inhibiting or enhancing
XX CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
XX CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
XX CC sequence, a substance such as an antibody or antigen-binding fragment
XX CC that specifically binds a desmosomal cadherin CAR sequence and/or a
XX CC polynucleotide encoding a desmosomal cadherin CAR sequence and/or a
XX CC cadherin CAR sequence or analogue. The modulating agents have
XX CC immunosuppressive, cytosstatic and antiapoptotic activity and are used to
XX CC facilitate wound healing and/or reduce scar tissue, for enhancing
XX CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
XX CC treating an autoimmune blistering disorder and to treat cancer
XX CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX SQ Sequence 8 AA:
Query Match 36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
DB 2 RALN 5

RESULT 28
ABB46204
ID ABB46204 standard; Peptide: 8 AA.
XX AC ABB46204;
XX DT 30-JAN-2002 (first entry)
XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 948.
XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
XX KW cytosstatic; antiapoptotic; wound healing; reduce scar tissue;
XX KW skin graft; organ implant; autoimmune blistering disorder; cancer;
XX KW apoptosis; cyclic.
XX OS Synthetic.
XX PN WO200172956-A2.
XX PD 04-OCT 2001.
XX PF 27-MAR-2001; 2001WO-1B01400.
XX PR 27-MAR-2000; 2000US-0535852.
XX PA (ADHEX) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuk OW, Symonds JM, Gaur RJ;
XX DR WPI: 2002-025778/03.
XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin
PT mediated cell adhesion, useful for facilitating wound healing and/or
PT reducing scar tissue, treating cancer and inducing apoptosis.
XX PS Claim 18; Page 100; 127pp; English.
XX CC The invention relates to modulating agents for inhibiting or enhancing
XX CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
XX CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
XX CC sequence, a substance such as an antibody or antigen-binding fragment
XX CC that specifically binds a desmosomal cadherin CAR sequence and/or a
XX CC polynucleotide encoding a desmosomal cadherin CAR sequence and/or a
XX CC cadherin CAR sequence or analogue. The modulating agents have
XX CC immunosuppressive, cytosstatic and antiapoptotic activity and are used to
XX CC facilitate wound healing and/or reduce scar tissue, for enhancing
XX CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
XX CC treating an autoimmune blistering disorder and to treat cancer
XX CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX SQ Sequence 8 AA:
Query Match 36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
DB 2 RALN 5

RESULT 29
ABB46209
ID ABB46209 standard; Peptide: 8 AA.
XX AC ABB46209;
XX DT 30-JAN-2002 (first entry)
XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 953.
XX
```

KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX Synthetic.
 CS
 XX WO2001:72956-A2.
 PN
 XX 04-OCT-2001.
 PU
 XX
 XX 27-MAR-2001; 2001WO-IB01400.
 PF
 XX
 XX 27-MAR-2000; 2000US-0535852.
 PR
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 PA
 PI Blaschuk OW, Symonds JM, Gour BJ;
 XX WPI: 2002-025778/03.
 DR
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 PT
 XX Claim 18: Page 100; 127pp: English.
 PS
 XX The invention relates to modulating agents for inhibiting or enhancing
 XX desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA:
 Query Match 36.4%, Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RALN 5
 LB IIII
 3 RALN 6
 RESULT 30
 ABB46215
 ID ABB46215 standard; Peptide; 8 AA.
 XX
 AC ABB46215;
 XX
 XX 30-JAN-2002 (first entry)
 UT
 XX Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 959.
 DE
 XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX Synthetic.
 OS
 XX WO2001:72956-A2.
 PN
 XX 04-OCT-2001.
 PU
 XX
 XX 27-MAR-2001; 2001WO-IB01400.
 PF
 XX
 XX 27-MAR-2000; 2000US-0535852.
 PR
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 PA
 PI Blaschuk OW, Symonds JM, Gour BJ;
 XX WPI: 2002-025778/03.
 DR
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 PT
 XX Claim 18: Page 100; 127pp: English.
 PS
 XX The invention relates to modulating agents for inhibiting or enhancing
 XX desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA:
 Query Match 36.4%, Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RALN 5
 LB IIII
 3 RALN 6

PF 27-MAR-2001; 2001WO-IB01400.
 XX
 XX 27-MAR-2000; 2000US-0535852.
 PR
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 PA
 PI Blaschuk OW, Symonds JM, Gour BJ;
 XX WPI: 2002-025778/03.
 DR
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 PT
 XX Claim 18: Page 100; 127pp: English.
 PS
 XX The invention relates to modulating agents for inhibiting or enhancing
 XX desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA:
 Query Match 36.4%, Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RALN 5
 DB IIII
 4 RALN 7
 RESULT 31
 ABB46222
 ID ABB46222 standard; Peptide; 8 AA.
 XX
 AC ABB46222;
 XX
 XX 30-JAN-2002 (first entry)
 DI
 XX Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 966.
 DE
 XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX Synthetic.
 OS
 XX WO2001:72956-A2.
 PN
 XX 04-OCT-2001.
 PU
 XX
 XX 27-MAR-2001; 2001WO-IB01400.
 PF
 XX
 XX 27-MAR-2000; 2000US-0535852.
 PR
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 PA
 PI Blaschuk OW, Symonds JM, Gour BJ;
 XX WPI: 2002-025778/03.
 DR
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 PT

PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 PS Claim 18: Page 100; 127pp; English.
 XX
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue. For enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer;
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 4 RALN 7

RESULT 32
 ABB46231
 ID ABB46231 standard; Peptide: 8 AA.
 XX
 AC ABB46231;
 XX
 LT 30 JAN-2002 (first entry)
 XX
 DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 975.
 XX
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX
 OS Synthetic.
 XX
 PN W0200172956-A2.
 XX
 PP 04 OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-1801400.
 XX
 PR 27-MAR-2000; 2000US-0535852.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Symonds JM, Gour BJ;
 XX
 DR WPI: 2002-025778/03.
 XX
 PT Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 PS Claim 18: Page 100; 127pp; English.
 XX
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA;

CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 2 RALN 5

RESULT 33
 ABB46232
 ID ABB46232 standard; Peptide: 8 AA.
 XX
 AC ABB46232;
 XX
 DT 30 JAN-2002 (first entry)
 XX
 DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 976.
 XX
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX
 OS Synthetic.
 XX
 PN W0200172956-A2.
 XX
 PP 04 OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-1801400.
 XX
 PR 27-MAR-2000; 2000US-0535852.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Symonds JM, Gour BJ;
 XX
 DR WPI: 2002-025778/03.
 XX
 PT Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 PS Claim 18: Page 100; 127pp; English.
 XX
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 23; Length 8;

```

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
DB 2 RALN 5

RESULT 34
ABB46247
ID ABB46237 standard; Peptide: 8 AA.
XX AC
AC ABB46247;
XX DT 30-JAN-2002 (first entry)
XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 987.
XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW skin graft; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis; cyclic.
XX OS Synthetic.
XX PN W0200172956 A2.
XX PD 04-OCT-2001.
XX PF 27-MAR-2001; 2001WO-B01400.
XX PR 27-MAR-2000; 2000US-0545852.
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuk OW, Symonds JM, Gour BJ;
XX WP1: 2002-025778/03.
XX PS Modulating agents for inhibiting or enhancing desmosomal cadherin
PI mediated cell adhesion, useful for facilitating wound healing and/or
PI reducing scar tissue, treating cancer and inducing apoptosis -
XX Claim 18; Page 100; 127pp; English.
XX CC The invention relates to modulating agents for inhibiting or enhancing
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
CC sequence, a substance such as an antibody or antigen-binding fragment
CC that specifically binds a desmosomal cadherin CAR sequence and/or a
CC polynucleotide encoding a polypeptide that comprises a desmosomal
CC cadherin CAR sequence or analogue. The modulating agents have
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC facilitate wound healing and/or reduce scar tissue, for enhancing
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC treating an autoimmune blistering disorder and to treat cancer
CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX Sequence 8 AA;
SQ Query Match 36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
DB 4 RALN 7

RESULT 35
ABB46250
ID ABB46250 standard; Peptide: 8 AA.
XX AC
AC ABB46250;
XX DT 30-JAN-2002 (first entry)
XX DE Desmoglein 1 CAR sequence cyclic peptide SEQ ID NO 994.
XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW skin graft; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis; cyclic.

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XX  OS   Synthesized.
XX  PN   W0200172956-A2.
XX  PD   04-OCT-2001.
XX  PF   27-MAR-2001: 2001WO-IB01400.
XX  PR   27-MAR-2000: 2000US-0535852.
XX  PA   (ADHEX) ADHEREX TECHNOLOGIES INC.
XX  PI   Blaschuk OW, Symonds JM, Gour BJ.
XX  DR   WPI: 2002-025778/03.
XX  PT   Modulating agents for inhibiting or enhancing desmosomal cadherin
PT   mediated cell adhesion, useful for facilitating wound healing and/or
PT   reducing scar tissue, treating cancer and inducing apoptosis.
XX  PS   Claim 18: Page 100; 127pp, English.
XX  CC   The invention relates to modulating agents for inhibiting or enhancing
CC   desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC   comprising a desmosomal cadherin cell adhesion recognition CAR sequence
CC   (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
CC   sequence, a substance such as an antibody or antigen-binding fragment
CC   that specifically binds a desmosomal cadherin CAR sequence and/or a
CC   polynucleotide encoding a polypeptide that comprises a desmosomal
CC   cadherin CAR sequence or analogue. The modulating agents have
CC   immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC   facilitate wound healing and/or reduce scar tissue, for enhancing
CC   adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC   treating an autoimmune blistering disorder and to treat cancer
CC   (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX  SQ   Sequence 8 AA:
XX
XX  Query Match: 36.4%; Score 4; DB 23; Length 8;
XX  Best Local Similarity 100.0%; Prod. No. 9.3e+05;
XX  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY   2 RALN 5
XX  DB   ||||
XX       2 RALN 5
XX
XX  RESULT 37
XX  ID   ABB46253
XX  AC   ABB46253
XX  DT   30-JAN-2002 (first entry)
XX  DE   Desmosomal CAR sequence cyclic peptide SEQ ID NO 1004.
XX  KW   Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
XX  KW   cytostatic; antiapoptotic; wound healing; reduce scar tissue;
XX  KW   skin graft; organ implant; autoimmune blistering disorder; cancer;
XX  KW   apoptosis; cyclic
XX  QS   Synthetic.
XX  PN   W0200172956-A2.
XX  PD   04-OCT-2001.
XX  PF   27-MAR-2001: 2001WO-IB01400.
XX  PR   27-MAR-2000: 2000US-0535852.
XX  PA   (ADHEX) ADHEREX TECHNOLOGIES INC.
XX  PI   Blaschuk OW, Symonds JM, Gour BJ.
XX  DR   WPI: 2002-025778/03.
XX  PT   Modulating agents for inhibiting or enhancing desmosomal cadherin
PT   mediated cell adhesion, useful for facilitating wound healing and/or
PT   reducing scar tissue, treating cancer and inducing apoptosis.
XX  PS   Claim 18, Page 100; 127pp, English.

```

XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA:

Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 2 RALN 5

RESULT 49
 ABB46265
 ID ABB46265 standard; Peptide: 8 AA.
 XX
 AC ABB46265;
 XX
 XX 30-JAN-2002 (first entry)
 XX Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1039
 XX
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX
 XX Synthetic.
 OS
 XX WO200172956 A2.
 XX
 XX 04-OCT-2001.
 XX
 XX 27-MAR-2001; 2001WO 1B01400.
 XX
 XX 27-MAR-2000; 2000US-0535852.
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 XX Blaschuk GW, Symonds JM, Gour PJ.
 XX WPI: 2002-025778/03.
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 XX Claim 18; Page 100; 127pp; English.
 XX
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing

CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA:

Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 3 RALN 6

RESULT 49
 ABB46271
 ID ABB46271 standard; Peptide: 8 AA.
 XX
 AC ABB46271;
 XX
 XX 30-JAN-2002 (first entry)
 XX Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1015.
 XX
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX
 XX Synthetic.
 OS
 XX WO200172956-A2.
 XX
 XX 04-OCT-2001.
 XX
 XX 27-MAR-2001; 2001WO 1B01400.
 XX
 XX 27-MAR-2000; 2000US-0535852.
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 XX Blaschuk GW, Symonds JM, Gour PJ.
 XX WPI: 2002-025778/03.
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 XX Claim 18; Page 100; 127pp; English.
 XX
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA:

Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5


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XX PD 04-OCT-2001.
XX PF 27-MAR-2001; 2001WO-1B01400.
XX PR 27-MAR-2000; 2000US-0535852.
XX PA (ADHEX) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuk OW, Symonds JM, Gour BJ;
XX PS WPI: 2002-025778/03.
XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin
XX PT mediated cell adhesion, useful for facilitating wound healing and/or
XX PT reducing scar tissue, treating cancer and inducing apoptosis.
XX PS Claim 18; Page 101; 127pp; English.
XX CC The invention relates to modulating agents for inhibiting or enhancing
XX CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
XX CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
XX CC sequence, a substance such as an antibody or antigen-binding fragment
XX CC that specifically binds a desmosomal cadherin CAR sequence and/or a
XX CC polynucleotide encoding a polypeptide that comprises a desmosomal
XX CC cadherin CAR sequence or analogue. The modulating agents have
XX CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
XX CC facilitate wound healing and/or reduce scar tissue, for enhancing
XX CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
XX CC treating an autoimmune blistering disorder and to treat cancer
XX CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX SQ Sequence 8 AA;
XX
XX Query Match 36.4%; Score 4; DB 23; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 RALN 5
XX DB 1111
XX 3 RALN 6
XX
XX RESULT: 45
XX ABB45299
XX ID ABB45299 standard; Peptide: 8 AA.
XX AC ABB46299;
XX DT 30-JAN-2002 (first entry)
XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1043.
XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
XX KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
XX KW skin graft; organ implant; autoimmune blistering disorder; cancer;
XX KW apoptosis; cyclic.
XX OS Synthetic.
XX PN W0200172956-A2.
XX PD 04-OCT-2001.
XX PF 27-MAR-2001; 2001WO-1B01400.
XX PR 27-MAR-2000; 2000US-0535852.
XX PA (ADHEX) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuk OW, Symonds JM, Gour BJ;
XX PS WPI: 2002-025778/03.
XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin
XX PT mediated cell adhesion, useful for facilitating wound healing and/or
XX PT reducing scar tissue, treating cancer and inducing apoptosis.
XX PS Claim 18; Page 101; 127pp; English.
XX CC The invention relates to modulating agents for inhibiting or enhancing
XX CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
XX CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
XX CC sequence, a substance such as an antibody or antigen-binding fragment
XX CC that specifically binds a desmosomal cadherin CAR sequence and/or a
XX CC polynucleotide encoding a polypeptide that comprises a desmosomal
XX CC cadherin CAR sequence or analogue. The modulating agents have
XX CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
XX CC facilitate wound healing and/or reduce scar tissue, for enhancing
XX CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
XX CC treating an autoimmune blistering disorder and to treat cancer
XX CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX SQ Sequence 8 AA;
XX
XX Query Match 36.4%; Score 4; DB 23; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 RALN 5
XX DB 1111
XX 2 RALN 5
XX
XX RESULT: 44
XX ABB46293
XX ID ABB46293 standard; Peptide: 8 AA.
XX AC ABB46293;
XX DT 30-JAN-2002 (first entry)
XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1037.
XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
XX KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
XX KW skin graft; organ implant; autoimmune blistering disorder; cancer;
XX KW apoptosis; cyclic.
XX OS Synthetic.
XX PN W0200172956-A2.
XX PD 04-OCT-2001.
XX PF 27-MAR-2001; 2001WO-1B01400.
XX PR 27-MAR-2000; 2000US-0535852.
XX PA (ADHEX) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuk OW, Symonds JM, Gour BJ;
XX PS WPI: 2002-025778/03.
XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin
XX PT mediated cell adhesion, useful for facilitating wound healing and/or
XX PT reducing scar tissue, treating cancer and inducing apoptosis.
XX PS Claim 18; Page 101; 127pp; English.
XX CC The invention relates to modulating agents for inhibiting or enhancing
XX CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
XX CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
XX CC sequence, a substance such as an antibody or antigen-binding fragment
XX CC that specifically binds a desmosomal cadherin CAR sequence and/or a
XX CC polynucleotide encoding a polypeptide that comprises a desmosomal
XX CC cadherin CAR sequence or analogue. The modulating agents have
XX CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
XX CC facilitate wound healing and/or reduce scar tissue, for enhancing
XX CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
XX CC treating an autoimmune blistering disorder and to treat cancer
XX CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX SQ Sequence 8 AA;

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CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX

XX SQ Sequence 8 AA:
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 4 RALN 7

RESULT 46
 ABB46306
 ID ABB46306 standard; Peptide: 8 AA.
 AC ABB46306;
 XX
 DT 30-JAN-2002 (first entry)
 DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1050.
 XX
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX
 OS Synthetic.
 XX
 PN WO200172956-A2.
 XX
 PD 04 OCT-2001.
 XX
 PE 27-MAR-2001; 2001WO-1801400.
 XX
 PR 27-MAR-2000; 2000US-0535852.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Symonds JM, Gour RJ;
 XX
 DP WPI: 2002-025778/03.
 XX
 PT Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 PS Claim 18; Page 101; 127pp; English.
 XX
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX

XX SQ Sequence 8 AA:
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 4 RALN 7

RESULT 47
 ABB46321
 ID ABB46321 standard; Peptide: 8 AA.
 AC ABB46321;
 XX
 DT 30-JAN-2002 (first entry)
 DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1065.
 XX
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX
 OS Synthetic.
 XX
 PN WO200172956-A2.
 XX
 PD 04 OCT-2001.
 XX
 PE 27-MAR-2001; 2001WO-1801400.
 XX
 PR 27-MAR-2000; 2000US-0545852.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Symonds JM, Gour RJ;
 XX
 DP WPI: 2002-025778/03.
 XX
 PT Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 PS Claim 18; Page 101; 127pp; English.
 XX
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX

XX SQ Sequence 8 AA:
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 2 RALN 5

```

RESULT 48
ABB46322
ID ABB46322 standard; Peptide: 8 AA.
XX
XX ABB46322;
XX
XX 30 JAN-2002 (first entry)
XX
XX Desmocleins-1 CAR sequence cyclic peptide SEQ ID NO 1071.
XX
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW skin graft; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis; cyclic.
XX
XX Synthetic.
XX
XX W0200172956-A2.
XX
XX 04 OCT-2001.
XX
XX 27-MAR-2001; 2001WO-1801400.
XX
XX 27-MAR-2000; 2000US-0535852.
XX
XX (ABBE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuk GW, Symonds JM, Gour BJ;
XX WPI: 2002-025778/03.
XX
XX Modulating agents for inhibiting or enhancing desmosomal cadherin
PT mediated cell adhesion, useful for facilitating wound healing and/or
PT reducing scar tissue, treating cancer and inducing apoptosis.
XX
XX Claim 18; Page 101; 127pp; English.
XX
XX The invention relates to modulating agents for inhibiting or enhancing
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC comprising a desmosomal cadherin mimetic or a desmosomal cadherin CAR
CC sequence, a substance such as an antibody or antigen-binding fragment
CC that specifically binds a desmosomal cadherin CAR sequence and/or a
CC polypeptide encoding a polypeptide that comprises a desmosomal
CC cadherin CAR sequence or analogue. The modulating agents have
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC facilitate wound healing and/or reduce scar tissue, for enhancing
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC treating an autoimmune blistering disorder and to treat cancer
CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX
XX Sequence 8 AA;
SQ
Query Match 36.4% Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RAIN 5
ID 1111
XX 1 RAIN 4
RESULT 49
ABB46326
ID ABB46326 standard; Peptide: 8 AA.
XX
XX ABB46326;
XX
XX 30 JAN-2002 (first entry)
XX
XX Desmocleins-1 CAR sequence cyclic peptide SEQ ID NO 1071.
XX
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW skin graft; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis; cyclic.
XX
XX Synthetic.
XX
XX W0200172956-A2.
XX
XX 04 OCT-2001.
XX
XX 27-MAR-2001; 2001WO-1801400.
XX
XX 27-MAR-2000; 2000US-0535852.
XX
XX (ABBE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuk GW, Symonds JM, Gour BJ;
XX WPI: 2002-025778/03.
XX
XX Modulating agents for inhibiting or enhancing desmosomal cadherin
PT mediated cell adhesion, useful for facilitating wound healing and/or
PT reducing scar tissue, treating cancer and inducing apoptosis.
XX
XX Claim 18; Page 101; 127pp; English.
XX
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CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC comprising a desmosomal cadherin mimetic or a desmosomal cadherin CAR
CC sequence, a substance such as an antibody or antigen-binding fragment
CC that specifically binds a desmosomal cadherin CAR sequence and/or a
CC polypeptide encoding a polypeptide that comprises a desmosomal
CC cadherin CAR sequence or analogue. The modulating agents have
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC facilitate wound healing and/or reduce scar tissue, for enhancing
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC treating an autoimmune blistering disorder and to treat cancer
CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX
XX Sequence 8 AA;
SQ
Query Match 36.4% Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RAIN 5
ID 1111
XX 2 RAIN 5
RESULT 50
ABB46326
ID ABB46326 standard; Peptide: 8 AA.
XX
XX ABB46326;
XX
XX 30 JAN-2002 (first entry)
XX
XX Desmocleins-1 CAR sequence cyclic peptide SEQ ID NO 1071.
XX
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW skin graft; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis; cyclic.
XX
XX Synthetic.
XX
XX W0200172956-A2.
XX
XX 04 OCT-2001.
XX
XX 27-MAR-2001; 2001WO-1801400.
XX
XX 27-MAR-2000; 2000US-0535852.
XX
XX (ABBE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuk GW, Symonds JM, Gour BJ;
XX WPI: 2002-025778/03.
XX
XX Modulating agents for inhibiting or enhancing desmosomal cadherin
PT mediated cell adhesion, useful for facilitating wound healing and/or
PT reducing scar tissue, treating cancer and inducing apoptosis.
XX
XX Claim 18; Page 101; 127pp; English.
XX
XX The invention relates to modulating agents for inhibiting or enhancing
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC comprising a desmosomal cadherin mimetic or a desmosomal cadherin CAR
CC sequence, a substance such as an antibody or antigen-binding fragment
CC that specifically binds a desmosomal cadherin CAR sequence and/or a
CC polypeptide encoding a polypeptide that comprises a desmosomal
CC cadherin CAR sequence or analogue. The modulating agents have
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC facilitate wound healing and/or reduce scar tissue, for enhancing
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC treating an autoimmune blistering disorder and to treat cancer
CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX
XX Sequence 8 AA;
SQ
Query Match 36.4% Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RAIN 5
ID 1111
XX 2 RAIN 5

```

XX 27-MAR-2000: 2000US-0535852.
XX (AHEX-) ADHEXEX TECHNOLOGIES INC
XX
XX Blasthek OW, Symonds JM, Gout RD
XX
XX WPI: 2002-025778/03
XX
XX Modulating agents for inhibited or enhanced cell adhesion, adhesion
XX mediated cell adhesion, agent for facilitated and inhibited adhesion
XX reducing scar tissue, treating cancer and inducing apoptosis
XX
XX Claim 18: Page 101: 127pp: English
XX
XX The invention relates to modulating agents for inhibition or enhancement
XX of desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX comprising a desmosomal cadherin CDS adhesion recognition (CAR) sequence
XX (AHH4341-ABH47262), a non peptide derivative of a desmosomal cadherin CAR
XX sequence, a substance such as an antibody or antigen binding fragment
XX that specifically binds a desmosomal cadherin CAR sequence and/or a
XX polypeptide encoding a polypeptide that comprises a desmosomal
XX cadherin CAR sequence or analogue. The modulating agents have
XX immunosuppressive, cytostatic and antiapoptotic activity and are used to
XX facilitate wound healing and/or reduce scar tissue, for enhancing
XX adhesion of foreign tissue implants (e.g. skin graft or organ transplant),
XX treating an autoimmune blistering disorder and to treat cancer
XX (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX
XX Sequence: 8 AA;
XX
XX Query Match: 36.4%; Score 4; IP 24; Length 9;
XX Best Local Similarity: 100.0%; Pred. No. 9; 4-06;
XX Matches: 4; Conservative 0; Mismatched 3; Gaps 0;
XX
XX 2 RALN 5
XX 111
XX 3 RALN 6
XX
XX Search Completed: September 30, 2003, 1:24:44
XX Job Time: 46.1667 secs

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cdm protein protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 41.5567 Seconds
(without adjustments)
62.639 Million cell updates/sec

Title: us-09-787-443-3

Perfect score: 11

Sequence: 1 ARALNWGAPK li

Scoring table: 0LIG0

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 25852604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3459

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: listing first 500 summaries

Database: SPTREMBL23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_oranelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp Vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriaph:
17: sp_archaeap:

Prod. No is the number of results for each the chosen database.
Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARY					Description	
Result No.	Score	Query Match	Length	DB ID		
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2	3	27.3	8	4	Q9UCN4	Q9UCN4 homo sapien
3	3	27.3	9	2	Q9R7ER	Q9R7ER escherichia
4	3	27.3	9	4	Q16605	Q16605 homo sapien
5	3	27.3	9	8	Q9T2L0	Q9T2L0 homo sapien
6	3	27.3	9	8	Q9T2L0	Q9T2L0 spinacia ol
7	3	27.3	10	3	Q8J0C2	Q8J0C2 encephalito
8	3	27.3	10	4	Q8T2A2	Q8T2A2 homo sapien
9	3	27.3	10	5	Q8WPE7	Q8WPE7 skogsbergia
10	3	27.3	10	11	Q9LWZ3	Q9LWZ3 rattus sp.
11	3	27.3	10	12	Q9Q0W9	Q9Q0W9 polymaviru
12	3	27.3	10	12	Q8JV70	Q8JV70 polymaviru
13	3	27.3	10	12	Q9Q0W1	Q9Q0W1 polymaviru
14	3	27.3	10	12	Q8J2V6	Q8J2V6 polymaviru
15	3	27.3	10	12	Q6V347	Q6V347 herpes simp
16	3	27.3	10	12	Q9Q0V9	Q9Q0V9 polymaviru

Q8JV84 polymaviru
Q9Q0W7 polymaviru
Q8JV66 polymaviru
Q9Q0V7 polymaviru
Q8JV82 polymaviru
Q8JV76 polymaviru
Q8JV74 polymaviru
Q9Q0X7 polymaviru
Q8JV78 polymaviru
Q9Q0W5 polymaviru
Q9Q0X3 polymaviru
Q9Q0X5 polymaviru
Q9Q0W3 polymaviru
Q8JV80 polymaviru
Q9Q0X1 polymaviru
Q9Q0X9 polymaviru
Q8JV72 polymaviru
Q8CD88 homo sapien
Q9TWX6 manduca sex
Q23876 dictyosteli
Q9TQS9 equus cabal
Q9QVH3 rattus sp.
Q8VLX8 thermus the
P94011 arabidopsis
Q34770 borrelia af
Q34622 borrelia bu
Q96P10 homo sapien
Q9U7D6 neospora ca
Q97122 toxoplasma
Q9GJU2 ovis aries
Q62355 mus musculu
Q9CU06 mus musculu
Q8CIW3 mus musculu
Q69394 pseudorabie
Q8X4F5 escherichia
Q8J192 ashbya goss
Q16232 homo sapien
Q9FUX5 symphoricar
P83291 arabidopsis
Q99PB8 mus musculu
Q8CFB7 mus musculu
Q85662 reovirus (t
Q85718 reovirus (t
O10228 human immun
O10232 human immun
O10233 human immun
O10227 human immun
O10226 human immun
O8UT17 human immun
Q9F598 micrococci
Q9F564 escherichia
Q9F5K5 comamonas a
Q8N0N6 brachiohisto
P92076 euhadra her
Q9T202 chlamydomon
Q9SQ16 oryza sativ
Q941J1 zea mays (m
Q9FYV6 gossypium h
Q8XQ9 xenopus lae
Q9Q090 human immun
Q97098 human immun
Q97099 human immun
Q97092 human immun
Q97094 human immun
Q9F5R2 shigella dy
P77556 escherichia
Q23560 escherichia
Q9Z1E9 neisseria m
Q9F4M3 enterococcu
Q9URB9 saccharomyc
Q15889 homo sapien
Q15900 homo sapien

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91	2	18.2	8	4	Q90J50	homo sapien	164	2	18.2	9	8	Q9TNF4	Q9tnf4 magnolia sc
92	2	18.2	8	5	P82685	periplaneta	165	2	18.2	9	8	Q9THL7	Q9thl7 magnolia si
93	2	18.2	8	5	P82686	periplaneta	166	2	18.2	9	8	Q9TNE0	Q9tne0 michelia co
94	2	18.2	8	5	P82687	periplaneta	167	2	18.2	9	8	Q95GN1	Q95gn1 pelargonium
95	2	18.2	8	5	P82688	periplaneta	168	2	18.2	9	8	Q9TNE4	Q9tne4 magnolia sa
96	2	18.2	8	5	P82689	periplaneta	169	2	18.2	9	8	Q95DS6	Q95ds6 magnolia wi
97	2	18.2	8	6	Q9TRX8	periplaneta	170	2	18.2	9	8	Q94NB2	Q94nb2 microcebus
98	2	18.2	8	6	Q8WNS1	bos taurus	171	2	18.2	9	8	Q9TNF6	Q9tnf6 magnolia gr
99	2	18.2	8	8	Q19957	gossypium h	172	2	18.2	9	8	Q9THL5	Q9thl5 magnolia li
100	2	18.2	8	8	Q19961	gossypium d	173	2	18.2	9	8	Q9TNF1	Q9tnf1 magnolia he
101	2	18.2	8	8	Q19958	gossypium b	174	2	18.2	9	8	Q94VH4	Q94vh4 varanus gla
102	2	18.2	8	8	Q9TND2	terratos	175	2	18.2	9	8	Q95DT3	Q95dt3 magnolia il
103	2	18.2	8	8	Q19960	gossypium m	176	2	18.2	9	8	Q9THM0	Q9thm0 magnolia fr
104	2	18.2	8	8	Q19959	gossypium t	177	2	18.2	9	8	Q94V18	Q94v18 varanus ere
105	2	18.2	8	8	Q19956	gossypium a	178	2	18.2	9	8	Q9T3P4	Q9t3p4 magnolia ma
106	2	18.2	8	8	Q8WGC7	petrolisthe	179	2	18.2	9	8	Q94NA9	Q94na9 daubentonia
107	2	18.2	8	9	Q8SBJ0	bacterioph	180	2	18.2	9	8	Q9THL8	Q9thl8 magnolia of
108	2	18.2	8	9	Q8H9K4	bacterioph	181	2	18.2	9	8	Q9TNE2	Q9tne2 magnolia ac
109	2	18.2	8	9	Q8H9K1	bacterioph	182	2	18.2	9	8	Q9TNF5	Q9tnf5 magnolia gu
110	2	18.2	8	9	Q8H9J9	bacterioph	183	2	18.2	9	8	Q9TNE3	Q9tne3 magnolia li
111	2	18.2	8	9	Q8H9J7	bacterioph	184	2	18.2	9	8	Q9TNE1	Q9tne1 magnolia st
112	2	18.2	8	9	Q8H9J5	bacterioph	185	2	18.2	9	8	Q9TND9	Q9tnd9 michelia fl
113	2	18.2	8	9	Q8H9J3	bacterioph	186	2	18.2	9	8	Q9THL6	Q9thl6 magnolia si
114	2	18.2	8	9	Q8H9J1	bacterioph	187	2	18.2	9	8	Q95DS4	Q95ds4 magnolia do
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118	2	18.2	8	9	Q8H9I4	bacterioph	191	2	18.2	9	8	Q95DS7	Q95ds7 magnolia si
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120	2	18.2	8	9	Q8H9I2	bacterioph	193	2	18.2	9	8	Q9TNE6	Q9tne6 magnolia ta
121	2	18.2	8	9	Q8H9H6	bacterioph	194	2	18.2	9	8	Q9T3P3	Q9t3p3 magnolia vi
122	2	18.2	8	9	Q8H9H5	bacterioph	195	2	18.2	9	8	Q9TNE7	Q9tne7 magnolia ni
123	2	18.2	8	9	Q8H9H3	bacterioph	196	2	18.2	9	8	Q94XE6	Q94xe6 tectocoris
124	2	18.2	8	10	Q40659	oryza sativ	197	2	18.2	9	8	Q95DR9	Q95dr9 manglietia
125	2	18.2	8	10	Q42507	tritium ae	198	2	18.2	9	8	Q94NB0	Q94nb0 microcebus
126	2	18.2	8	11	Q9ERK2	mus musculus	199	2	18.2	9	8	Q8W8W6	Q8w8w6 diadema ant
127	2	18.2	8	11	Q9JLD7	mesocricetu	200	2	18.2	9	8	Q95DR8	Q95dr8 michelia ma
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130	2	18.2	8	11	Q9K4R8	mus musculus	203	2	18.2	9	11	Q924N8	Q924n8 mus musculus
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132	2	18.2	8	11	Q62528	mus spretus	205	2	18.2	9	11	Q9QVH9	Q9qvhi9 mus sp. sup
133	2	18.2	8	12	Q9WJ33	pseudorabie	206	2	18.2	9	11	Q9QW70	Q9qwt0 mus musculus
134	2	18.2	8	13	Q9PS69	gallus gall	207	2	18.2	9	11	Q61723	Q61723 mus musculus
135	2	18.2	8	13	Q8JFNE	gallus gall	208	2	18.2	9	12	Q69473	Q69473 human herpe
136	2	18.2	9	1	Q50832	methanococc	209	2	18.2	9	12	Q9E107	Q9el07 hepatitis b
137	2	18.2	9	2	Q5E214	sodalis glo	210	2	18.2	9	12	Q71067	Q71067 canine dist
138	2	18.2	9	2	P72145	pseudomonas	211	2	18.2	9	12	Q82622	Q82622 avian infec
139	2	18.2	9	2	Q53914	streptomyce	212	2	18.2	9	12	P90359	P90359 barley mild
140	2	18.2	9	2	Q57428	aeromonas s	213	2	18.2	9	12	Q71069	Q71069 canine dist
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142	2	18.2	9	2	Q93LE4	heliobacilli	215	2	18.2	9	12	Q84333	Q84333 simian viru
143	2	18.2	9	2	Q44377	aeromonas t	216	2	18.2	9	12	Q71068	Q71068 canine dist
144	2	18.2	9	2	Q44468	aeromonas v	217	2	18.2	9	12	Q89491	Q89491 murine minu
145	2	18.2	9	2	Q9R735	streptomyce	218	2	18.2	9	12	Q91A14	Q91a14 gallus gall
146	2	18.2	9	2	P72145	pseudomonas	219	2	18.2	9	13	Q8JFA7	Q8jfa7 ficedula al
147	2	18.2	9	2	Q43928	aeromonas f	220	2	18.2	9	13	Q8JFA6	Q8jfa6 ficedula hy
148	2	18.2	9	2	Q43301	aeromonas c	221	2	18.2	9	13	Q92009	Q92009 gallus gall
149	2	18.2	9	2	Q51765	pseudomonas	222	2	18.2	9	13	Q8AYL5	Q8ayl5 carassius a
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151	2	18.2	9	4	Q9H461	homo sapien	224	2	18.2	9	13	Q50843	Q50843 methanococc
152	2	18.2	9	4	Q15692	homo sapien	225	2	18.2	9	13	Q9F9H5	Q9f9h5 helicobacte
153	2	18.2	9	4	Q9UCN5	homo sapien	226	2	18.2	10	1	Q9F9H5	Q9f9h5 clostridium
154	2	18.2	9	5	Q91WD6	leptinotars	227	2	18.2	10	2	Q9F9H5	Q9f9h5 clostridium
155	2	18.2	9	5	Q9TVF1	trypanosoma	228	2	18.2	10	2	Q9F9H5	Q9f9h5 clostridium
156	2	18.2	9	5	Q9MW43	homo sapien	229	2	18.2	10	2	Q9F9H5	Q9f9h5 clostridium
157	2	18.2	9	8	Q95DS5	magnolia sa	230	2	18.2	10	2	Q47651	Q47651 escherichia
158	2	18.2	9	8	Q8WFS4	diadema mex	231	2	18.2	10	2	Q47651	Q47651 escherichia
159	2	18.2	9	8	Q95DS0	manglietia	232	2	18.2	10	2	Q47651	Q47651 escherichia
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238	2	18.2	10	2	Q47475	Q47475 escherichia	311	2	18.2	11	2	Q9A127	Q9A127 carsonella
239	4	18.2	10	2	Q8RSU1	Q8RSU1 helicobacte	312	2	18.2	11	2	Q8RKN1	Q8RKN1 escherichia
240	2	18.2	10	2	Q9F5W1	Q9F5W1 vibrio chol	313	2	18.2	11	2	Q8KHL0	Q8KHL0 streptococc
241	2	18.2	10	2	Q9K343	Q9K343 escherichia	314	2	18.2	11	2	Q9R4B1	Q9R4B1 streptococc
242	2	18.2	10	2	Q95421	Q95421 escherichia	315	2	18.2	11	2	Q9X5S6	Q9X5S6 streptomyc
243	2	18.2	10	2	Q8R171	Q8R171 anaplasmia p	316	2	18.2	11	2	Q9S618	Q9S618 prochloroc
244	2	18.2	10	2	Q47694	Q47694 escherichia	317	2	18.2	11	2	Q9F023	Q9F023 escherichia
245	2	18.2	10	2	P96306	P96306 aeromonas s	318	2	18.2	11	2	Q47600	Q47600 escherichia
246	2	18.2	10	2	P83367	P83367 bacillus ce	319	2	18.2	11	2	Q87882	Q87882 mycobacteri
247	2	18.2	10	2	P83160	P83160 anabaena sp	320	2	18.2	11	2	Q9RF22	Q9RF22 mycoplasma
248	2	18.2	10	2	P83154	P83154 anabaena sp	321	2	18.2	11	2	P95518	P95518 pasteurella
249	2	18.2	10	2	P82386	P82386 streptococc	322	2	18.2	11	2	Q47604	Q47604 escherichia
250	2	18.2	10	2	Q8GDC0	Q8GDC0 escherichia	323	2	18.2	11	2	Q47345	Q47345 escherichia
251	2	18.2	10	4	Q8NEK0	Q8NEK0 homo sapien	324	2	18.2	11	2	Q47420	Q47420 escherichia
252	2	18.2	10	4	Q9R369	Q9R369 homo sapien	325	2	18.2	11	2	Q8KKA1	Q8KKA1 streptococc
253	2	18.2	10	4	Q8UNF2	Q8UNF2 homo sapien	326	2	18.2	11	2	Q56411	Q56411 escherichia
254	2	18.2	10	4	Q14096	Q14096 homo sapien	327	2	18.2	11	2	Q47059	Q47059 escherichia
255	2	18.2	10	4	Q9UCS3	Q9UCS3 homo sapien	328	2	18.2	11	2	Q9R446	Q9R446 neisseria g
256	2	18.2	10	4	Q9UJ48	Q9UJ48 homo sapien	329	2	18.2	11	2	Q8GMU3	Q8GMU3 acinetobact
257	2	18.2	10	4	Q9UE86	Q9UE86 homo sapien	330	2	18.2	11	3	Q60005	Q60005 aspergillus
258	2	18.2	10	5	Q91FW1	Q91FW1 fusinus fer	331	2	18.2	11	3	Q60007	Q60007 emericella
259	2	18.2	10	5	Q25356	Q25356 locusta mig	332	2	18.2	11	3	Q60192	Q60192 aspergillus
260	2	18.2	10	5	Q8WFL6	Q8WFL6 oikopleura	333	2	18.2	11	3	Q6C1R7	Q6C1R7 saccharomyc
261	2	18.2	10	6	P82383	P82383 drosophila	334	2	18.2	11	3	Q60006	Q60006 aspergillus
262	2	18.2	10	6	Q9TS43	Q9TS43 sus scrofa	335	2	18.2	11	4	Q60614	Q60614 homo sapien
263	2	18.2	10	6	Q8WFO4	Q8WFO4 atelies belz	336	2	18.2	11	4	Q14759	Q14759 homo sapien
264	2	18.2	10	6	Q95NB1	Q95NB1 eulemur ful	337	2	18.2	11	4	Q9UCP2	Q9UCP2 homo sapien
265	2	18.2	10	6	Q95NH0	Q95NH0 eulemur ful	338	2	18.2	11	4	Q9KX38	Q9KX38 homo sapien
266	2	18.2	10	6	Q8SPN8	Q8SPN8 macaca mulia	339	2	18.2	11	4	Q60761	Q60761 homo sapien
267	2	18.2	10	6	Q95M70	Q95M70 trichosurus	340	2	18.2	11	4	Q73811	Q73811 homo sapien
268	2	18.2	10	6	P83205	P83205 ovis aries	341	2	18.2	11	4	Q15997	Q15997 homo sapien
269	2	18.2	10	8	Q9XMB4	Q9XMB4 acgilops ta	342	2	18.2	11	4	Q96QF8	Q96QF8 homo sapien
270	2	18.2	10	8	Q912P3	Q912P3 rattus sp.	343	2	18.2	11	4	Q9UCP5	Q9UCP5 homo sapien
271	2	18.2	10	8	Q912P4	Q912P4 rattus sp.	344	2	18.2	11	4	Q9UE69	Q9UE69 homo sapien
272	2	18.2	10	8	Q95D10	Q95D10 magnolia po	345	2	18.2	11	4	Q9HCN5	Q9HCN5 homo sapien
273	2	18.2	10	8	Q95D58	Q95D58 magnolia de	346	2	18.2	11	5	Q26092	Q26092 pisaster oc
274	2	18.2	10	8	Q95D58	Q95D58 magnolia sp	347	2	18.2	11	5	Q95PX6	Q95PX6 caenorhabdi
275	2	18.2	10	8	Q91347	Q91347 ophisaurus	348	2	18.2	11	5	Q9NFX0	Q9NFX0 drosophila
276	2	18.2	10	8	Q8W8C2	Q8W8C2 anolis punc	349	2	18.2	11	6	Q95J20	Q95J20 eulemur ful
277	2	18.2	10	8	Q91G32	Q91G32 ophisaurus	350	2	18.2	11	6	Q95NB6	Q95NB6 eulemur ful
278	2	18.2	10	8	Q95D53	Q95D53 magnolia me	351	2	18.2	11	6	Q95J19	Q95J19 eulemur ful
279	2	18.2	10	8	Q8WD18	Q8WD18 anolis tran	352	2	18.2	11	7	Q77914	Q77914 oreochromis
280	2	18.2	10	8	Q8W8C3	Q8W8C3 anolis nite	353	2	18.2	11	7	Q9UEX7	Q9UEX7 homo sapien
281	2	18.2	10	8	Q91368	Q91368 gerthomotis	354	2	18.2	11	7	Q78118	Q78118 oreochromis
282	2	18.2	10	8	Q8W8C4	Q8W8C4 anolis punc	355	2	18.2	11	7	Q77872	Q77872 oreochromis
283	2	18.2	10	8	Q95D12	Q95D12 magnolia pa	356	2	18.2	11	7	Q78120	Q78120 oreochromis
284	2	18.2	10	8	Q95D11	Q95D11 magnolia yo	357	2	18.2	11	7	Q77873	Q77873 oreochromis
285	2	18.2	10	8	Q95D17	Q95D17 magnolia sc	358	2	18.2	11	7	Q77871	Q77871 oreochromis
286	2	18.2	10	8	Q8H0H4	Q8H0H4 anomobryum	359	2	18.2	11	8	Q9G622	Q9G622 salea horsf
287	2	18.2	10	9	Q38217	Q38217 lactococcus	360	2	18.2	11	8	Q95E14	Q95E14 dendrochilu
288	2	18.2	10	10	Q95926	Q95926 glycine max	361	2	18.2	11	8	Q9G359	Q9G359 japalura fl
289	2	18.2	10	10	Q41788	Q41788 zea mays (m	362	2	18.2	11	8	Q9G649	Q9G649 otocryptis
290	2	18.2	10	10	Q94119	Q94119 zea mays (m	363	2	18.2	11	8	Q9G528	Q9G528 acanthosaur
291	2	18.2	10	10	Q08938	Q08938 nicotiana t	364	2	18.2	11	8	Q94VH7	Q94VH7 varanus gil
292	2	18.2	10	10	P82414	P82414 nicotiana t	365	2	18.2	11	8	Q9G619	Q9G619 ceratophora
293	2	18.2	10	11	Q9QVK8	Q9QVK8 mus sp. mep	366	2	18.2	11	8	Q8WER7	Q8WER7 ceratophora
294	2	18.2	10	11	C70580	C70580 mus musculu	367	2	18.2	11	8	Q8WD50	Q8WD50 ceratophora
295	2	18.2	10	11	Q9K320	Q9K320 mus musculu	368	2	18.2	11	8	Q35374	Q35374 paramacium
296	2	18.2	10	11	Q8H0H2	Q8H0H2 mus musculu	369	2	18.2	11	8	Q9G5X1	Q9G5X1 trapelus pe
297	2	18.2	10	12	Q9J348	Q9J348 hepatitis q	370	2	18.2	11	8	Q8WER4	Q8WER4 ceratophora
298	2	18.2	10	12	Q90349	Q90349 hepatitis q	371	2	18.2	11	8	Q9G682	Q9G682 cheilosania
299	2	18.2	10	12	Q90347	Q90347 hepatitis q	372	2	18.2	11	8	Q9G655	Q9G655 japalura tr
300	2	18.2	10	12	Q90346	Q90346 hepatitis q	373	2	18.2	11	8	Q9G637	Q9G637 calotes lio
301	2	18.2	10	13	Q9P507	Q9P507 alligator m	374	2	18.2	11	9	Q38415	Q38415 bacterioph
302	2	18.2	10	13	Q9P801	Q9P801 cynops pyr	375	2	18.2	11	10	Q06626	Q06626 solanum tub
303	2	18.2	10	13	Q73588	Q73588 gallus gall	376	2	18.2	11	10	Q65901	Q65901 leavenworth
304	2	18.2	10	13	Q73594	Q73594 gallus gall	377	2	18.2	11	10	Q8RV30	Q8RV30 zea mays (m
305	2	18.2	10	13	P82080	P82080 limnodynast	378	2	18.2	11	10	Q9S8X4	Q9S8X4 glycine max
306	2	18.2	10	13	P82084	P82084 limnodynast	379	2	18.2	11	10	Q39784	Q39784 gossypium h
307	2	18.2	10	15	Q85598	Q85598 moloney mur	380	2	18.2	11	10	Q9T019	Q9T019 brassica ol
308	2	18.2	10	15	Q85619	Q85619 moloney mur	381	2	18.2	11	10	Q941R5	Q941R5 pinus radia

382	2	18.2	11	Q99JC3	Q99JC3 rattus sp.	455	2	18.2	12	8	Q95EL0	Q95el0 dendrochilu
383	2	18.2	11	Q99XN6	Q99XN6 mus musculus	456	2	18.2	12	8	Q95EK0	Q95ek0 dendrochilu
384	2	18.2	11	Q99N81	Q99N81 mus musculus	457	2	18.2	12	8	Q95EL6	Q95el6 dendrochilu
385	2	18.2	11	Q9JLE6	Q9JLE6 rattus noir	458	2	18.2	12	8	Q95EM2	Q95em2 dendrochilu
386	2	18.2	11	Q9JLH5	Q9JLH5 mus musculus	459	2	18.2	12	8	Q31851	Q31851 arbidopsis
387	2	18.2	11	Q96866	Q96866 lymphocytic	460	2	18.2	12	8	Q95EK8	Q95ek8 dendrochilu
388	2	18.2	11	Q94084	Q94084 lecania sp.	461	2	18.2	12	8	Q95EL2	Q95el2 dendrochilu
389	2	18.2	11	Q98808	Q98808 lymphocytic	462	2	18.2	12	8	Q95EM0	Q95em0 dendrochilu
390	2	18.2	11	Q96874	Q96874 feline cali	463	2	18.2	12	8	Q95EJ3	Q95eJ3 dendrochilu
391	2	18.2	11	Q94247	Q94247 poliovirinu	464	2	18.2	12	8	Q03816	Q03816 metasequoia
392	2	18.2	11	Q98511	Q98511 tude rubrip	465	2	18.2	12	8	Q95EL8	Q95el8 dendrochilu
393	2	18.2	11	Q9AX69	Q9AX69 oreochromis	466	2	18.2	12	8	Q95EK6	Q95ek6 dendrochilu
394	2	18.2	11	Q9AX68	Q9AX68 oreochromis	467	2	18.2	12	8	Q95EK2	Q95ek2 dendrochilu
395	2	18.2	11	Q94110	Q94110 mouse mamma	468	2	18.2	12	8	Q03815	Q03815 abies alba
396	2	18.2	11	Q95620	Q95620 honey mdr	469	2	18.2	12	8	Q95EJ1	Q95eJ1 dendrochilu
397	2	18.2	12	Q9R5F7	Q9R5F7 helicobacte	470	2	18.2	12	8	Q95E12	Q95e12 dendrochilu
398	2	18.2	12	Q9K149	Q9K149 fischerella	471	2	18.2	12	8	P92457	P92457 ephedra sp.
399	2	18.2	12	Q9R5F5	Q9R5F5 helicobacte	472	2	18.2	12	8	Q95E18	Q95e18 dendrochilu
400	2	18.2	12	Q9L8H8	Q9L8H8 enterococu	473	2	18.2	12	8	Q95EK4	Q95ek4 dendrochilu
401	2	18.2	12	Q9R7E1	Q9R7E1 staphylococ	474	2	18.2	12	8	P92454	P92454 cymas revol
402	2	18.2	12	Q9K8T5	Q9K8T5 campylobact	475	2	18.2	12	8	Q95EL4	Q95el4 dendrochilu
403	2	18.2	12	Q9K1H4	Q9K1H4 enterococu	476	2	18.2	12	8	P82164	P82164 spinacia ol
404	2	18.2	12	Q9X6Y0	Q9X6Y0 aquilex pyr	477	2	18.2	12	8	Q36668	Q36668 pinus sylve
405	2	18.2	12	Q46747	Q46747 escherichia	478	2	18.2	12	8	Q37791	Q37791 larix eurol
406	2	18.2	12	Q9L8H6	Q9L8H6 enterococu	479	2	18.2	12	8	Q36669	Q36669 pinus sylve
407	2	18.2	12	Q9L4M9	Q9L4M9 streptococu	480	2	18.2	12	8	Q37790	Q37790 larix eurol
408	2	18.2	12	Q05128	Q05128 sphingomora	481	2	18.2	12	8	Q8H093	Q8H093 bryum donia
409	2	18.2	12	Q01275	Q01275 neurospora	482	2	18.2	12	8	Q8HB27	Q8HB27 picea glauc
410	2	18.2	12	Q8J0A7	Q8J0A7 saccharomyc	483	2	18.2	12	8	Q8HB26	Q8HB26 picea maria
411	2	18.2	12	Q9UMR0	Q9UMR0 homo sapien	484	2	18.2	12	8	Q8HB25	Q8HB25 picea ruben
412	2	18.2	12	Q95PH0	Q95PH0 homo sapien	485	2	18.2	12	10	Q8L3X3	Q8L3X3 pinus radia
413	2	18.2	12	Q9UC37	Q9UC37 homo sapien	486	2	18.2	12	10	Q8SAS2	Q8SAS2 pinus sylve
414	2	18.2	12	Q16452	Q16452 homo sapien	487	2	18.2	12	10	Q9JX21	Q9JX21 zea mays (m
415	2	18.2	12	Q9UMZ9	Q9UMZ9 homo sapien	488	2	18.2	12	10	Q945C3	Q945C3 crypthecodi
416	2	18.2	12	Q9HB04	Q9HB04 homo sapien	489	2	18.2	12	10	Q9S938	Q9S938 beta vulgar
417	2	18.2	12	Q9HB32	Q9HB32 homo sapien	490	2	18.2	12	10	Q9FSA9	Q9FSA9 silene aega
418	2	18.2	12	Q9UMZ8	Q9UMZ8 homo sapien	491	2	18.2	12	10	Q9AXW1	Q9AXW1 brassica na
419	2	18.2	12	Q13865	Q13865 homo sapien	492	2	18.2	12	10	Q8SAS3	Q8SAS3 pinus sylve
420	2	18.2	12	Q9B4X3	Q9B4X3 homo sapien	493	2	18.2	12	10	P83196	P83196 oryza sativ
421	2	18.2	12	Q9NR17	Q9NR17 homo sapien	494	2	18.2	12	10	P82325	P82325 pisum sativ
422	2	18.2	12	Q8MYG1	Q8MYG1 drosophila	495	2	18.2	12	10	P82328	P82328 pisum sativ
423	2	18.2	12	Q9TWV4	Q9TWV4 lymnaea sta	496	2	18.2	12	10	Q8H6B6	Q8H6B6 hordeum vul
424	2	18.2	12	Q61574	Q61574 estertagia	497	2	18.2	12	11	Q8K303	Q8K303 mus musculu
425	2	18.2	12	Q9JHY4	Q9JHY4 sus sp. ies	498	2	18.2	12	11	Q35868	Q35868 mus musculu
426	2	18.2	12	Q8MJL0	Q8MJL0 suainus iu	499	2	18.2	12	11	Q9QVX4	Q9QVX4 rattus sp.
427	2	18.2	12	Q9JLY4	Q9JLY4 bos taurus	500	2	18.2	12	15	G12110	G12110 caprine art
428	2	18.2	12	Q8MJL6	Q8MJL6 callithrix							
429	2	18.2	12	Q9JLY4	Q9JLY4 callithrix							
430	2	18.2	12	Q9JLY4	Q9JLY4 bos taurus							
431	2	18.2	12	Q9XSV1	Q9XSV1 sus scrofa							
432	2	18.2	12	Q8MJL7	Q8MJL7 callithrix							
433	2	18.2	12	Q8MJL9	Q8MJL9 leontopitue							
434	2	18.2	12	Q8MJL6	Q8MJL6 cebuella py							
435	2	18.2	12	Q95NB4	Q95NB4 eulemur fu							
436	2	18.2	12	Q9NT18	Q9NT18 bos taurus							
437	2	18.2	12	Q8MJL3	Q8MJL3 saimiri sci							
438	2	18.2	12	Q8MJL1	Q8MJL1 atelies fusc							
439	2	18.2	12	Q8MJL2	Q8MJL2 cebus apeli							
440	2	18.2	12	Q8MJL4	Q8MJL4 aotus azara							
441	2	18.2	12	Q91129	Q91129 saguinus oe							
442	2	18.2	12	Q9TR17	Q9TR17 bos taurus							
443	2	18.2	12	Q83127	Q83127 bos indicus							
444	2	18.2	12	Q77891	Q77891 oreochromis							
445	2	18.2	12	Q77820	Q77820 pseudotroph							
446	2	18.2	12	Q77890	Q77890 oreochromis							
447	2	18.2	12	Q77889	Q77889 oreochromis							
448	2	18.2	12	Q8MES0	Q8MES0 anoda crist							
449	2	18.2	12	Q9T203	Q9T203 bos taurus							
450	2	18.2	12	Q95EJ8	Q95EJ8 dendrochilu							
451	2	18.2	12	Q95E16	Q95E16 dendrochilu							
452	2	18.2	12	Q8XN16	Q8XN16 malva nega							
453	2	18.2	12	Q8XN16	Q8XN16 palatella i							
454	2	18.2	12	Q95E15	Q95E15 dendrochilu							

ALIGNMENTS

RESULT 1

ID	P83333	PRELIMINARY:	PRT:	15 AA.
AC	P83333			
DT	01-JUN-2002 (TREMBLEI. 21, Created)			
DT	01-JUN-2002 (TREMBLEI. 21, Last sequence update)			
DT	01-OCT-2002 (TREMBLEI. 22, Last annotation update)			
DE	Lysozyme C III (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) (Fragment).			
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;			
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.			
OX	NCBI_TaxID=8022;			
RP	[1]			
RA	SEQUENCE, CATALYTIC ACTIVITY, AND MASS SPECTROMETRY.			
RT	TISSUE=Skin mucus;			
RT	Fernandes J.M.O., Kemp G.D., Smith V.J.;			
RT	*Characterisation of two muramidases from skin mucus of rainbow trout.*;			
KL	Submitted (APR-2002) to the SWISS-PROT data bank.			
CC	!- FUNCTION: LYSOZYMES HAVE PRIMARILY A BACTERIOLYTIC FUNCTION; THOSE			

CC IN TISSUES AND BODY FLUIDS ARE ASSOCIATED WITH THE MONOCYTE
 CC MACROPHAGE SYSTEM AND ENHANCE THE ACTIVITY OF IMMUNOAGENTS.
 CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4 BETA-LINKAGES BETWEEN N-
 CC ACETYL-D-GLUCOSAMINE AND N-ACETYL-MURAMIC ACID IN PEPTIDOGLYCAN
 CC HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.
 CC -1- MASS SPECTROMETRY: MW-14235; MTR0.00 MALDI.
 CC -1- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
 DR INTERPRO: IPR001916; Glyco_hydro_22.
 DR PROSITE: PS00128; LACTALBUMIN-LYSOZYME, PARTIAL.
 KW Hydrolase; Glycosidase; Bacteriolytic enzyme.
 FT NON_TER 15
 SQ SEQUENCE 15 AA: 1665 MW: 40516; 2568870 CRC64;
 Query Match 36.4%; Score 4; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKAL 4
 DB 9 AKAL 12
 RESULT 2
 Q9UCN4 PRELIMINARY: PRT; 8 AA.
 AC Q9UCN4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Cell-surface heparin/HEPARANSULFATE binding protein peptide 3
 DE (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE:92291055; PubMed:1601862;
 RA Reboudi N., Julian J., Rohde E.H., Carson E.D.
 RT "Identification of cell-surface heparin/heparan sulfate-binding
 RT proteins of a human uterine epithelial cell line (HUS-1)."
 RI J. Biol. Chem. 267:11930-11939(1992)
 SQ SEQUENCE 8 AA: 689 MW: 808733; 10540970 CRC64;
 Query Match 27.3%; Score 3; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.4e+0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GAK 9
 DB 2 GAK 4
 RESULT 3
 Q9R7E8 PRELIMINARY: PRT; 4 AA.
 AC Q9R7E8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE KdsB (Fragment).
 OS Escherichia coli.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Bacteriia; Proteobacteria; Escherichia.
 CC Enterobacteriaceae; Escherichia.
 CX NCBI_TaxID:562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:95180691; PubMed:7875564;
 RA Roseow C., Roberts J.S., Jann K.
 RT "Isolation from recombinant Escherichia coli, and characterization of
 RT CMP-Kds synthetase, involved in the expression of the capsular K5

RT polysaccharide (K-C5).";
 RL FEMS Microbiol. Lett. 125:159-164(1995).
 DR EMBL: S76943; AAB3585.1; .
 FT plasmid.
 FT NON_TER 1
 SQ SEQUENCE 9 AA: 899 MW: 388872042C33DD8 CRC64;
 Query Match 27.3%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GAK 9
 DB 2 GAK 4
 RESULT 4
 Q16605 PRELIMINARY: PRT; 9 AA.
 AC Q16605;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Glutathione S-transferase 2 (Fragment).
 DE GSTA2 OR GST2.
 GN GSTA2 OR GST2.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:88330756; PubMed:3138230;
 RA Chow N.W., Whang-Peng J., Kao-Shan C.S., Tam M.F., Lai H.C., Tu C.P.;
 RT "Human glutathione S transferases. The Ha multigene family encodes
 RT products of different but overlapping substrate specificities.";
 RI J. Biol. Chem. 263:12797-12800(1988).
 RL EMBL: M21867; AAA52617.1; .
 DR EMBL; M21866; AAA35918.1; .
 FT NON_TER 9
 SQ SEQUENCE 9 AA: 1116 MW: 1168E72327633B1D CRC64;
 Query Match 27.3%; Score 3; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 KPK 11
 DB 4 KPK 6
 RESULT 5
 Q9T2L0 PRELIMINARY: PRT; 9 AA.
 AC Q9T2L0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE LHC II-LIGHT-harvesting chlorophyll protein II (Fragment).
 GS Spinacia oleracea (Spinach).
 CC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
 CX NCBI_TaxID:3562;
 RN [1]
 RP SEQUENCE
 RX MEDLINE:91373386; PubMed:1894641;
 RA Michel H., Griffin P.R., Shabanowitz J., Hunt D.F., Bennett J.;
 RT "Tandem mass spectrometry identifies sites of three post-translational
 RT modifications of spinach light-harvesting chlorophyll protein II.
 RT Proteolytic cleavage, acetylation, and phosphorylation.";
 RI J. Biol. Chem. 266:17584-17591(1991).
 FT NON_TER 1


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FT NON_TER      9 AA: 999 MW: 5439276338 Da Lys 17654.
SQ SEQUENCE      27.3% Score 4: DB 4: Length 9:
Query Match     100.0% Pred. No. 6.5e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 6 KPK 8

RESULT 6
QNTZ11
ID QNTZ11 PRELIMINARY: PRI: 9 AA:
AC QNTZ11 (TEMBLrel. 13, Created)
DT 01-MAY-2003 (TEMBLrel. 13, Last sequence update)
DT 01-MAY-2003 (TEMBLrel. 13, Last sequence update)
DE LNC 11-LIGHT-harvesting chlorophyll protein 11 (Fragment)
OS Spinacia oleracea (Spinach)
OC Chloroplast
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Spinacia
CX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9137495; PubMed=1844841;
RA Michel H., Griffin P.R., Shabarwal Z.J., Bodo J.P., Bennett J.J.
RT "Random mass spectrometry identifies sites of three post-translational
RT modifications of spinach light-harvesting chlorophyll protein 11."
RT Proteolytic cleavage, acetylation, and phosphorylation."
RL J. Biol. Chem. 266:17584-17591(1991);
DR EMBL: AY171239; AAN73417.1;
FT NON_TER      9 AA: 985 MW: 5439276338 Da Lys 17654.
SQ SEQUENCE      27.3% Score 4: DB 4: Length 9:
Query Match     100.0% Pred. No. 6.5e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 6 KPK 8

RESULT 7
QBJUC2
ID QBJUC2 PRELIMINARY: PRI: 9 AA:
AC QBJUC2 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE Hsp70 (Fragment)
OS Eucaryota; Fungi; Microsporidia; Unikonta; Eukaryota; Eukaryota;
CX NCBI_TaxID=27973;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=RV6/95, and pV7/95;
RA Rao M., del Aquila C., Fenoy S., Benjamins J., N.
RT "Genotype variability in the microsporidian Encephalitozoon hellem."
RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY171238; AAN73415.1;
DR EMBL: AY171239; AAN73417.1;
FT NON_TER      10 AA: 1100 MW: 107614725 Da Lys 17654.
SQ SEQUENCE      27.3% Score 6: DB 5: Length 10:
Query Match     100.0% Pred. No. 6.5e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALN 5
DB 1 ALN 3

RESULT 10
Q91W73

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QY 3 ALN 5
DB 6 ALN 8

RESULT 8
Q81ZA2
ID Q81ZA2 PRELIMINARY: PRI: 10 AA:
AC Q81ZA2 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE Cardiac troponin 2 (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Blood;
RA Hahli A., Kubo T., Steffensen U., Steffensen M., McKenna W.J.,
RA Mogensen J.;
RT "Homo sapiens Troponin T (TNNT2) introns 6 and 7 and exon 7."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY160215; AAN71550.1;
FT NON_TER      10 AA: 1099 MW: AB245C6325BB1B16 CRC64;
SQ SEQUENCE      27.3% Score 3: DB 4: Length 10:
Query Match     100.0% Pred. No. 6.5e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 7 KPK 9

RESULT 9
Q8WPE7
ID Q8WPE7 PRELIMINARY: PRI: 10 AA:
AC Q8WPE7 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DE Opsin (Fragment)
OS Skogsbergia ferberii
OC Eukaryota; Metazoa; Artibeidae; Chiroptera; Ostracoda; Myodocopa;
CX NCBI_TaxID=176979;
RN [1]
RP SEQUENCE FROM N.A.
RA ISSUE=Entire organism;
RA Oakley T.H., Huber D.R.;
RT "Eye-specific expression of multiple opsin loci in ostracod
RT crustaceans."
RL Submitted (FEB 2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF353372; AAL37547.1;
FT NON_TER      10 AA: 1035 MW: 1F4B117672DDDD4 CRC64;
SQ SEQUENCE      27.3% Score 3: DB 5: Length 10:
Query Match     100.0% Pred. No. 6.5e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALN 5
DB 1 ALN 3

RESULT 10
Q91W73

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ID Q91WZ3 PRELIMINARY; PRT: 10 AA.
AC Q91WZ3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Luteinizing hormone/chorionic gonadotropin receptor homolog
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE=96147985; PubMed=8571710;
RA Shen Q.X., Liu H.H., Chen W.Y., Bahl C.P.;
RT "[Cloning and overexpression of rat ovary LH/hCG receptor cDNA in
RI insect cells].";
RL Shih Yen Sheng Wu Hsueh Pao 28:283-290(1995).
DR EMBL: S80660; AAB50710.1; -.
KW Chorion; Receptor.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1129 MW: 09A5F22DC4177760 CRC64:

Query Match 27.3%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAL 4
DB 6 RAL 8

RESULT 11
ID Q9Q0W9 PRELIMINARY; PRT: 10 AA.
AC Q9Q0W9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-UMEA3;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RI populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119350; AAF24106.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64:

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 12
ID Q8JV70 PRELIMINARY; PRT: 10 AA.
AC Q8JV70;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-USA 6;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,

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OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-USA 5;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RI gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL: AF304387; AAM97804.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64:

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 13
ID Q9Q0W1 PRELIMINARY; PRT: 10 AA.
AC Q9Q0W1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CSFB;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RI populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119354; AAF24114.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64:

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 14
ID Q8JV68 PRELIMINARY; PRT: 10 AA.
AC Q8JV68;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-USA 6;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,

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RA Girones R.;
RT "Potential transmission of human polyomavirus through the
KI gastrointestinal tract after exposure to virions or viral DNA.";
KL J. Virol. 75:10290-10299(2001).
DR EMBL: AF304388; AAM97806.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 15
Q69347 ID Q69347 PRELIMINARY: PRT: 10 AA.
AC Q69347
DT 01-NOV-1996 (TREMBlrel. 0; Created)
DI 01-NOV-1996 (TREMBlrel. 0; Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19; Last annotation update)
DE Hypothetical 1.1 kDa protein.
OS Herpes simplex virus (type 1 / strain: KOS)
OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KOS;
RX MEDLINE=86068025; PubMed=2999787;
RA Gibbs J.S., Chou H.C., Hali J.D., Mount D.W., Retondo M.J.,
RA Weller S.K., Coen D.M.;
RT "Sequence and mapping analyses of the herpes simplex virus DNA
KI polymerase gene predict a C-terminal, substrate binding domain.";
KL Proc. Natl. Acad. Sci. U.S.A. 82:7969-7973(1985).
DR EMBL: M10792; AAA66437.1; -;
KW Hypothetical protein.
SQ SEQUENCE 10 AA; 1057 MW; C45DF775BDC420 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAA 3
DB 3 AAA 5

RESULT 16
Q69349 ID Q69349 PRELIMINARY: PRT: 10 AA.
AC Q69349
DT 01-MAY-2000 (TREMBlrel. 13; Created)
DI 01-MAY-2000 (TREMBlrel. 13; Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13; Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses: dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSPE;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
KI populations by studying their presence in urban sewage.";
KL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119355; AAF24116.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 17
Q8JV84 ID Q8JV84 PRELIMINARY: PRT: 10 AA.
AC Q8JV84
DT 01-OCT-2002 (TREMBlrel. 22; Created)
DI 01-OCT-2002 (TREMBlrel. 22; Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22; Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses: dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G3;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
KI gastrointestinal tract after exposure to virions or viral DNA.";
KL J. Virol. 75:10290-10299(2001).
DR EMBL: AF303943; AAM97790.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1180 MW; 4CD6A97AF1A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 18
Q900W7 ID Q900W7 PRELIMINARY: PRT: 10 AA.
AC Q900W7
DT 01-MAY-2000 (TREMBlrel. 13; Created)
DI 01-MAY-2000 (TREMBlrel. 13; Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13; Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses: dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NANCY2;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
KI populations by studying their presence in urban sewage.";
KL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119351; AAF24108.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

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RESULT 19
Q8JV66 ID Q8JV66 PRELIMINARY; PRT; 10 AA.
AC Q8JV66;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSF K;
RX MEDLINE=21465052; PubMed=11581397;
RA Bojill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions of viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL: AF304389; AAM97808.1; -.
FT NON_TER 1
FT SEQUENCE 10 AA; 1167 MW; 4C06A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB [1]
3 KPK 5

RESULT 20
Q8JV7 ID Q8JV7 PRELIMINARY; PRT; 10 AA.
AC Q8JV7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSF2;
RX MEDLINE=2007544; PubMed=10618230;
RA Bojill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119356; AAF24118.1; -.
FT NON_TER 1
FT SEQUENCE 10 AA; 1167 MW; 4C06A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB [1]
3 KPK 5

RESULT 21
Q8JV82 ID Q8JV82 PRELIMINARY; PRT; 10 AA.
AC Q8JV82;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

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DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL;
RX MEDLINE=21465052; PubMed=11581397;
RA Bojill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions of viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL: AF303944; AAM97792.1; -.
FT NON_TER 1
FT SEQUENCE 10 AA; 1167 MW; 4C06A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB [1]
3 KPK 5

RESULT 22
Q8JV76 ID Q8JV76 PRELIMINARY; PRT; 10 AA.
AC Q8JV76;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA2;
RX MEDLINE=21465052; PubMed=11581397;
RA Bojill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions of viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL: AF303947; AAM97798.1; -.
FT NON_TER 1
FT SEQUENCE 10 AA; 1167 MW; 4C06A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB [1]
3 KPK 5

RESULT 23
Q8JV74 ID Q8JV74 PRELIMINARY; PRT; 10 AA.
AC Q8JV74;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.

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KC STRAIN-USA3;
RX MEDLINE-21465052; PubMed-11591392;
RA Bo111-Mas S., Formiga-Cruz M., Clemente-Saunders P., Calatell F.,
RA Girones R.;
RT *Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to viruses of viral [NA.];
RL J. Virol. 75:10290-10299(2003);
DR EMBL: AF303948; AAM97800.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4006A97771A32763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 24
Q9Q0X7 PRELIMINARY: PRT: 10 AA.
AC Q9Q0X7;
DT 01-MAY-2000 (TREMBlrel. 13; Created);
DI 01-MAY-2000 (TREMBlrel. 13; Last sequence update);
DE Large T antigen (Fragment);
OS Polyomavirus JC;
OC Viruses; dSDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN-BCN2;
RX MEDLINE-20087544; PubMed-10618230;
RT Bo111-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000);
DR EMBL: AF119346; AAF4098.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1180 MW: 4016A4172A1A29118064;

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 25
Q8JW78 PRELIMINARY: PRT: 10 AA.
AC Q8JW78;
DI 01-OCT-2002 (TREMBlrel. 22; Created);
DI 01-OCT-2002 (TREMBlrel. 22; Last sequence update);
DE Large T antigen (Fragment);
OS Polyomavirus JC;
OC Viruses; dSDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN-USA1;
RX MEDLINE-21465052; PubMed-11591392;
RA Bo111-Mas S., Formiga-Cruz M., Clemente-Saunders P., Calatell F.,
RA Girones R.;
RT *Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to viruses of viral [NA.];
RL J. Virol. 75:10290-10299(2003);
DR EMBL: AF303948; AAM97796.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4006A97771A32763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

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FT NON_TER 1
SQ SEQUENCE 10 AA: 1183 MW: 40D6A97771A32763 CRC64;

Query Match 27.4% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 26
Q9Q0W5 PRELIMINARY: PRT: 10 AA.
AC Q9Q0W5;
DT 01-MAY-2000 (TREMBlrel. 13; Created);
DT 01-MAY-2000 (TREMBlrel. 13; Last sequence update);
DT 01-MAY-2000 (TREMBlrel. 13; Last annotation update);
DE Large T antigen (Fragment);
OS Polyomavirus JC;
OC Viruses; dSDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN-PRETORIA3;
RX MEDLINE-20087544; PubMed-10618230;
RA Bo111-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000);
DR EMBL: AF119352; AAF24110.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 40D6A97771A32763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 27
Q9Q0X3 PRELIMINARY: PRT: 10 AA.
AC Q9Q0X3;
DT 01-MAY-2000 (TREMBlrel. 13; Created);
DT 01-MAY-2000 (TREMBlrel. 13; Last sequence update);
DT 01-MAY-2000 (TREMBlrel. 13; Last annotation update);
DE Large T antigen (Fragment);
OS Polyomavirus JC;
OC Viruses; dSDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN-BCN8;
RX MEDLINE-20087544; PubMed-10618230;
RA Bo111-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000);
DR EMBL: AF119348; AAF24102.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 40D6A97771A32763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

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Db          3 KPK 5

RESULT 28
Q900X5      PRELIMINARY;          PRT: 10 AA.
AC Q900X5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DI 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment);
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN BCN16;
RX MEDLINE=20087544; PubMed=10612230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119347; AAF24100.1;
FT NON_TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
Db 11
3 KPK 5

RESULT 29
Q900W3      PRELIMINARY;          PRT: 10 AA.
AC Q900W3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DI 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment);
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN PRETORIAL;
RX MEDLINE=20087544; PubMed=10612230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119353; AAF24112.1;
FT NON_TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
Db 11
3 KPK 5

RESULT 30
Q8JVB0      PRELIMINARY;          PRT: 10 AA.
AC Q8JVB0;
DI 01-OCT-2002 (TReMBLrel. 22, Created)
DI 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

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UT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment);
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-E2;
RX MEDLINE=21465052; PubMed=11581497;
RA Bofill-Mas S., Fortiga-Cruz M., Clemente-Casares P., Calafell F.,
   Girones R.;
RT "Potential transmission of human polyomaviruses through the
   gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:19290-19299(2001).
DR EMBL; AF303945; AAY97794.1;
FT NON_TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
Db 11
3 KPK 5

RESULT 31
Q900X1      PRELIMINARY;          PRT: 10 AA.
AC Q900X1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DI 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment);
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN15;
RX MEDLINE=20087544; PubMed=10612230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119349; AAF24104.1;
FT NON_TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
Db 11
3 KPK 5

RESULT 32
Q900X9      PRELIMINARY;          PRT: 10 AA.
AC Q900X9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DI 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment);
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN10;

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RX MEDLINE:20087544; PubMed=10518240;
RA Botilli-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polioviruses in human
R populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
OR EMBL: AF119345; AAF24096.1;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4206A97771A42763 CR*64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 13
ID Q8JV72 PRELIMINARY; PRT; 16 AA.
AC Q8JV72;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Poliovirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polioviridae; Poliovirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=USA 4;
MEDLINE=21465052; PubMed=11561347;
RA Botilli-Mas S., Formiga-Cruz M., Clemente-Diazos E., Calatell F.,
KA Girones R.;
RT "Potential transmission of human polioviruses through the
RT gastrointestinal tract after exposure to viruses of viral DNA.";
RL J. Virol. 75:10290-10295(2001).
OR EMBL: AF304386; AAM57802.1;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4206A97771A42763 CR*64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 14
ID Q8TDAB PRELIMINARY; PRT; 11 AA.
AC Q8TDAB;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DI 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glutathione synthetase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cho Y. W., Lee Y.-Y., Lim C.-J.;
RT "Cloning and characterization of glutathione synthetase gene from
R human placenta DNA.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.
OR EMBL: AF485789; AAL91591.1;
FT NON_TER 11
SQ SEQUENCE 11 AA; 1235 MW; 1CB2831E59F64374 CR*64;

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Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NMG 7
DB 4 NMG 6

RESULT 35
ID Q9IWX6 PRELIMINARY; PRT; 11 AA.
AC Q9IWX6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Juvenile hormone binding protein, JHBP-12.5 kDa CNBR peptide
DE (Fragment).
OS Manduca sexta (Tobacco hornmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Spingioidea;
OC Spingidae; Spinginae; Manduca.
CX NCBI_TaxID=7140;
RN [1]
RP SEQUENCE.
RX MEDLINE=92134256; PubMed=1734862;
RA Touhara K., Prestwich G.D.;
RT "Binding site mapping of a photoaffinity-labeled juvenile hormone
RT binding protein.";
RL Biochem. Biophys. Res. Commun. 182:466-473(1992).
FT NON_TER 11
SQ SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CR*64;

Query Match 27.3%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 9 GAK 11

RESULT 36
ID Q23876 PRELIMINARY; PRT; 11 AA.
AC Q23876;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 04, Last annotation update)
DE Actin 4.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
CX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82260445; PubMed=6286214;
RA McKeown M., Firtel R.A.;
RT "Actin multigene family of Dictyostelium.";
RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
OR EMBL: K02957; AAA33150.1;
DR EMBL; K02956; AAA33150.1; JOINED.
SQ SEQUENCE 11 AA; 1205 MW; 728B4C14C6C2CAAB CR*64;

Query Match 27.3%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALN 5
DB 9 ALN 10

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RESULT 37
Q9TOS9          PRELIMINARY;      PRT:      11 AA.
AC Q9TOS9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Transferrin (Fragment).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Giffard J.M., Brandon R.B., Bell T.K.;
RT "Further identification of single nucleotide polymorphisms in the
RL equine transferrin gene.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF185800; AAF05495.1; -
DR EMBL: AF185797; AAF05492.1; -
DR EMBL: AF185798; AAF05493.1; -
DR EMBL: AF185799; AAF05494.1; -
FT NON_TER 11
SQ SEQUENCE 11 AA; 1231 MW; 6586121E2DC4905D CRC64;

Query Match      27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KAK 4
DB 6 KAL 8

RESULT 38
Q9QVH3          PRELIMINARY;      PRT:      11 AA.
AC Q9QVH3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chromogranin-B, CGB-GLUCAGONOMA peptide (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92064871; PubMed=1954899;
RA Nielsen E., Wellinder B.S., Madsen A.L.;
RT "Chromogranin-B, a putative precursor of eight novel rat glucagonoma
RL peptides through processing at mono-, di-, or tri-basic residues.";
RL Endocrinology 129:3147-3156(1991).
DR InterPro; IPR001990; Granin.
DR Pfam; PF01271; Granin; 1.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1342 MW; 6C82C3734525AAB CRC64;

Query Match      27.3%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWG 7
DB 7 NWG 9

RESULT 39
Q8VLX8          PRELIMINARY;      PRT:      12 AA.
AC Q8VLX8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)

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DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Lysyl-tRNA synthetase (Fragment).
GN LYSS.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K18;
RA Spada S., Fembroke J.T., Wall J.G.;
RT "Cloning and characterisation of the czrB metal cation efflux protein
RL from T. thermophilus.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AJ307316; CAC83721.1; -
KW Aminocyl-tRNA synthetase.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1327 MW; 502A33E27ECDD813 CRC64;

Query Match      27.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 2 KPK 4

RESULT 40
P94011          PRELIMINARY;      PRT:      12 AA.
ID P94011;
AC P94011;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Elongation factor EF-1 alpha A4 (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN=cv. Columbia; TISSUE=Green siliques;
RA Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
DR EMBL: Z27066; CAA81582.1; -
FT NON_TER 1
SQ SEQUENCE 12 AA; 1229 MW; CEDA9EA59422CDD CRC64;

Query Match      27.3%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 10 GAK 12

RESULT 41
O34770          PRELIMINARY;      PRT:      13 AA.
ID O34770;
AC O34770;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE GUAA (Fragment).
GN GUAA.
OS Borrelia afzelii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=29518;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN PKO, VS461, and J11
RX MEDLINE-97426044; PubMed-9282746;
RA Tilly K., Casjens S., Stevenson H., Bono J.L., Samuels D.S., Hogan D.,
  Rosa P.;
RI "The Borrelia burgdorferi circular plasmid cp26: conservation of
  plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL: U93698; AAC45530.1;
DR EMBL: U93695; AAC45524.1;
DR EMBL: U94697; AAC45528.1;
FT NON_TER 13
SQ SEQUENCE 13 AA; 1421 MW; 08FAR3930E197220 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
DB 3 ARA 5

RESULT 42
Q34622
AC Q34622 PRELIMINARY; PRT; 13 AA.
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DI 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DI 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE GUAA (Fragment).
GN GUAA.
OS
OC Borrelia burgdorferi (Lyme disease spirochete).
OX NCBI_TaxID:135;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CT19, UN127C19-2, and 25015;
RX MEDLINE-97426044; PubMed-9282746;
RA Tilly K., Casjens S., Stevenson H., Bono J.L., Samuels D.S., Hogan D.,
  Rosa P.;
RI "The Borrelia burgdorferi circular plasmid cp26: conservation of
  plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL: U93694; AAC45522.1;
DR EMBL: U04280; AAC45543.1;
DR EMBL: U04282; AAC45541.1;
FT NON_TER 13
SQ SEQUENCE 13 AA; 1407 MW; 08FAR3930E197220 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
DB 3 ARA 5

RESULT 43
Q96PT0
ID Q96PT0 PRELIMINARY; PRT; 13 AA.
AC Q96PT0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

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DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Epilysin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21167821; PubMed-1121198;
RA Lohi J., Willson C.L., Roby J.D., Parks W.C.;
RI "Epilysin, a novel human matrix metalloproteinase (MMP-28) expressed
  in testis and keratinocytes and in response to injury.";
RL J. Biol. Chem. 276:10134-10144(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-21458570; PubMed-11574168;
RA Lilman S.A., Keski-Oja J., Lohi J.;
RI "Promoter characterization of the human and mouse epilysin (MMP-28)
  genes.";
RL Gene 275:185-194(2001).
DR EMBL: AF336346; AAL15619.1;
FT NON_TER 13
SQ SEQUENCE 13 AA; 1440 MW; 2F1EE783D61E2728 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAL 4
DB 10 RAL 12

RESULT 44
Q907D6
ID Q907D6 PRELIMINARY; PRT; 13 AA.
AC Q907D6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ycf24 protein (fragment).
GN YCF24.
OS Neospora caninum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
  Neospora.
OX NCBI_TaxID:29176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NC1;
RX MEDLINE-20074141; PubMed-10508442;
RA Lang-Unnasch N., Aiello D.P.;
RI "Sequence evidence for an altered genetic code in the Neospora caninum
  plastid.";
RL Int. J. Parasitol. 29:1557-1562(1999).
DR EMBL: AF138960; AAP14260.1;
FT NON_TER 1
SQ SEQUENCE 13 AA; 1532 MW; CC8DB4011FCDC40D CRC64;

Query Match 27.3%; Score 3; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
DB 6 ARA 8

RESULT 45
Q97122
ID Q97122 PRELIMINARY; PRT; 13 AA.
AC Q97122;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DI 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

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BT 01-MAY-1999 (TRENBLREL. 10, Last annotation update)
DN YCF24.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae.
CX Toxoplasma.
GX NCBI_TaxID=5811.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH.
RA Atello D.P., Lang-Unnasch N.J.
RT "Analysis of the rpoB gene product of Toxoplasma gondii."
RL Submitted (SEP-1998) to the EMBL/GenBank/Trna databases.
DR EMBL: AF095904; AAD17841.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA: 1532 MW: 1690640115167430.76664;
      Query Match      27.3% Score 3; DB 11; Length 13;
      Best local Similarity 100.0%; Pred. No. 8.2e+03;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
DB 6 ARA 8
      |||

RESULT 46
Q9GJC2 ID Q9GJC2 PRELIMINARY; PRT; 13 AA.
AC Q9GJC2
DT 01-MAR-2001 (TRENBLREL. 16, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DE Calpastatin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
GX NCBI_TaxID=9440.
RN [1]
RP SEQUENCE FROM N.A.
RA Noneman D., Geesink G.H., Kachmarian M.
RT "Differential splicing and protein isoforms of calpastatin."
RL Submitted (OCT-1999) to the EMBL/GenBank/Trna databases.
DR EMBL: AF192536; AAC31688.1; -.
DR EMBL: AF192535; AAC31687.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA: 1335 MW: 41671309666.63661;
      Query Match      27.3% Score 3; DB 11; Length 13;
      Best local Similarity 100.0%; Pred. No. 8.2e+03;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 4 KPK 6
      |||

RESULT 47
Q62455 ID Q62455 PRELIMINARY; PRT; 13 AA.
AC Q62455
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Trypsin (Fragment).
OS TrxA.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
GX NCBI_TaxID=10090.
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=A/1;
RX MEDLINE=87066713; Pubmed=3641189;
RA Stevenson B.J., Hagenbuechle C., Wellauer P.K.;
RT "Sequence organisation and transcriptional regulation of the mouse
   elastase II and trypsin genes.";
RL Nucleic Acids Res. 14:8307-8330(1986).
DR EMBL: X04580; CAA28248.1; -.
DR MGD: MGI:102757; Try4.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1346 MW: 20554200214D729 CRC64;
      Query Match      27.3% Score 3; DB 11; Length 13;
      Best local Similarity 100.0%; Pred. No. 8.2e+03;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAI 4
DB 2 RAI 4
      |||

RESULT 48
Q9CU06 ID Q9CU06 PRELIMINARY; PRT; 13 AA.
AC Q9CU06
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
DE Zona pellucida binding protein (Fragment).
OS Gn ZPBP.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
GX NCBI_TaxID=10090.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; Pubmed11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukushima Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuwamura P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Bellotti D., Bejanda N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustigich S., Hill D., Holtmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni E., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordenskiöld P., King B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:555-600(2001);
DR EMBL: AK018876; BAB31470.1; -.
DR MGD: MGI:1855701; Zpbp.
FT NON_TER 1
SQ SEQUENCE 13 AA: 1404 MW: 1644220999576842 CRC64;
      Query Match      27.3% Score 3; DB 11; Length 13;
      Best local Similarity 100.0%; Pred. No. 8.2e+03;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CAK 9
DB 8 CAK 10
      |||

RESULT 49
Q62455 ID Q62455 PRELIMINARY; PRT; 13 AA.
AC Q62455
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Trypsin (Fragment).
OS TrxA.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
GX NCBI_TaxID=10090.
RN [1]
RP SEQUENCE FROM N.A.

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ID Q6C1W3 PRELIMINARY: ERF: 14 AA.
AC Q6C1W3
DT 01-MAR-2003 (TrEMBLrel. 23, created)
DI 01-MAR-2003 (TrEMBLrel. 23, last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
DE MOF4-related protein (Fragment).
GN FEX189
GN Mus musculus (Mouse).
OS Mammalia: Eutheria: Chordata: Mammalia: Vertebrata: Euteleostomi:
OC Euteleostomi: Euteleostomi: Euteleostomi: Euteleostomi: Euteleostomi:
OX NCBI_TaxID:10090
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN 129/SvEv.
RA MEDLINE: 22220132; PubMed: 12274461.
RA Tomizaga K., Pereira-Smith O.,
RI "The genomic organization, promoter position and expression profile of
R2 the mouse MOF15 gene."
RL Gene 294:215-215(2002).
DR EMBL: AY072694; AAL67900.1; -.
FT NON-TER 13 13
SQ SEQUENCE 13 AA: 1544 MW: 980388/254276A (M024)

Query Match 27.38; Score 3; 16 hits; Length 14;
Best Local Similarity 100.0%; Pval No. 8; 400; 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 9 KPK 11
IB 111
IB 6 KPK 10

RESULT 50
Q69394 PRELIMINARY: ERF: 14 AA.
AC Q69394
DT 01-NOV-1996 (TrEMBLrel. 01, created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, last annotation update)
DE Glycoprotein precursor (Fragment).
OS Pseudorabies virus.
OC Viruses: dsDNA viruses, to RNA stage: Herpesviridae:
OX Alphaherpesvirinae: Varicellovirinae.
GN NCBI_TaxID:10445;
RN 111
RP SEQUENCE FROM N.A.
RC MEDLINE: 94227568; PubMed: 8485646;
RA Ryan P., Robbins A., Whealy M., Enquist W.
RC "Overall signal sequence hydrophobicity, polarity, and the in vitro
RI translocation efficiency of a herpesvirus signal peptide."
RL Virus Genes 7:5-21(1993).
DR EMBL: M77773; AAA73134.1; -.
KW Signal.
FT SIGNAL 1 12 POTENTIAL.
FT CHAIN 13 >13 POTENTIAL.
FT NON-TER 13 13
SQ SEQUENCE 13 AA: 1274 MW: 2036675/264644A (M024)

Query Match 27.38; Score 3; 16 hits; Length 14;
Best Local Similarity 100.0%; Pval No. 8; 400; 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 ASA 3
IB 111
IB 5 ASA 7

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Search completed: September 30, 2003, 11:17:50
 Job time : 45.6667 secs

GenCore version 5.1.1.6

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OM protein - protein search, using SW model

Run on: September 30, 2003, 10:07:04 : Search time 6.26 Seconds
 (without alignments)
 82 767 Million cell updates/sec

Title: us-09-787-443-3

Perfect score: 11

Sequence: 1 ARALWGAKPK 11

Scoring table: GLI30

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 4702605 residues

Word size : 9

Total number of hits satisfying chosen parameters: 707

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : SwissProt_41.*

Note: No. is the number of results predicted by chance to have a
 score greater than or equal to the score if the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	13	1	CH60_CANFA
2	3	27.3	10	1	COXQ_SHEEP
3	3	27.3	10	1	H1E1_ROMM
4	3	27.3	10	1	H1E2_ROMM
5	3	27.3	11	1	RS30_ONCMY
6	3	27.3	15	1	FGF1_CANFA
7	2	18.2	8	1	ACT_THETA
8	2	18.2	8	1	AKH_MELM
9	2	18.2	8	1	ALH4_CYTO
10	2	18.2	8	1	ALH5_CYTO
11	2	18.2	8	1	FAR4_CANFA
12	2	18.2	8	1	FAR5_CANFA
13	2	18.2	8	1	GLUR_HUMAN
14	2	18.2	8	1	H1E1_PERAM
15	2	18.2	8	1	H1E2_PERAM
16	2	18.2	8	1	H1E3_PERAM
17	2	18.2	8	1	LCK1_LEUMA
18	2	18.2	8	1	LCK2_LEUMA
19	2	18.2	8	1	LCK3_LEUMA
20	2	18.2	8	1	LCK4_LEUMA
21	2	18.2	8	1	LCK5_LEUMA
22	2	18.2	8	1	LCK6_LEUMA
23	2	18.2	8	1	LCK7_LEUMA
24	2	18.2	8	1	LCK8_LEUMA
25	2	18.2	8	1	NS1_MYCTU
26	2	18.2	8	1	RQIE_PANBO
27	2	18.2	8	1	RS1_ERWCH
28	2	18.2	8	1	RS7_MYCTU
29	2	18.2	8	1	TF34_RGVIN
30	2	18.2	8	1	UF06_M4USE
31	2	18.2	8	1	WPI_PEHAI
32	2	18.2	9	1	CON2_LUNGE
33	2	18.2	9	1	COM2_CONVE

34	2	18.2	9	1	FAR4_CALVO
35	2	18.2	9	1	FAR5_ASCSU
36	2	18.2	9	1	FAR5_PANRE
37	2	18.2	9	1	LMP1_LOCHI
38	2	18.2	9	1	NEUX_HUMAN
39	2	18.2	9	1	PSP_BOMMO
40	2	18.2	9	1	R133_BOVIN
41	2	18.2	9	1	IHYF_PIG
42	2	18.2	9	1	UPA6_HUMAN
43	2	18.2	10	1	BPP2_BOTJA
44	2	18.2	10	1	BPP8_BOTJA
45	2	18.2	10	1	BPP_VIPAS
46	2	18.2	10	1	CATB_SHEEP
47	2	18.2	10	1	COXA_ONCMY
48	2	18.2	10	1	COXQ_RABIT
49	2	18.2	10	1	FAR2_PENNO
50	2	18.2	10	1	FAR5_MACRS
51	2	18.2	10	1	FAR6_PANRE
52	2	18.2	10	1	FARP_MYTED
53	2	18.2	10	1	FIBB_CERSI
54	2	18.2	10	1	GLEM_HUMAN
55	2	18.2	10	1	GON1_CHEPR
56	2	18.2	10	1	GON3_PETMA
57	2	18.2	10	1	HTF_HELZE
58	2	18.2	10	1	HTF_NAUCI
59	2	18.2	10	1	LABA_JATMU
60	2	18.2	10	1	NS1_MYCTU
61	2	18.2	10	1	PAP1_PARMA
62	2	18.2	10	1	PNEU_HUMAN
63	2	18.2	10	1	PNEU_RAT
64	2	18.2	10	1	RCA_PINPS
65	2	18.2	10	1	RL16_ACHLA
66	2	18.2	10	1	TKN1_SCYCA
67	2	18.2	10	1	TKU2_UREUN
68	2	18.2	10	1	TPIS_NICPL
69	2	18.2	10	1	UPA5_HUMAN
70	2	18.2	10	1	URA6_HUMAN
71	2	18.2	10	1	XYNB_DICB4
72	2	18.2	11	1	BPPB_AKRIA
73	2	18.2	11	1	CAZ1_LITCI
74	2	18.2	11	1	CAZ2_LITCI
75	2	18.2	11	1	CS15_BACSU
76	2	18.2	11	1	ESL_RAT
77	2	18.2	11	1	LPW_THETH
78	2	18.2	11	1	MHB1_KLEPN
79	2	18.2	11	1	NUHM_CANFA
80	2	18.2	11	1	PVK1_PERAM
81	2	18.2	11	1	Q20A_COMTE
82	2	18.2	11	1	RRPL_CHAV
83	2	18.2	11	1	TKN2_UPERU
84	2	18.2	11	1	TKNA_GADMO
85	2	18.2	11	1	TKNA_HORSE
86	2	18.2	11	1	TKNA_ONCMY
87	2	18.2	11	1	TKNA_RANCA
88	2	18.2	11	1	TKNA_RANR1
89	2	18.2	11	1	TKNA_SCYCA
90	2	18.2	11	1	TKND_RANCA
91	2	18.2	11	1	ULAG_HUMAN
92	2	18.2	11	1	UXB2_YEAST
93	2	18.2	12	1	FAR7_PENNO
94	2	18.2	12	1	FRE1_LITIN
95	2	18.2	12	1	H2AX_ONCMY
96	2	18.2	12	1	HEP1_BACSE
97	2	18.2	12	1	LMT1_LOCHI
98	2	18.2	12	1	PORD_METTM
99	2	18.2	12	1	PSP3_PHYPA
100	2	18.2	12	1	RS19_CLYEP
101	2	18.2	12	1	RS19_ELYEP
102	2	18.2	12	1	SO15_BACSU
103	2	18.2	12	1	
104	2	18.2	12	1	
105	2	18.2	12	1	
106	2	18.2	12	1	

P1859	calliphora
P3170	ascaris suu
P8261	panagrellus
P31799	locusta mig
P04277	homo sapien
P82003	bombyx mori
P29226	bos taurus
P01255	sus scrofa
P30092	homo sapien
P30422	bothrops ja
P01022	bothrops ja
P30426	bothrops in
P31351	vipera aspi
P83205	ovis aries
P80328	oncorhynch
P80336	oryctolagus
P83317	penaeus mon
P83278	macrobachi
P26660	panagrellus
P14537	mytilus edu
P02728	homo sapien
P80677	chelyosoma
P04378	petromyzon
P30948	petromyzon
P16353	heliothis z
P10939	nauphoeta c
P14596	tabanus atr
P13270	jatropha mu
P81135	mycobacteri
P81863	pardachirus
P22103	homo sapien
P21996	rattus norv
P81084	pinus pinas
P29221	acholeplasm
P08608	scyllorhinu
P40752	urechis uni
P19118	nicotiana p
P30091	homo sapien
P32080	homo sapien
P80717	dictyoglomu
P01021	akistodon
P82087	litoria cit
P82088	litoria cit
P81095	batillus su
P56571	rattus norv
P83321	penaeus mon
P05624	thermus the
P80580	klebsiella
P49820	canis fami
P41837	periplaneta
P80464	comamonas t
P13179	chandiura
P08616	uperoleia r
P28498	gadus morhu
P01290	equus cabal
P28499	oncorhynch
P22688	rana catesb
P29207	rana ridibu
P41333	scyllorhinu
P22691	rana catesb
P31933	homo sapien
P99013	saccharomyc
P83322	penaeus mon
P82021	litoria inf
P83327	oncorhynch
P83054	bacteroides
P23395	locusta mig
P80903	methanobact
P80662	physcomitre
O46400	clover yell
O47881	elm yellows
P80863	bacillus su

253	1	9.1	8	1	CC26_MAIZE	P80632	zea mays (m	326	1	9.1	9	1	TKC1_CALVO	P41517	calliphora
254	1	9.1	8	1	UH09_RAT	P56575	rattus norv	327	1	9.1	9	1	TKL1_LOEMI	P16223	locusta mig
255	1	9.1	8	1	UPA1_HUMAN	P30087	homo sapien	328	1	9.1	9	1	TRP4_LEUMA	P81736	leucophaea
256	1	9.1	8	1	UPA2_HUMAN	P30296	homo sapien	329	1	9.1	9	1	ULAD_HUMAN	P31929	homo sapien
257	1	9.1	8	1	VG03_HSV2H	P81780	herpes simp	330	1	9.1	9	1	ULAE_HUMAN	P31931	homo sapien
258	1	9.1	9	1	AL10_CARMA	P81813	carcinus ma	331	1	9.1	9	1	ULAH_HUMAN	P31934	homo sapien
259	1	9.1	9	1	AL11_CARMA	P81814	carcinus ma	332	1	9.1	9	1	ULAK_MOUSE	P99031	mus musculus
260	1	9.1	9	1	AL12_CARMA	P82678	chlamydomon	333	1	9.1	9	1	UN19_CLOPA	P81355	clostridium
261	1	9.1	9	1	BS41_SERP2	P81375	serattia p.	334	1	9.1	9	1	UPA3_HUMAN	P30089	homo sapien
262	1	9.1	9	1	BUX_CLOPA	P81377	clostridium	335	1	9.1	9	1	UPA7_HUMAN	P30093	homo sapien
263	1	9.1	9	1	CCAP_CARMA	P36556	carcinus ma	336	1	9.1	9	1	XY1A_STRSQ	P19149	streptomyce
264	1	9.1	9	1	CUN1_CUNST	P05487	conus striat	337	1	9.1	9	1	YHFR_AZOV1	P25825	azotobacter
265	1	9.1	9	1	CUXE_THUOB	P89575	thunnus obo	338	1	9.1	10	1	AEGL_AGRAE	P83465	agrocyste ae
266	1	9.1	9	1	DEL_NEPNO	P24616	nephrops mi	339	1	9.1	10	1	AH3_PRUSE	P29261	prunus sero
267	1	9.1	9	1	GNF1_LOEMI	P76334	locusta mig	340	1	9.1	10	1	AKHX_LOEMI	P81626	locusta mig
268	1	9.1	9	1	GSIP_RABIT	P01158	oryctolagus	341	1	9.1	10	1	AL19_CARMA	P81822	carcinus ma
269	1	9.1	9	1	FAR1_CALVO	P41856	calliphora	342	1	9.1	10	1	AMPN_HELAM	P81731	helicoverpa
270	1	9.1	9	1	FAR2_CALVO	P41857	calliphora	343	1	9.1	10	1	ANGL_BOTJA	Q10581	bothrops ja
271	1	9.1	9	1	FAR3_PANRE	P41873	panagrellus	344	1	9.1	10	1	ANGT_BOVIN	P01017	bos taurus
272	1	9.1	9	1	FAR4_CALVO	P41858	calliphora	345	1	9.1	10	1	ANGT_CHICK	P01018	gallus gall
273	1	9.1	9	1	FAR5_MACRS	P83276	macrobrachi	346	1	9.1	10	1	APE_CACGI	P80474	capnocytoph
274	1	9.1	9	1	FAR6_PENMO	P83318	penaeus mon	347	1	9.1	10	1	BRK_ONCMY	Q9prz1	oncorhynch
275	1	9.1	9	1	FAR7_PENMO	P83319	penaeus mon	348	1	9.1	10	1	CAJ2_LITCI	P82086	litoria cit
276	1	9.1	9	1	FAR8_CALVO	P41860	calliphora	349	1	9.1	10	1	CAER_LITXA	P56264	litoria xan
277	1	9.1	9	1	FAR9_PENMO	P83420	penaeus mon	350	1	9.1	10	1	COXH_ONCMY	P80331	oncorhynch
278	1	9.1	9	1	FAR0_CALVO	P41861	calliphora	351	1	9.1	10	1	COXX_ONCMY	P80332	oncorhynch
279	1	9.1	9	1	FAR6_MACRS	P83279	macrobrachi	352	1	9.1	10	1	COXM_RAT	P80431	rattus norv
280	1	9.1	9	1	FAR7_CALVO	P41862	calliphora	353	1	9.1	10	1	COXO_RAT	P80432	rattus norv
281	1	9.1	9	1	FAR8_MACRS	P83261	macrobrachi	354	1	9.1	10	1	COXO_THUOB	P80982	thunnus obo
282	1	9.1	9	1	FAR9_ASHSB	P43172	ascaris suu	355	1	9.1	10	1	CU30_LOEMI	P11735	locusta mig
283	1	9.1	9	1	FAR0_CALVO	P41865	calliphora	356	1	9.1	10	1	ESL_LACCA	P81758	lactobacilli
284	1	9.1	9	1	FAR1_CALVO	P41868	calliphora	357	1	9.1	10	1	ESTA_SCHGA	P81012	schizaphis
285	1	9.1	9	1	FAR2_CALSI	P18495	callinectes	358	1	9.1	10	1	FAR7_MACRS	P83280	macrobrachi
286	1	9.1	9	1	FAR3_ERYP2	P19346	erythrocybe	359	1	9.1	10	1	FARC_CALVO	P41867	calliphora
287	1	9.1	9	1	FAR4_MACFC	P19345	macaca fusc	360	1	9.1	10	1	FARP_LOEMI	P38553	locusta mig
288	1	9.1	9	1	FAR5_PAPAN	P19344	papio anabi	361	1	9.1	10	1	FARP_RANSE	P18523	manduca sex
289	1	9.1	9	1	FAR6_PAPHA	P19343	papio hamad	362	1	9.1	10	1	GAJU_HUMAN	P01358	homo sapien
290	1	9.1	9	1	FAR7_TREGE	P19342	theropitheci	363	1	9.1	10	1	GONI_ALLMI	P37041	alligator m
291	1	9.1	9	1	FAR8_SARBU	P80359	treponema h	364	1	9.1	10	1	GONI_CLOPA	P81749	clupea pall
292	1	9.1	9	1	FAR9_KLEAE	P83350	sarcophaqa	365	1	9.1	10	1	GON2_CHEPR	P80678	chelyosoma
293	1	9.1	9	1	HPIC_KLEAE	P12361	kiepsicla	366	1	9.1	10	1	GON3_CHICK	P37043	gallus gall
294	1	9.1	9	1	LPYR_RHOVI	P82492	rhodopsendo	367	1	9.1	10	1	GON3_ONCRE	P20367	oncorhynch
295	1	9.1	9	1	ISO_CYPGA	P42493	cyprinus ca	368	1	9.1	10	1	GONL_SQUAC	P27429	squalus aca
296	1	9.1	9	1	KNL3_BOMVA	P83058	bombina var	369	1	9.1	10	1	GRP_RANRI	P23260	rana ridibu
297	1	9.1	9	1	LITR_LITAU	P08945	litoria aur	370	1	9.1	10	1	GS09_BACSU	P80243	bacillus su
298	1	9.1	9	1	LITR_PHYKO	P08946	phyllomedus	371	1	9.1	10	1	LCMS_LEUMA	P21144	leucophaea
299	1	9.1	9	1	LMG3_LOEMI	P41489	locusta mig	372	1	9.1	10	1	LPK2_LOEMI	P41488	locusta mig
300	1	9.1	9	1	LPK3_STAGU	P36884	staphylococ	373	1	9.1	10	1	LSK2_LEUMA	P09039	leucophaea
301	1	9.1	9	1	MCMT_BOVIN	P29177	bos taurus	374	1	9.1	10	1	MALE_KLEPN	Q05564	klebsiella
302	1	9.1	9	1	MOSH_CLYJA	P19853	clypeaster	375	1	9.1	10	1	MOSQ_CLYJA	P19962	clypeaster
303	1	9.1	9	1	MOSH_CLYJA	P19854	clypeaster	376	1	9.1	10	1	MP2_MICOC	P81533	microplitis
304	1	9.1	9	1	NEF_HV125	P12481	human immun	377	1	9.1	10	1	NO40_TOBAC	P55962	nicotiana t
305	1	9.1	9	1	NEUO_CAVPO	P34966	cavia porce	378	1	9.1	10	1	ODP2_BOVIN	P11180	bos taurus
306	1	9.1	9	1	NSK1_SARBU	P41492	sarcophaqa	379	1	9.1	10	1	POPB_METTM	P80901	methanobact
307	1	9.1	9	1	OXVA_SCYCA	P42956	scyllorhinu	380	1	9.1	10	1	PPCK_FASHE	P80525	fasciola he
308	1	9.1	9	1	OXVA_SQUAC	P42959	squalus aca	381	1	9.1	10	1	PSBF_CAPAN	Q03367	capsicum an
309	1	9.1	9	1	OXVE_SCYCA	P42957	scyllorhinu	382	1	9.1	10	1	PVK_LOEMI	P83382	locusta mig
310	1	9.1	9	1	OXVI_RUFEC	P42955	bufo requia	383	1	9.1	10	1	Q20B_COMTE	P80465	comamonas t
311	1	9.1	9	1	OXVI_CYPGA	P23879	cyprinus ca	384	1	9.1	10	1	Q20G_COMTE	P80466	comamonas t
312	1	9.1	9	1	OXVI_ESEFO	P42968	eisenia foe	385	1	9.1	10	1	RRPL_PHODV	P35946	phocine dis
313	1	9.1	9	1	OXVT_OATVC	P80027	octopus vul	386	1	9.1	10	1	RT02_BOVIN	P82923	bos taurus
314	1	9.1	9	1	OXYT_RAHIT	P12878	oryctolagus	387	1	9.1	10	1	SLAP_BACTG	P49325	baillus th
315	1	9.1	9	1	OXYT_PALCI	P42994	raja clavac	388	1	9.1	10	1	SP34_DICMU	P81545	dictyosteli
316	1	9.1	9	1	OXVY_SQUAC	P43000	squalus aca	389	1	9.1	10	1	SPI_HALRO	Q10997	halocynthia
317	1	9.1	9	1	PGJR_DIAAB	P81179	diaprepes a	390	1	9.1	10	1	SYK_CAMUP	Q46464	campylobact
318	1	9.1	9	1	PPH1_LYCES	P83380	lycopersico	391	1	9.1	10	1	TENK_RANTE	P56923	rana tempor
319	1	9.1	9	1	PPK1_PERAM	P82591	periplaneta	392	1	9.1	10	1	TKL2_LOEMI	P16224	locusta mig
320	1	9.1	9	1	RE42_LITRU	P82075	litoria rub	393	1	9.1	10	1	TKL3_LOEMI	P30249	locusta mig
321	1	9.1	9	1	RS10_SERMA	Q68936	serratia ma	394	1	9.1	10	1	TKL4_LOEMI	P30250	locusta mig
322	1	9.1	9	1	SAMP_MUSCA	P19095	musculus ca	395	1	9.1	10	1	TKNB_CHICK	P19851	gallus gall
323	1	9.1	9	1	SAP_STOVA	P24047	stomopreute	396	1	9.1	10	1	TKNB_ONCMY	P28500	oncorhynch
324	1	9.1	9	1	TAL1_PICGA	P17440	piechia jadi	397	1	9.1	10	1	TKNB_RANCA	P22689	rana catesb
325	1	9.1	9	1	TAL3_PICGA	P17441	piechia jadi	398	1	9.1	10	1	TKNB_RANRI	P29135	rana ridibu

399	1	9.1	10	1	TKNC_RANCA	P22690 rana catesb	472	1	9.1	12	1	CD14_LITXA	P56246 litoria xan
400	1	9.1	10	1	TKNC_PIG	P01292 sus scrofa	473	1	9.1	12	1	CXAL_CONIM	P50983 conus imper
401	1	9.1	10	1	TKN_PHYBI	P08610C phyllorcedus	474	1	9.1	12	1	CXL3_CONMR	P58809 conus marmo
402	1	9.1	10	1	TKS1_AEGAE	P42634 acedus aegypt	475	1	9.1	12	1	CXST_CONTE	P58846 conus texti
403	1	9.1	10	1	TKS2_AEGAE	P42635 acedus aegypt	476	1	9.1	12	1	FART_CALVO	P41869 calliphora
404	1	9.1	10	1	TKU1_UPERN	P40751 urechis uni	477	1	9.1	12	1	FLF1_SARBU	P83349 sarcophaga
405	1	9.1	10	1	TKOF_AEGAE	P19425 aedes aegypt	478	1	9.1	12	1	GRAP_RANRU	P40754 rana rugosa
406	1	9.1	10	1	TRP5_LEUMA	P81747 leucophaea	479	1	9.1	12	1	HCY1_CARMA	P83176 carcinus ma
407	1	9.1	10	1	TRP6_LEUMA	P81748 leucophaea	480	1	9.1	12	1	HCY8_MEGCR	Q10584 carcinus ma
408	1	9.1	10	1	TRP7_LEUMA	P81749 leucophaea	481	1	9.1	12	1	HSYA_RAT	Q10584 megathura c
409	1	9.1	10	1	TRP8_LEUMA	P81746 leucophaea	482	1	9.1	12	1	LICH_BACLI	P82995 rattus norv
410	1	9.1	10	1	TRP9_LEUMA	P81744 leucophaea	483	1	9.1	12	1	LOSC_LOCM1	P82907 bacillus li
411	1	9.1	10	1	UHU5_RAT	P56573 rattus norv	484	1	9.1	12	1	LOSC_LOCM1	P47733 locusta mig
412	1	9.1	10	1	UHA3_HUMAN	P40949 homo sapien	485	1	9.1	12	1	NO40_LOTJA	Q22426 lotus japon
413	1	9.1	10	1	UPA2_HUMAN	P50088 homo sapien	486	1	9.1	12	1	NO40_SESRO	Q24369 sesbania ro
414	1	9.1	10	1	UPA4_HUMAN	P40396 homo sapien	487	1	9.1	12	1	NO40_SOYBN	P55960 glycine max
415	1	9.1	10	1	UPA8_HUMAN	P40394 homo sapien	488	1	9.1	12	1	NUDM_CANFA	P54713 canis famli
416	1	9.1	10	1	UPA9_HUMAN	P40395 homo sapien	489	1	9.1	12	1	OPS3_DROVI	P17645 drosophila
417	1	9.1	10	1	URAI_HUMAN	P32118 homo sapien	490	1	9.1	12	1	PA21_MIFPM	P25072 micrurus fu
418	1	9.1	10	1	URAT_HUMAN	P34940 homo sapien	491	1	9.1	12	1	PA28_VIPBO	P31859 vipera beru
419	1	9.1	10	1	URE3_MORMO	P12349 morganella	492	1	9.1	12	1	PPK4_PERPU	P82619 periplaneta
420	1	9.1	10	1	UXA2_CHLIR	P16003 chlamydia t	493	1	9.1	12	1	PPK4_PERPU	P82690 periplaneta
421	1	9.1	10	1	UXA6_CHLIR	P38007 chlamydia t	494	1	9.1	12	1	PVK2_PERAM	P81555 periplaneta
422	1	9.1	10	1	YEH1_YEAST	P59012 saccharomyc	495	1	9.1	12	1	RPI1_CONSP	P58805 conus spuri
423	1	9.1	10	1	YEG3_BACSU	P66699 bacillus su	496	1	9.1	12	1	RI16_GINB1	P36207 ginkgo bilo
424	1	9.1	11	1	ANG1_CRIGE	P09037 citinia geor	497	1	9.1	12	1	RS19_TOBBP	Q56251 tomato big
425	1	9.1	11	1	ASL1_BACSE	P83146 bacteroides	498	1	9.1	12	1	TA10_TREME	P01371 tremella me
426	1	9.1	11	1	ASL2_BACSE	P83147 bacteroides	499	1	9.1	12	1	TIN2_HOPTI	P82652 hoplobatrac
427	1	9.1	11	1	BPF3_BOVIN	P30426 bothrops in	500	1	9.1	12	1	TIN3_HOPTI	P82653 hoplobatrac
428	1	9.1	11	1	BPF4_BOVIN	P30424 bothrops in						TKN2_KASMA	P08614 kassina mac
429	1	9.1	11	1	BEP4_AGRIF	P04562 agkistrodon							
430	1	9.1	11	1	BKK_MEJFL	P12797 megalocolla							
431	1	9.1	11	1	CAL1_HITCI	P82089 litoria cit							
432	1	9.1	11	1	CAS2_HITCI	P82090 litoria cit							
433	1	9.1	11	1	CAL1_HITCI	P82091 litoria cit							
434	1	9.1	11	1	CAS2_HITCI	P82092 litoria cit							
435	1	9.1	11	1	CEP1_AHFT	P22790 achelonia lu							
436	1	9.1	11	1	GOR2_PERAM	P11496 periplaneta							
437	1	9.1	11	1	CUXA_CANFA	P59501 canis famli							
438	1	9.1	11	1	CXSA_CONAL	P58846 conus aulic							
439	1	9.1	11	1	CX5R_CONAL	P58849 conus aulic							
440	1	9.1	11	1	CXLI_CONMR	P58807 conus marmo							
441	1	9.1	11	1	EFQ2_COPPA	P81350 elostriadum							
442	1	9.1	11	1	FAR4_CALVO	P41864 calliphora							
443	1	9.1	11	1	HS72_FINES	P81672 pinus pine							
444	1	9.1	11	1	CADU_CONMY	P84016 cancorystha							
445	1	9.1	11	1	LSK1_LEUMA	P84328 leucophaea							
446	1	9.1	11	1	LSK2_PERAM	P86855 periplaneta							
447	1	9.1	11	1	MLG2_HETS	P41489 thermomyza							
448	1	9.1	11	1	MCRN_HUMAN	P01763 homo sapien							
449	1	9.1	11	1	NXSN_PSETE	P59072 pseudonaja							
450	1	9.1	11	1	PKC1_CARMO	P82684 caradacus m							
451	1	9.1	11	1	PUGC_PSEFL	P55373 pseudomora							
452	1	9.1	11	1	PUGC_RANP1	P08051 rana pipien							
453	1	9.1	11	1	REA1_LLIRD	P82074 litoria rib							
454	1	9.1	11	1	REP2_CONAM	P42441 comopholis							
455	1	9.1	11	1	T2P1_PPROVO	P31041 proteus vti							
456	1	9.1	11	1	TINI_HOPTI	P82651 heplotracc							
457	1	9.1	11	1	TINI_HOPTI	P82654 hoplobatrac							
458	1	9.1	11	1	TKC2_CALVO	P41518 calliphora							
459	1	9.1	11	1	TKN1_PSEBU	P42486 pseudophryn							
460	1	9.1	11	1	TKN1_UPERN	P82026 uperoleia i							
461	1	9.1	11	1	TKN1_UPERN	P08612 uperoleia r							
462	1	9.1	11	1	TKN2_PSEBU	P42487 pseudophryn							
463	1	9.1	11	1	TKN1_PSEBU	P42488 pseudophryn							
464	1	9.1	11	1	TKN1_PSEBU	P42489 pseudophryn							
465	1	9.1	11	1	TKN5_PSEBU	P42490 pseudophryn							
466	1	9.1	11	1	TKNA_CHLIR	P19480 gallus gal							
467	1	9.1	11	1	TKNA_ELEMO	P01293 eleodone mos							
468	1	9.1	11	1	TKN_PSEBU	P08615 physalaema							
469	1	9.1	11	1	UE05_MOUSE	P48643 mus musculu							
470	1	9.1	12	1	CALM_TETIT	G05555 tetrahymen							
471	1	9.1	12	1	CD14_LITXA	P56246 litoria xan							

ALIGNMENTS

CH60_CANFA	STANDARD:	PRT:	13 AA.
AC P49818;			
DT 01-OCT-1996 (Ref. 34, Created)			
DT 01-OCT-1996 (Ref. 34, Last sequence update)			
DT 16-OCT-2001 (Ref. 40, Last annotation update)			
DE 60 kDa heat shock protein, mitochondrial (Hsp60) (60 kDa chaperonin)			
DE (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein			
DE P1) (Fragment).			
DE HSP60 OR HSP60.			
CS Canis familiaris (Dog).			
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
CX NCBI_TaxID=9615;			
RN [1]			
RP SEQUENCE.			
RC TISSUE=Heart;			
RC MEDLINE=98163440; PubMed=9504812;			
RC Dunn M.J., Corbett J.M., Wheeler C.H.;			
RT *HSC-2DPAGE and the two-dimensional gel electrophoresis database of			
RT dog heart proteins.			
RL Electrophoresis 18:2795-2802(1997).			
CC -1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND			
CC MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF			
CC REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED			
CC UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX.			
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.			
CC -1- SIMILARITY: Belongs to the chaperonin (HSP60) family.			
DR HSC-2DPAGE; P49818; DOG.			
DR InterPro: IPR001844; Chaperin_Cpn60.			
DR PROSITE: PS00296; CHAPERONIN_CPN60; PARTIAL.			
KW Chaperone; ATP-binding; Mitochondrion.			
FT NON_TER 13			
SQ SEQUENCE 13 AA: 1363 MW: C6571E012DBFE879 CRC64;			
Query Match 94.4%; Score 4; DB 1; Length 13;			
Best Local Similarity 100.0%; Pred. No. 1.3e+02;			

KT "A unique charged tyrosine-containing member of the adipokinetic
 RT hormone/red-pigment-concentrating hormone peptide family isolated and
 RL sequenced from two beetle species.";
 RN Biochem. J. 275:671-677(1991).
 RP [2]

RP SPECIES-P. marginata; TISSUE=Corpora cardiaca;
 RX MEDLINE=92265187; PubMed=1586453;
 RA Gaede G., Lopata A., Kellner R., Rinehart K.L. Jiro.
 RI "Primary structures of neuropeptides isolated from the corpora
 RT cardiaca of various cetonid beetle species determined by
 KT pulsed liquid phase sequencing and tandem fast atom bombardment mass
 KT spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).

CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HETH / RPCH FAMILY.

DR PIR: A58641; A58641.
 DR PIR: S15422; S15422.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH: 1.
 KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.
 FT MOD_RES 8 1 PYROGLUTAMINE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 1022 MW: 867AB775AB54736 CRC64:

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 I,
 DB 2 LN 3

RESULT 9

ALL4_CVDPO STANDARD: PRT: # AA.
 AC P82155;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Cydiastatin 4.
 OS Cydia pomonella (Codling moth).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Davey M., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).

CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 910 MW: 92287905AB477400 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2
 I,
 DB 1 AR 2

RESULT 10

ALL5_CVDPO STANDARD: PRT: 8 AA.
 AC P82155;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Cydiastatin 5.
 OS Cydia pomonella (Codling moth).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Davey M., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA Davey M., East P.D., Thorpe A.;
 RT "Lepidopteran peptides of the allatostatin superfamily.";
 RL Peptides 18:1301-1309(1997).

CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 898 MW: 922879CABB58640D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2
 I,
 DB 1 AR 2

RESULT 11

FAR4_MACRS STANDARD: PRT: 8 AA.
 AC P83277;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE FMRFamide-like neuropeptide Flp4 (APALRFR-amide).
 OS Macrobrachium rosenbergii (Giant fresh water prawn).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 OX NCBI_TaxID=79674;
 RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Eye stalk;
 RA Sithigornkul P., Sarathongkum W., Jaidechoey S., Longyant S.,
 RA Sithigornkul W.;
 RT "Novel FMRFamide-like neuropeptides from the eye stalk of the giant
 RT freshwater prawn Macrobrachium rosenbergii.";
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -!- MASS SPECTROMETRY: MW-943; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.

DR GO: GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 943 MW: 9CD40734072DC76D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AL 4
 I,
 DB 3 AL 4

RESULT 12

FARB_CALVO
 ID FARB_CALVO STANDARD: PRI: 5 AA.
 AC P41863;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Callipremamide 8.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Musciformia; Tsetseidra;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN 1;
 RP SEQUENCE.
 RC TISSUE Thoracic ganglion;
 RX MEDLINE=62196111; PubMed=1549595;
 RA Dave B., Johnson A.H., Sewell J.C., Scott A.G., Orchard L.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of the Met Arg-Pho-NH2
 RT neuropeptides (designated callipremamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1 SIMILARITY: BELONGS TO THE FARB (PMKFAAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC PIR: H41978; H41978.
 DR Neuropeptide; Amidation.
 KW MOD.RES 8 8 AMIDATION
 FT SEQUENCE 8 AA; 957 MW; 72245699CAA444045 (Unk4);
 SQ
 Query Match 18.2% Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GA 8
 1 GA 2
 QY 1 GA 2
 RESULT 13
 GLUR_HUMAN
 ID GLUR_HUMAN STANDARD: PRI: 8 AA.
 AC P02729;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urine glycopeptide.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Platyhelminthes; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Paranthropus; Hominidae; Homo;
 OX NCBI_TaxID=9606;
 RN 1;
 RP SEQUENCE.
 RC MEDLINE=72062338; PubMed=5126885;
 RA Lohr C.J., Weiss J.B.;
 RT "Identification in urine of a low molecular weight highly polar
 RT glycopeptide containing cysteinyl-galactose.";
 RL Biochem. J. 123:25P-25P(1971).
 CC -1- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
 CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
 CC ATTRIBUTED. AN ERTHROCYTE MEMBRANE GLYCOPROTEIN HAVING A
 CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
 CC PIR: A03188; XGHUEU.
 DR G01300C5576; C10extracellular; NAS.
 DR Glycoprotein.
 KW CARBOHYD 1 1 S-LINKED (GLUCOSE)
 FT SEQUENCE 8 AA; 855 MW; C2D87AALF5BIEBIE (Unk4).
 SQ
 Query Match 18.2% Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GA 8
 11

Db 7 GA 8
 RESULT 14
 HTFL_PERAM
 ID HTFL_PERAM STANDARD: PRI: 8 AA.
 AC P04548;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-1994 (Rel. 41, Last annotation update)
 DE Hypertrahaloemic factor I (Neuropeptide M-I) (Periplanetin CC-I)
 DE (PeA-CAH-I) (LeD CC-I) (Hypertrahaloemic neuropeptide I).
 OS Periplaneta americana (American cockroach).
 OS Leptinotarsa decemlineata (Colorado potato beetle), and
 OS Blatta orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
 OC Blattellidae; Periplaneta.
 OX NCBI_TaxID=6978; 7539; 6976;
 RN 1;
 RP SEQUENCE.
 RC SPECIES-P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schafer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L. Jr.;
 RT "Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN 12;
 RP SEQUENCE.
 RC SPECIES-P.americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Willer C.A., Schooley D.A.;
 RT "Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN 3;
 RP SEQUENCE.
 RC SPECIES-I.decemlineata; TISSUE-Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN 14;
 RP SEQUENCE.
 RC SPECIES-B.orientalis; TISSUE-Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrahaloemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphodrhina portentosa, Blattella germanica and Blatta orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: HYPERTRHALOEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
 CC PIR: A44960; A44960.
 DR PIR: A49823; A49823.
 DR PIR: S08995; S08995.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation.
 FT MOD.RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD.RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;


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RI *Isolation, primary structure and synthesis of two neuropeptides
RI from Leucophaea maderae: members of a new family of
RI Cephalomyotropins.*
RI Comp. Biochem. Physiol. 84C:205-211(1986).
CC !- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTHORUM (HINDCUT).
CC !- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
KW MOD_RES 8 B AMIDATION.
SQ SEQUENCE 8 AA: 893 MW: 1063658449C866DA CRC64:

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WS 7
II
DB 7 WS 8

RESULT 18
ID LCK2_LEUMA STANDARD: PRI: 8 AA.
AC P21142:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
LE Leucokinin II (L-II).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
CX NCBI_TaxID:6988;
RN [1]
RP TISSUE:Head;
RC Helman G.M., Cook H.J., Nachman R.J.;
RI *Isolation, primary structure and synthesis of two neuropeptides
RI from Leucophaea maderae: members of a new family of
RI Cephalomyotropins.*
RI Comp. Biochem. Physiol. 84C:205-211(1986).
CC !- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTHORUM (HINDCUT).
CC !- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
KW MOD_RES 8 B AMIDATION.
SQ SEQUENCE 8 AA: 852 MW: 1063658449C866DA CRC64:

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WS 7
II
DB 7 WS 8

RESULT 19
ID LCK3_LEUMA STANDARD: PRI: 8 AA.
AC P21142:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
LE Leucokinin III (L-III).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
CX NCBI_TaxID:6988;
RN [1]
RP TISSUE:Head;
RC Helman G.M., Cook H.J., Nachman R.J.;
RI *Isolation, primary structure and synthesis of two additional neuropeptides
RI from Leucophaea maderae: members of a new family of
RI Cephalomyotropins.*
RI Comp. Biochem. Physiol. 84C:271-276(1986).
CC !- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTHORUM (HINDCUT).
CC !- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
KW MOD_RES 8 B AMIDATION.
SQ SEQUENCE 8 AA: 906 MW: 1063658449C866DA CRC64:

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WS 7
II
DB 7 WS 8

RESULT 20
ID LCK4_LEUMA STANDARD: PRI: 8 AA.
AC P21144:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin IV (L-IV).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
CX NCBI_TaxID:6988;
RN [1]
RP TISSUE:Head;
RC Helman G.M., Cook H.J., Nachman R.J.;
RI *Isolation, primary structure and synthesis of two additional neuropeptides
RI from Leucophaea maderae: members of a new family of
RI Cephalomyotropins.*
RI Comp. Biochem. Physiol. 84C:271-276(1986).
CC !- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTHORUM (HINDCUT).
CC !- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
KW MOD_RES 8 B AMIDATION.
SQ SEQUENCE 8 AA: 906 MW: 1063658449C866DA CRC64:

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WS 7
II
DB 7 WS 8

RESULT 21
ID LCK5_LEUMA STANDARD: PRI: 8 AA.
AC P19887:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 19, Last annotation update)
DE Leucokinin V (L-V).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
CX NCBI_TaxID:6988;
RN [1]
RP TISSUE:Head;

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RA Holman G.M., Cook H.J., Nachman R.J.;
RI *Primary structure and synthesis of two additional neuropeptides
RI from Leucophaea maderae: members of a new family of
RI Cephalomyotropins.*
RI Comp. Biochem. Physiol. 84C:271-276(1986).
CC !- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTHORUM (HINDCUT).
CC !- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
KW MOD_RES 8 B AMIDATION.
SQ SEQUENCE 8 AA: 910 MW: 1063658449C866DA CRC64:

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WS 7
II
DB 7 WS 8

RESULT 22
ID LCK6_LEUMA STANDARD: PRI: 8 AA.
AC P21145:
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
CX NCBI_TaxID:6988;
RN [1]
RP TISSUE:Head;
RC Helman G.M., Cook H.J., Nachman R.J.;
RI *Primary structure and synthesis of two additional neuropeptides
RI from Leucophaea maderae: members of a new family of
RI Cephalomyotropins.*
RI Comp. Biochem. Physiol. 84C:271-276(1986).
CC !- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTHORUM (HINDCUT).
CC !- SIMILARITY: TO THE OTHER LEUCOKININS.
KW Neuropeptide; Amidation.
KW MOD_RES 8 B AMIDATION.
SQ SEQUENCE 8 AA: 906 MW: 1063658449C866DA CRC64:

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WS 7
II
DB 7 WS 8

RESULT 23
ID LCK7_LEUMA STANDARD: PRI: 8 AA.
AC P19887:
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 30-MAY-2000 (Rel. 19, Last annotation update)
DE Leucokinin VII (L-VII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
CX NCBI_TaxID:6988;
RN [1]
RP TISSUE:Head;

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RC TISSUE-Head;
RX MEDLINE:87052651; PubMed:2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VII:
RI myotropic peptides of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:27-34(1987).
CC -|- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC -|- ACTIVITY OF COCKROACH PROCTODEUM (HINDGUT).
CC -|- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0315; JS0315.
KW Neuropeptide; Amidation.
FT MOD.RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 784 MW; 246365A59766 CRC64.

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WG 7
DB 7 WG 8

RESULT 24
LOCK8_LEUMA STANDARD; PRT; 4 AA.
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leucokinin VI (L-VI).
OS Leucophaea maderae (Madeira cockroach).
OC Neoptera; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
CX NCBI_TaxID:6988;
RN 11;
RP SEQUENCE.
RC TISSUE-Head;
RX MEDLINE:87052651; PubMed:2877794;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VII:
RI myotropic peptides of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:27-34(1987).
CC -|- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC -|- ACTIVITY OF COCKROACH PROCTODEUM (HINDGUT).
CC -|- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0416; JS0416.
KW Neuropeptide; Amidation; Pteridine; Pteridine; Pteridine.
FT MOD.RES 1 1 PERKOLIN-NEURONAL ACTIO.
FT MOD.RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 935 MW; 406365B1E91A766 CRC64.

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WG 7
DB 7 WG 8

RESULT 24
LOCK7_LEUMA STANDARD; PRT; 8 AA.
AC P19988;
DT 01-FEB-1991 (Rel. 17, Created);
DT 01-FEB-1994 (Rel. 17, Last sequence update);
DT 01-FEB-1994 (Rel. 17, Last annotation update);
DE Leucokinin VII (L-VII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota.

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OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
CX NCBI_TaxID:6988;
RN 11;
RP SEQUENCE.
RC TISSUE-Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RI VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -|- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC -|- ACTIVITY OF COCKROACH PROCTODEUM (HINDGUT).
CC -|- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0317; JS0317.
KW Neuropeptide; Amidation.
FT MOD.RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9CD76A CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WG 7
DB 7 WG 8

RESULT 24
LOCK8_LEUMA STANDARD; PRT; 8 AA.
AC P19990;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Leucokinin VIII (L-VIII).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberoidea; Leucophaea.
CX NCBI_TaxID:6988;
RN 11;
RP SEQUENCE.
RC TISSUE-Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucokinin VII and
RI VIII: the final members of this new family of cephalomyotropic
RT peptides isolated from head extracts of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:31-34(1987).
CC -|- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC -|- ACTIVITY OF COCKROACH PROCTODEUM (HINDGUT).
CC -|- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: JS0318; JS0318.
KW Neuropeptide; Amidation.
FT MOD.RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 902 MW; 736365AB59CAADD8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WG 7
DB 7 WG 8

RESULT 25
NS3_MYCTU STANDARD; PRT; 8 AA.
AC P81152;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE 30 kDa non secretory protein 3 (Fragment).
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID:1773;
LN [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN H37Rv;
RA Prasad H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS PROTEIN database.
CC -! CAUTION: We are unable to find this protein in the translations of
CC the genome of strain H37Rv.
FT NUN_TER 1 8
FT NUN_TER 8 8
SQ SEQUENCE 8 AA: 919 MW: 85566.40Da pI:4.292 Charge:4;

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 2 RA 3
DB 1 1
5 RA 7

RESULT 26
RSL_ERWCH
ID RSL_ERWCH STANDARD; PRT; 8 AA.
AC P04949;
DT 01-NOV-1988 (Rel. 09, Created)
DI 01-FEB-1994 (Rel. 28, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Red pigment concentrating hormone (RPCH).
OS Pandanus borealis (Northern red shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;
OC Pandallidae; Pandallus.
CX NCBI_TaxID:6704;
LN [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN H37Rv;
RA Prasad H.K., Annapurna P.S.;
RL Submitted (DEC-1997) to the SWISS PROTEIN database.
CC -! CAUTION: We are unable to find this protein in the translations of
CC the genome of strain H37Rv.
FT NUN_TER 1 8
FT NUN_TER 8 8
SQ SEQUENCE 8 AA: 919 MW: 85566.40Da pI:4.292 Charge:4;

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 4 LN 5
DB 1 1
2 LN 3

RESULT 27
RSL_ERWCH
ID RSL_ERWCH STANDARD; PRT; 8 AA.
AC P47985;
DT 01-OCT-1994 (Rel. 30, Created)
DI 01-OCT-1994 (Rel. 30, Last sequence update)
DI 01-NOV-1995 (Rel. 42, Last annotation update)

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DE 30S ribosomal protein S1 (Fragment).
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteobacterium.
CX NCBI_TaxID:556;
LN [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN 1947;
RA Douville A., Toussaint A., Faellen M.;
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: BINDS MRNA; THUS FACILITATING RECOGNITION OF THE
CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT
CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC
DB EMBL: X74750; GAA52769.1;
DB PIR: S37141; S37141
KW Ribosomal protein; Repeat; RNA-binding.
FT NUN_TER 1
SQ SEQUENCE 8 AA: 847 MW: 9E18733DC5B339CD CRC64;

Query Match 18.2% Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Gaps 0;

QY 8 AK 9
DB 1 1
5 AK 6

RESULT 28
RSL_MYCIT
ID RSL_MYCIT STANDARD; PRT; 8 AA.
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DI 01-FEB-1994 (Rel. 28, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S7 (Fragment).
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID:1767;
LN [1]
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94197130; PubMed=8451173;
RA Nair J., Rouse D.A., Morris S.L.;
RT "Nucleotide sequence analysis of the ribosomal S12 gene of
RT Mycobacterium intracellulare".
RL Nucleic Acids Res. 21:1039-1039(1993).
CC -! FUNCTION: One of the primary rRNA binding proteins, it binds
CC directly to 16S rRNA where it nucleates assembly of the head
CC domain of the 30S subunit. Is located at the subunit interface
CC close to the decoding center, probably blocks exit of the E-site
CC tRNA (By similarity).
CC -! SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
CC and S11 (By similarity).
CC -! SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR EMBL: J08171; AAA25376.1; -;
 DR PIR: S35538; S35538;
 UR HAMAP: MF_00480; -; 1;
 DR InterPro: IPR000235; Ribosomal_S7;
 DR PROSITE: PS00052; RIBOSOMAL_S7; PARTIAL;
 KW Ribosomal protein: RNA-binding; tRNA binding;
 FT INTMET 0 0 BY SIM:LABITY;
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 850 MW: 63276Da76e742417 CRC64;

Query Match 18.2% Score 2: DB 1: Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PK 11
 DB 7 PK 8

RESULT 29
 ID R134_BOVIN STANDARD: PRT: 8 AA.
 AC P82929;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S14 (S14nt) (MRP-S14) (Fragment).
 GN MRPS14.
 OS Bos taurus (Bovine).
 CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=5913;
 RN [1]
 RP SEQUENCE
 EC TISSUE: Liver;
 RX MEDLINE-21276436; PubMed-11276123;
 RA Koe E.C., Burkart W., Blackburn K., Mosely A., Spremull L.L.;
 RT "The small subunit of the mammalian mitochondrial ribosome:
 RT identification of the full complement of ribosomal proteins present.";
 RL J. Biol. Chem. 276:19363-19374(2001).
 CC -!- SUBUNIT: Component of the mitochondria: ribosome small subunit.
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 KW Ribosomal protein; Mitochondrial.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 935 MW: 9639Da7205e47b70e4;

Query Match 18.2% Score 2: DB 1: Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WG 7
 DB 2 WG 3

RESULT 30
 ID JF006_MOUSE STANDARD: PRT: 8 AA.
 AC P18644;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 20-page of fibroblasts (p50) (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CC NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE-95009907; PubMed-7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:745-745(1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 817 MW: A35DD878676805B1 CRC64;

Query Match 18.2% Score 2: DB 1: Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GA 8
 DB 6 GA 7

RESULT 31
 WPL_PERAT STANDARD: PRT: 8 AA.
 ID AC P83195;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Wall protein-3 (WPP-1) (Fragment).
 OS Perkinsus atlanticus.
 CC Eukaryota; Alveolata; Perkinsa; Perkinsida; Perkinsidae; Perkinsus.
 CC NCBI_TaxID=106964;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RX MEDLINE-22044350; PubMed-12049410;
 RA Montes J.F., Burford M., Llado A., Garcia-Valero J.;
 RT "Characterization and immunolocalization of a main proteinaceous
 RT component of the cell wall of the protozoan parasite Perkinsus
 RT atlanticus.";
 RL Parasitology 124:477-484(2002).
 CC -!- FUNCTION: Is a major protein component of the cell wall. May play
 CC a key role in the organization of the cell wall and in promoting
 CC the survival of this parasite.
 CC -!- SUBCELLULAR LOCATION: Cell wall. Disulfide-linked to other cell
 CC wall components.
 CC -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental
 CC stages.
 KW Cell wall.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA: 765 MW: F1787D87B1AAB16 CRC64;

Query Match 18.2% Score 2: DB 1: Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GA 8
 DB 5 GA 6

RESULT 32
 ID CONO_CONGE STANDARD: PRT: 9 AA.
 AC P05486;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lys-conopressin G.
 OS Conus geographus (Geography cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 CC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.


```

DX NCBI_TaxID:6491;
RN
RP
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Kamito J.A., Zeikus R.D.
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs: characterization of
KT peptides from Conus geographus and Conus striatus venoms";
RL J. Biol. Chem. 262:15821-15824(1987);
RN
RP REVIEW
RX MEDLINE=59024586; PubMed=3652286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails";
RL Annu. Rev. Biochem. 57:665-700(1988);
CC -1- SURCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DK InterPro: IPR000981; Neurohyp-10rm.
DK Pfam: PF00220; hormone4; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1037 MW: 14062.668 Da:
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 KP 11
DB 7 KP 8

RESULT 34
CONV CONVE STANDARD: PRI: 9 AA.
AC P83047;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Contryphan-Vn.
OS Conus ventricosus (Mollusca: Mollusca)
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Artibeus topoda;
OC Apogastropoda; Caenogastropoda; Sorbeopoda; Aplysioleptopoda;
OC Neogastropoda; Conus; Conus; Conus;
OX NCBI_TaxID:117492;
RN
RP SEQUENCE: SYNTHESIS, AND MASS SPECTROMETRY
RX MEDLINE=21547785; PubMed=11688995;
RA Massilia G.R., Schinina M.E., Ascaris P., Collinelli F.;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
RL snail Conus ventricosus";
RL Biochem. Biophys. Res. Commun. 288:908-914(2001)
CC -1- SURCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1388.6; METHOD MALDI.
CC -1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW TISSUE: Amidation; D-amino acid.
FT DISULFID 3 9
FT MOD_RES 5 5 D-TRYPTOPHAN.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1091 MW: 80386.7632 Da:
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 KP 10
DB 6 KP 7

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RESULT 34
FAR4 CALVO STANDARD: PRI: 9 AA.
AC P41859;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 4.
OS Calliphora vomitoria (Insecta: Diptera).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID:27454;
RN
RP SEQUENCE.
RX TISSUE: Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnson A.H., Scwell J.C., Scott A.G., Orchard I.;
RA Renfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRamides) from the blowfly
RT Calliphora vomitoria";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
DK PIR: D41978; D41978.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1162 MW: 317306.99 Da:
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 KP 10
DB 1 KP 2

RESULT 35
FAR5 ASCSU STANDARD: PRI: 9 AA.
AC P43170;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF5.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID:6253;
RN
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
RT Ascaris suum";
RL Peptides 16:491-500(1995).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1052 MW: 340800.59 Da:
Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 KP 10
DB 3 KP 4

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RESULT 36
ID FAF5_PANKE STANDARD: PRT: 9 AA.
AC P82661
DT 16 OCT 2001 (Rel. 40, Created)
DT 16 OCT 2001 (Rel. 40, Last sequence update)
DT 16 OCT 2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF5 (AMRNALVFMamide)
OS Panagrellus redivivus
OC Eukaryota; Metazoa; Nematoea; Chromadorea; Platyhelminthes
OC Panagrellidae; Panagrellinae; Panagrellus
OX NCBI_TaxID-6233;
[[[
RN SEQUENCE, FUNCTION, AND ANIMATION.
RA Moffet G.L., Marks N.J., Halton D.W., Thomson D.B., Goody J.G.,
MAule A.G.;
RT "Isolation, characterization and pharmacology of FMRFamide-related
peptides (FaRpe) from free-living nematode, Panagrellus redivivus."
RL Submitted (JUL-2000) to the SWISS-PROT data bank.
CC - FUNCTION: MYOACTIVE.
CC - SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
KW Neuropeptide; Amidation.
FT MCB_RES 9 9 AMIDATION
SQ SEQUENCE 9 AA: 1077 MW: 40012672DE4446 QCR64;

Query Match 18.2% Score 2; DB 1; Length 9;
Best local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AL 4
DB 5 AL 6

RESULT 37
ID FAF5_PANKE STANDARD: PRT: 9 AA.
AC P41799;
DT 01 JUL 1994 (Rel. 26, Created)
DT 01 JUL 1994 (Rel. 26, Last sequence update)
DT 01 OCT 1994 (Rel. 27, Last annotation update)
DE Locustamininhibiting peptide (LDM-MIP)
OS Locusta migratoria (Migratory locust)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
Acrididae; Acridinae; Oedipodinae; Oedipodini
OX NCBI_TaxID-7004;
[[[
RN SEQUENCE.
RA Scholtz L., Helman G.M., Hayes T.K., Nishida K., de Groot A.,
Scholtz L.;
RT "Isolation, identification and synthesis of locustamininhibiting
peptide (LDM-MIP), a novel bioactivity active neuropeptide from
Locusta migratoria."
RL Locusta migratoria;
CC - FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINDGUT AND
IN THE SUBESOPHAGEAL GANGLION.
CC - TISSUE SPECIFICITY: NEURONS LOCATED IN THE VENTRAL CELL CLUSTERS
OF THE HINDGUT.
CC - IN THE SUBESOPHAGEAL GANGLION.
KW Amidation; Neuropeptide.
FT MCB_RES 9 9 AMIDATION
SQ SEQUENCE 9 AA: 1060 MW: 4576137256073 QCR4;

Query Match 18.2% Score 2; DB 1; Length 9;
Best local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AL 5
DB 5 AL 6

RESULT 38
ID NEUX_HUMAN STANDARD: PRT: 9 AA.
AC P04277;
DT 20 MAR 1987 (Rel. 04, Created)
DT 20 MAR 1987 (Rel. 04, Last sequence update)
DT 28 FEB 2003 (Rel. 41, Last annotation update)
DE Neurotensin-related peptide (NRP) (Kinetensin).
OS Homo sapiens (Human);
OC Bos taurus (Bovine); and
OC Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID-9606, 9913, 9946;
[[[
RN SEQUENCE.
RA MEDLINE-86242180; PubMed-3087352;
RA Modard M.H., Kobayashi R., Chen C.F., Lee T.D., Reeve J.R. Jr.,
Shively J.E., Walsh J.H.;
RT "The amino acid sequence of kinetensin, a novel peptide isolated from
pepsin-treated human plasma: homology with human serum albumin,
neurotensin and angiotensin."
RT Biochem. Biophys. Res. Commun. 136:983-988(1986).
OX NCBI_TaxID-9606, 9913, 9946;
[[[
RN SEQUENCE.
RA SPECIES=Human;
RA MEDLINE-87194805; PubMed-2437111;
RA Carraway R.E., Mitra S.P., Cochran D.E.;
RT "Structure of a biologically active neurotensin-related peptide
obtained from pepsin-treated albumin(s).";
RL J. Biol. Chem. 262:5968-5973(1987).
CC - FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND
BLOOD FLOW (PORENTAL).
CC PIR: A36895; ABR05.
DR GO: GO:0005576; Cerebrocellular; NAS.
DR GO: GO:0005180; Peptide hormone; NAS.
DR GO: GO:0007599; Pilemostasis; IDA.
DR GO: GO:0006629; Lipid metabolism; NAS.
KW Hormone.
SQ SEQUENCE 9 AA: 1172 MW: C804DB4761F4140D QCR64;

Query Match 18.2% Score 2; DB 1; Length 9;
Best local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2
DB 2 AR 3

RESULT 39
ID PTSP_BOMBYX STANDARD: PRT: 9 AA.
AC P82593;
DT 16 OCT 2001 (Rel. 40, Created)
DT 16 OCT 2001 (Rel. 40, Last sequence update)
DT 28 FEB 2003 (Rel. 41, Last annotation update)
DE Prothoracicostatic peptide (Bom PTSP).
OS Bombyx mori (Silk moth)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;
Bombycidae; Bombyx.
OX NCBI_TaxID-7091;
[[[
RN SEQUENCE.
RA STRAIN-0145 X N140; TISSUE Brain;
RA MEDLINE-2332614; PubMed-10531408;
RA Hsu Y.-C., Tzeng Y., Nakamura K., Sakakibara M., Nadata S.,
Kikuchi H.;

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RI Identification of a prothoracicostatic peptide in the larva, brain of
 KT the silkworm, *Bombyx mori*.
 RL J. Biol. Chem. 274:31169-31173(1999).
 RN [2]

RP ERKATUM.
 RA Hua Y., Tanaka Y., Nakamura K., Sakakibara M., Nakanishi S.,
 KA Katoaka H.,
 RL J. Biol. Chem. 275:9892-9897(2000).
 CC 1- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
 CC gland.
 CC 1- SUBCELLULAR LOCATION: Secreted.
 CC 1- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR
 KW Hormone; Amidation.
 FT MOD_RES 9 AA: 1090 MW: 38780*64472AA660A CR64;
 SQ SEQUENCE 9 AA: 1090 MW: 38780*64472AA660A CR64;

Query Match 18.2% Score 2; DB 1; Length 9;
 Best local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 DB 5 LN 6

RESULT 40
 ID PT33_HUMAN STANDARD; PRT; 9 AA
 AC P62926;
 DT 26-FEB-2003 (Rel. 41, Created)
 DI 28-FEB-2003 (Rel. 41, Last sequence update)
 DI 29-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S28 (S28mt) (CYP S28) (Fragment).
 GN MRS21.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Ruminata; Cetartiodactyla; Ruminantia; Bovidae; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE

RC TISSUE=Liver;
 RX MEDLINE=21276446; PubMed=21276446;
 RA Koe E.C., Burkhardt W., Blackburn K., Moscovici A., Spradford L.L.
 RT The small subunit of the mammalian cytochrome P-450 2C8.
 RT Identification of the full complement of cDNAs of proteins present.
 RL J. Biol. Chem. 276:19363-19374(2001)
 CC 1- SURFING: Component of the cytochrome P-450 2C8, subunit
 CC (28S) which comprises a 12S P450 and a 12S cytochrome P-450
 CC 1- SUBCELLULAR LOCATION: Mitochondrion.
 KW Ribosomal protein; Mitochondrion
 FT NON_TER 1
 FT NON_TER 9
 SQ SEQUENCE 9 AA: 1032 MW: 104107.07(66058) CR64;

Query Match 18.2% Score 2; DB 1; Length 9;
 Best local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AK 9
 DB 8 AK 9

RESULT 41
 ID THYF_PIG STANDARD; PRT; 9 AA
 AC P31255;
 DT 21-JUL-1986 (Rel. 01, Created)
 DI 21-JUL-1986 (Rel. 01, Last sequence update)
 DI 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thymic factor.
 OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=74026571; PubMed=914862;
 RA Plehn J.M., Gaido M., Walschitz Y., Bach J.-F.,
 RT Structural study of circulating thymic factor: a peptide isolated
 RT from pig serum. Its amino acid sequence.
 RL J. Biol. Chem. 252:8045-8047(1977).
 CC 1- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
 CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
 CR PIR, A01523; YFIS.
 KW Pyroglutamate; Carboxylic acid
 FT MOD_RES 1 1 1
 SQ SEQUENCE 9 AA: 876 MW: 15008*786585B33D CR64;

Query Match 18.2% Score 2; DB 1; Length 9;
 Best local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AK 9
 DB 2 AK 3

RESULT 42
 ID UPA6_HUMAN STANDARD; PRT; 9 AA
 AC P30092;
 DT 01-APR-1993 (Rel. 25, Created)
 DI 01-APR-1993 (Rel. 25, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2B page of plasma (Spot 14) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Plasma;
 RX MEDLINE=93092947; PubMed=14595937;
 RA Hughes G.J., Fraliger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., Camus R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.,
 RT Plasma protein maps: an update by microsequencing.
 RL Electrophoresis 13:707-714(1992).
 CC 1- MISCELLANEOUS: ON THE 2D GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.1; IS MW IS: 48 kDa.
 DB SWISS-2DPAGE; P30092; HUMAN.
 FT NON_TER 1
 FT NON_TER 9
 SQ SEQUENCE 9 AA: 935 MW: 5282*2CAA8676447 CR64;

Query Match 18.2% Score 2; DB 1; Length 9;
 Best local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 DB 2 LN 3

RESULT 43
 ID BPP2_BOTIN STANDARD; PRT; 10 AA
 AC P30422;
 DT 01-APR-1993 (Rel. 25, Created)
 DI 01-FEB-1994 (Rel. 28, Last sequence update)
 DI 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).

ID	BPBP8_BOTIN	STANDARD:	PRT:	10 AA:
AC	P30426;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Bradykinin-potentiating peptide S5,1 (Angiotensin-converting enzyme inhibitor)			
OS	Bothrops insularis (Island jararaca) (Queimada Jararaca)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;			
CC	Viperidae; Crotalinae; Bothrops;			
NCBI_TaxID	8723;			
RN	[1]			
SEQUENCE				
TISSUE	Venom;			
RC				
RX	MEDLINE=50351557; PubMed=2386615;			
RA	Canfra A.C.O., Vieira C.A., Giglio J.R.;			
RT	*Primary structure and biological activity of bradykinin potentiating peptides from bothrops insularis snake venom.*;			
RT	J. Protein Chem. 9:221-227(1990).			
CC	-I- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.			
CC	It acts as an indirect hypotensive agent.			
CC	PIR: H37196; H37196.			
DR	Hypotensive agent; Pyrolidone carboxylic acid.			
FT	MOD_RES			
KW	Hypotensive agent; 1 PYROLIDONE CARBOXYLIC ACID.			
SEQUENCE	10 AA; 117 MW; 2FF835545761F6D8 CRC64;			
Query Match	18.2%; Score 2; DB 1; Length 10;			
Best Local Similarity	100.0%; Pred. No. 1.3e+04;			
Matches	2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	6 WG 7			
DB	1			
DB	2 WG 3			
RESULT 45				
BPP_VIPAS				
ID	BPP_VIPAS	STANDARD:	PRT:	10 AA:
AC	P31351;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Bradykinin-potentiating peptide (Angiotensin-converting enzyme inhibitor)			
OS	Vipera aspis (Asp. Vipet)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;			
CC	Viperidae; Viperinae; Vipera.			
NCBI_TaxID	8706;			
RN	[1]			
SEQUENCE				
TISSUE	Venom;			
RC				
RX	MEDLINE=90382616; PubMed=2159439;			
RA	Komori Y., Sugihara H.;			
RT	*Characterization of a new inhibitor for angiotensin converting enzyme from the venom of Vipera aspis aspis.*;			
RT	Int. J. Biochem. 22:767-771(1990).			
CC	-I- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.			
CC	It acts as an indirect hypotensive agent.			
CC	PIR: A60377; XASNPC.			
DR	Hypotensive agent; Pyrolidone carboxylic acid.			
KW	Hypotensive agent; 1 PYROLIDONE CARBOXYLIC ACID.			
FT	MOD_RES			
SEQUENCE	10 AA; 1062 MW; 3BA827C327686773 CRC64;			
Query Match	18.2%; Score 2; DB 1; Length 10;			
Best Local Similarity	100.0%; Pred. No. 1.3e+04;			
Matches	2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

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QY      10 PK 11
DB      6 PK 7

RESULT 47
CAIR_SHEEP
ID CATH_SHEEP STANDARD: PRT: 10 AA.
AC P81205:
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B) (Fragment).
GN CTSB
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RV SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22394055; PubMed=12506352;
RA El Amir B., Remy B., Sousa N.M., Joris B., Ottens N.G., Perenyi Z.,
RA Muko H.B., Beckers J.-F.M.P.;
RT *Isolation and partial characterization of three pregnancy associated
RT glycoproteins from the ewe placenta.*;
RL Mol. Reprod. Dev. 64:199-206(2003);
CC -!- FUNCTION: Thiol protease which is believed to participate in
CC intracellular degradation and turnover of proteins. Has also been
CC implicated in tumor invasion and metastasis.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
CC for peptide bonds. Preferentially cleaves -Arg-Arg- and Xaa bonds in
CC small molecule substrates (thus differing from cathepsin L). In
CC addition to being an endopeptidase, shows peptidyl-dipeptidase
CC activity, liberating C-terminal dipeptides.
CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
CC by a disulfide bond (By similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal (by similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR InterPro: IPR001049; SHProl_acsite.
DR PROSITE: PS00640; THIOL_PROTEASE_ASN; PARTIAL.
DR PROSITE: PS00139; THIOL_PROTEASE_CYS; PARTIAL.
DR PROSITE: PS00639; THIOL_PROTEASE_HIS; PARTIAL.
KW Hydrolase; Thiol protease; Lysosome.
ST NON_TER 10 10
SQ SEQUENCE 10 AA: 1177 MW: 9795;PGLDAAIPLPRAQHWG;

Query Match 19.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AR 2
DB      7 AR 8

RESULT 48
COXA_OMCY
ID CATH_OMCY STANDARD: PRT: 10 AA.
AC P80428:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RV SEQUENCE.
RC TISSUE=Liver;

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RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT *Identification of tissue specific isoforms for subunits Vb and Vila
RT of cytochrome c oxidase isolated from rainbow trout.*;
RL Eur. J. Biochem. 221:1111-1116(1994);
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE. THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) -> 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR PIR: S43625; S43625
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1144 MW: C535C5B1A802C33D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 AK 9
DB      3 AK 4

RESULT 49
COXQ_RABIT
ID COXQ_RABIT STANDARD: PRT: 10 AA.
AC P80336:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
GN COX8B.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RV SEQUENCE.
RC TISSUE=Heart, and liver;
RA Freund R., Kadenbach B.;
RT Submitted (MAR-1994) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) -> 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1027 MW: 2C325CB40DC76338 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AR 2
DB      6 AR 7

RESULT 50
FAR2_PENMO
ID FAR2_PENMO STANDARD: PRT: 10 AA.
AC P83317:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP2 (AYSNLNYLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

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OC Eumalacostraca, Eucarida: Decapoda; Decapoda; Penaeoidea;
 OC Penaeidae; Penaeus.
 CX NCBI_taxid:6687;
 RN {}
 RP SEQUENCE AND MASS SPECTROMETRY.
 RC TISSUE: Eyestalk;
 RX MEDLINE:21956277; PubMed:11959019;
 RA Sathigorsqui P., Pupem J., Kungkasom C., Lanyant S.,
 RA Chavitsuthangkura P., Sathigorsqui W., Porasm A.:
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 RI of the giant tiger prawn *Penaeus monodon*."
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 MASS SPECTROMETRY: MW:1260.67; METHOD: MALDI
 CC -1 SIMILARITY: BELONGS TO THE FAXP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1260 MW; 8BF92B95472455 CRC64;

Query Match 18.2% Score 2; 10b 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1;36+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 DB 5 LN 6

Search completed: September 30, 2003, 10:26:00
 Job time: 8.25 secs

SeqWare version 5.1.1.6
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CM protein protein search, using SW model

Run on: September 30, 2003, 10: 7:04 Search time: 11:45:55 Seconds
(with 1000000 updates/sec)

Title: US-09-787-443-3

Perfect score: 11

Sequence: 1 ARALNWCAR 11

Scoring table: GCIGD

Gapop 60.0, Gapext 50.0

Searched: 283308 seqs, 5616682 residues

Word size: 0

Total number of hits satisfying chosen parameters 204

Maximum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database:

1: PIR76.8

2: PIR2.8

3: PIR1.8

4: PIR4.8

Prod. No. is the number of results predicted by the program to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	13	2	protein 17 - home
2	3	27.3	8	2	hypothetical prote
3	3	27.3	8	4	hypothetical hist
4	3	27.3	9	2	hypothetical hist
5	3	27.3	10	2	hypothetical hist
6	3	27.3	10	2	hypothetical hist
7	3	27.3	10	2	hypothetical hist
8	3	27.3	10	2	hypothetical hist
9	3	27.3	10	2	hypothetical hist
10	3	27.3	10	2	hypothetical hist
11	3	27.3	11	2	hypothetical hist
12	3	27.3	11	2	hypothetical hist
13	3	27.3	11	2	hypothetical hist
14	3	27.3	12	2	hypothetical hist
15	3	27.3	12	2	hypothetical hist
16	3	27.3	12	2	hypothetical hist
17	3	27.3	13	2	hypothetical hist
18	3	27.3	13	2	hypothetical hist
19	3	27.3	13	2	hypothetical hist
20	3	27.3	14	2	hypothetical hist
21	3	27.3	14	2	hypothetical hist
22	3	27.3	14	2	hypothetical hist
23	3	27.3	14	2	hypothetical hist
24	3	27.3	14	2	hypothetical hist
25	3	27.3	15	2	hypothetical hist
26	3	27.3	15	2	hypothetical hist
27	3	27.3	15	2	hypothetical hist
28	3	27.3	15	2	hypothetical hist
29	3	27.3	15	2	hypothetical hist

T-cell receptor al
mixed lymphocyte r
red pigment-concen
hypertrehalosemic
hypertrehalosemic
hypertrehalosemic
adipokinetic hormo
adipokinetic hormo
neuropeptide Led-C
neuropeptide Led-C
adipokinetic hormo
hypertrehalosemic
hypertrehalosemic
adipokinetic hormo
lg heavy chain V r
sperm-activating p
sperm-activating p
sperm-activating p
urine glycopeptide
angiotensin-conver
rpsA protein - Brw
glycine reductase
endoglycosylcerami
R-phycoerythrin ga
unidentified 6.5/3
neuropeptide M-1 -
leucokinin V - Mad
leucokinin VII - M
leucokinin VIII -
neuropeptide - flo
p element, P cytot
calliphramide 8 -
acetylcholinestera
aspartate transami
serum albumin - do
thymic humoral fac
apolipoprotein A-1
lg H chain V-D-J r
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
thymic factor - pi
locustamininhibiti
dihydrolipoamide S
conopressin G - co
thymocyte growth p
adipokinetic hormo
ribosomal protein
calsequestrin, car
xenopsin-related p
xenopsin-related p
vitamin B3 26-mono
sperm-activating p
photosystem II pro
alpha/beta-gliadin
neuropeptide Grb-A
neuropeptide Grb-A
calliphramide 4 -
c-rel protein - ch
118K stomach cance
gene NF2 protein -
lg heavy chain CRD
macrophage cytotox
zymogen granule me
alpha-2-macroglobu
alpha-2-macroglobu
ribosomal protein
lg H chain V-D-J r
lg heavy chain V r

103	2	18.2	9	2	P10644	T-cell receptor be	176	2	18.2	10	2	S71948	matrix metalloprot
104	2	18.2	9	2	P07078	unidentified 48.7K	177	2	18.2	10	2	C19398	Ec mu (IgM) recept
105	2	18.2	9	2	P59350	gene c-mpl protei	178	2	18.2	10	2	P01633	Ig H chain V-D-J r
106	2	18.2	9	2	A15523	fructose-2,6-bisph	179	2	18.2	10	2	P01592	Ig H chain V-D-J r
107	2	18.2	9	2	S78420	tubosomal protein	180	2	18.2	10	2	S16849	Ig heavy chain V r
108	2	18.2	9	2	P06945	T-cell receptor be	181	2	18.2	10	2	P13932	Ig mu chain J regi
109	2	18.2	9	2	P06946	T-cell receptor be	182	2	18.2	10	2	P13932	T-cell receptor al
110	2	18.2	9	2	S19046	lysine-conopressin	183	2	18.2	10	2	P18887	T-cell receptor ga
111	2	18.2	9	2	P07073	ubiquinol-cytochro	184	2	18.2	10	2	A47364	placental lactogen
112	2	18.2	9	2	S15553	ori 2 para 5'-regi	185	2	18.2	10	2	A55695	proteoglycan core
113	2	18.2	10	1	XAV113	anaphase-promover	186	2	18.2	10	2	C10572	T-cell receptor be
114	2	18.2	10	1	XASNP3	anaphase-promover	187	2	18.2	10	2	P06946	T-cell receptor be
115	2	18.2	10	1	RUMOS	quadrifoliate - se	188	2	18.2	10	2	P06923	T-cell receptor be
116	2	18.2	10	2	C24947	unspecific monooxy	189	2	18.2	10	2	S68033	cytochrome P450 1A
117	2	18.2	10	2	S11118	diacylglycerol red:	190	2	18.2	10	2	S53789	neuropeptide pec-H
118	2	18.2	10	2	A50410	beta-mesendorphin	191	2	18.2	10	2	A59173	nuclease Bhl (EC 3
119	2	18.2	10	2	A50421	hyper-trehalosemic	192	2	18.2	10	2	A14871	monodehydroascorba
120	2	18.2	10	2	S08997	hyper-trehalosemic	193	2	18.2	10	2	P07988	NADH2 dehydrogenas
121	2	18.2	10	2	S08998	hyper-trehalosemic	194	2	18.2	10	2	P07984	NADH2 dehydrogenas
122	2	18.2	10	2	A26361	hyper-trehalosemic	195	2	18.2	10	2	P00783	bradykinin-potent
123	2	18.2	10	2	A15571	hypertrehalosemic/	196	2	18.2	10	1	XASNEA	substance P - hors
124	2	18.2	10	2	S13945	hypertrehalosemic h	197	2	18.2	10	1	SPHO	substance P - quin
125	2	18.2	10	2	P12171	triacylglycerol li	198	2	18.2	10	1	A60654	probable trypsin lea
126	2	18.2	10	2	P60758	sperm-activating p	199	2	18.2	10	1	LF1WME	alcohol dehydrogen
127	2	18.2	10	2	P60759	sperm-activating p	200	2	18.2	10	2	S66196	rhodopsin homolog
128	2	18.2	10	2	P60760	sperm-activating p	201	2	18.2	10	2	A38841	substance P - rain
129	2	18.2	10	2	P60761	sperm-activating p	202	2	18.2	10	2	S23308	substance P - Atla
130	2	18.2	10	2	A60762	sperm-activating p	203	2	18.2	10	2	S23306	beta-glucosidase (
131	2	18.2	10	2	A60763	sperm-activating p	204	2	18.2	10	2	A61033	quinoline 2-oxidor
132	2	18.2	10	2	G09527	sperm-activating p	205	2	18.2	10	2	D61033	nifs protein - Bra
133	2	18.2	10	2	G09589	sperm-activating p	206	2	18.2	10	2	S42449	anti protein - pha
134	2	18.2	10	2	E62589	sperm-activating p	207	2	18.2	10	2	A58502	38K kidney stone p
135	2	18.2	10	2	H63588	sperm-activating p	208	2	18.2	10	2	C58501	42K bile stone pro
136	2	18.2	10	2	S15527	sperm-activating p	209	2	18.2	10	2	J00395	hypothetical prote
137	2	18.2	10	2	X0005	erythrocyte membra	210	2	18.2	10	2	P00231	beta-glucosidase (
138	2	18.2	10	2	A24867	erythrocyte membra	211	2	18.2	10	2	S66606	quinoline 2-oxidor
139	2	18.2	10	2	R13143	pneumonia - human	212	2	18.2	10	2	S04875	nifs protein - Bra
140	2	18.2	10	2	A33143	pneumonia - rat	213	2	18.2	10	2	S41138	acetyl ornithine d
141	2	18.2	10	2	S07697	hypothetical prote	214	2	18.2	10	2	S42587	hypothetical prote
142	2	18.2	10	2	S07698	hypothetical prote	215	2	18.2	10	2	B43669	58K heat shock pro
143	2	18.2	10	2	G58501	48K bile/pancreatic	216	2	18.2	10	2	P02372	probable antigen 5
144	2	18.2	10	2	A60762	cryptic material p	217	2	18.2	10	2	E41476	seed protein ws-23
145	2	18.2	10	2	P64442	cytochrome c553	218	2	18.2	10	2	G61497	ribosomal protein
146	2	18.2	10	2	S48184	bacteriostatin -	219	2	18.2	10	2	P04267	unidentified 5,7/3
147	2	18.2	10	2	S42449	paraspinal crystal	220	2	18.2	10	2	P00731	6-phosphofructokin
148	2	18.2	10	2	S42449	paraspinal crystal	221	2	18.2	10	2	A26120	probable substance
149	2	18.2	10	2	P64442	glyoxal reductase	222	2	18.2	10	2	S33000	gallbladder stone
150	2	18.2	10	2	P64442	glyoxal reductase	223	2	18.2	10	2	S57389	Ig heavy chain CRD
151	2	18.2	10	2	P64442	glyoxal reductase	224	2	18.2	10	2	P10243	T-cell receptor al
152	2	18.2	10	2	P64442	glyoxal reductase	225	2	18.2	10	2	S51732	collistatin - bovi
153	2	18.2	10	2	A27617	triose phosphate 1	226	2	18.2	10	2	A33571	ribosomal protein
154	2	18.2	10	2	P50451	24K protein 4302 -	227	2	18.2	10	2	S78765	6-phosphofructokin
155	2	18.2	10	2	P50209	24K protein 4407	228	2	18.2	10	2	A14454	6-phosphofructokin
156	2	18.2	10	2	B61449	polylactonase	229	2	18.2	10	2	P00664	Ig H chain V-D-J r
157	2	18.2	10	2	S61449	polylactonase	230	2	18.2	10	2	P01632	Ig H chain V-D-J r
158	2	18.2	10	2	P00165	polylactonase	231	2	18.2	10	2	P01600	Ig H chain V-D-J r
159	2	18.2	10	2	S56137	triose-phosphate 1	232	2	18.2	10	2	P01583	Ig H chain V-D-J r
160	2	18.2	10	2	A34365	neuropeptide tRNA	233	2	18.2	10	2	P01584	Ig H chain V-D-J r
161	2	18.2	10	2	A49187	neuropeptide-tRNA	234	2	18.2	10	2	P10209	T-cell receptor al
162	2	18.2	10	2	C39111	Ig heavy chain CRD	235	2	18.2	10	2	P10214	T-cell receptor be
163	2	18.2	10	2	A24136	acetylcholinestera	236	2	18.2	10	2	PTC218	T-cell receptor be
164	2	18.2	10	2	S43625	cytochrome c oxida	237	2	18.2	10	2	P00441	translation elonga
165	2	18.2	10	2	S37196	cytochrome c oxida	238	2	18.2	10	2	S65377	cytochrome-c oxida
166	2	18.2	10	2	H37196	bradykinin-potent	239	2	18.2	10	2	S09349	microtubule-associ
167	2	18.2	10	2	A35556	hypothetical prote	240	2	18.2	10	2	P00939	T-cell receptor be
168	2	18.2	10	2	P10245	Ig heavy chain CRD	241	2	18.2	10	2	P00903	T-cell receptor be
169	2	18.2	10	2	P00309	Ig heavy chain CRD	242	2	18.2	10	2	S19015	hypothetical prote
170	2	18.2	10	2	PT0316	Ig heavy chain CRD	243	2	18.2	10	2	S19081	retinoic acid rece
171	2	18.2	10	2	P01344	Ig heavy chain CRD	244	2	18.2	10	2	A43975	locustanatotropin -
172	2	18.2	10	2	H45482	patcher activatin	245	2	18.2	10	2	P00578	tyrosine 3-monooxy
173	2	18.2	10	2	E40334	T-cell receptor qu	246	2	18.2	10	2	P00578	tyrosine 3-monooxy
174	2	18.2	10	2	F49033	T-cell receptor qu	247	2	18.2	10	2	P00579	tyrosine 3-monooxy
175	2	18.2	10	2	S26500	cellular alpha 1V	248	2	18.2	10	2	P00580	tyrosine 3-monooxy

395	2	18.2	13	2	PH0789	T-cell receptor al	468	2	18.2	14	2	PH1768	T cell receptor al
396	2	18.2	13	2	PH0805	T-cell receptor al	469	2	18.2	14	2	PH1769	T cell receptor al
397	2	18.2	13	2	PH0948	unidentified GMS2	470	2	18.2	14	2	S57572	insulin-like grow
398	2	18.2	13	2	PH0728	T-cell receptor be	471	2	18.2	14	2	JH0516	leukotriene B-4 12
399	2	18.2	13	2	C47650	Iq kappa chain J r	472	2	18.2	14	2	A47421	glycoprotein compo
400	2	18.2	13	2	H47530	Iq kappa chain J r	473	2	18.2	14	2	F48394	thrombospondin 2 -
401	2	18.2	13	2	F51905	collecting duct wa	474	2	18.2	14	2	D45474	tubulin beta-3 cha
402	2	18.2	13	2	G84988	hypothetical prote	475	2	18.2	14	2	A39703	hypothetical 1.5K
403	2	18.2	13	2	S64558	serine proteinase	476	2	18.2	14	2	JS0272	Ig H chain V-D-J r
404	2	18.2	13	2	H85575	hypothetical prote	477	2	18.2	14	2	PH1626	Ig H chain V-D-J r
405	2	18.2	13	2	S54144	glyceroldehyde-3-p	478	2	18.2	14	2	PH1628	Ig H chain V-D-J r
406	2	18.2	13	2	F70076	glycophorin B/alyc	479	2	18.2	14	2	PH1639	Ig H chain V-D-J r
407	2	18.2	14	1	NP0214	hypothalamic tetra	480	2	18.2	14	2	PH1617	Ig H chain V-D-J r
408	2	18.2	14	1	NP04AV	mastoparan - yello	481	2	18.2	14	2	PH1623	Ig H chain V-D-J r
409	2	18.2	14	1	QMVHMM	mastoparan M - hor	482	2	18.2	14	2	PH1586	Ig H chain V-D-J r
410	2	18.2	14	1	QMVHMM	mastoparan X - hor	483	2	18.2	14	2	PH1594	Ig H chain V-D-J r
411	2	18.2	14	1	QMVHXX	mastoparan C - Eur	484	2	18.2	14	2	PH1597	Ig H chain V-D-J r
412	2	18.2	14	1	LFEBWI	trp operon leader	485	2	18.2	14	2	PH1598	Ig H chain V-D-J r
413	2	18.2	14	2	A33798	D-amino-acid oxida	486	2	18.2	14	2	PH1608	Ig H chain V-D-J r
414	2	18.2	14	2	JN0389	histamine-releasin	487	2	18.2	14	2	PH1448	T-cell receptor al
415	2	18.2	14	2	PH1677	Iq heavy chain V r	488	2	18.2	14	2	PH0800	T-cell receptor al
416	2	18.2	14	2	F51430	hemoglobin beta ch	489	2	18.2	14	2	PH0795	T-cell receptor al
417	2	18.2	14	2	F51432	histone H4-1 prec	490	2	18.2	14	2	PH0776	T-cell receptor al
418	2	18.2	14	2	A35377	GIP-binding protei	491	2	18.2	14	2	PH1450	T-cell receptor al
419	2	18.2	14	2	A42473	ermk leader peptid	492	2	18.2	14	2	PT0210	T-cell receptor al
420	2	18.2	14	2	A44515	trp EG leader pept	493	2	18.2	14	2	PH0765	T-cell receptor be
421	2	18.2	14	2	S27140	hypothetical prote	494	2	18.2	14	2	PH0747	T-cell receptor be
422	2	18.2	14	2	JH0328	probrusin tetrad	495	2	18.2	14	2	E35141	T-cell receptor de
423	2	18.2	14	2	S29532	xylan: 1,4-beta-xy	496	2	18.2	14	2	F49037	TCR delta chain V-
424	2	18.2	14	2	F39753	nitrogenase (EC 1.	497	2	18.2	14	2	S65392	cytochrome-c oxida
425	2	18.2	14	2	F10142	carbon-monoxide de	498	2	18.2	14	2	C48394	major fat-globule
426	2	18.2	14	2	S07768	soluble coenzyme M	499	2	18.2	14	2	H83778	hypothetical prote
427	2	18.2	14	2	S14864	methyl coenzyme M	500	2	18.2	14	2	E81280	probable proteolys
428	2	18.2	14	2	S29789	hypothetical prote							
429	2	18.2	14	2	H56319	PS 1 complex subu							
430	2	18.2	14	2	PA0111	protein GAI00654							
431	2	18.2	14	2	S09721	2S albumin small c							
432	2	18.2	14	2	PT0206	calotropin D1 - ma							
433	2	18.2	14	2	G44957	photosystem II oxy							
434	2	18.2	14	2	S34801	chaperone, TCP1-re							
435	2	18.2	14	2	S34802	chaperone, TCP1-re							
436	2	18.2	14	2	S34803	chaperone, TCP1-re							
437	2	18.2	14	2	PS0252	16K protein 5404 -							
438	2	18.2	14	2	PS-258	48K protein 3228 -							
439	2	18.2	14	2	PS0298	unidentified 6.0/k							
440	2	18.2	14	2	H56381	malate dehydrogena							
441	2	18.2	14	2	PI0229	karagasin - karata							
442	2	18.2	14	2	PA0094	lysylamine (65)-di							
443	2	18.2	14	2	PA0103	protein QF20020 -							
444	2	18.2	14	2	B34135	DNA-binding protei							
445	2	18.2	14	2	S14336	mastoparan B - hor							
446	2	18.2	14	2	S04530	Iq heavy chain J r							
447	2	18.2	14	2	S62374	alpha-1-antichymot							
448	2	18.2	14	2	F54815	carbonic anhydrase							
449	2	18.2	14	2	B61235	fibroblast-activat							
450	2	18.2	14	2	PT0223	Iq heavy chain CDR							
451	2	18.2	14	2	PT0232	Iq heavy chain CDR							
452	2	18.2	14	2	PH1347	Iq heavy chain DJ							
453	2	18.2	14	2	PH1348	Iq heavy chain DJ							
454	2	18.2	14	2	PH1327	Iq heavy chain DJ							
455	2	18.2	14	2	PH1356	Iq heavy chain DJ							
456	2	18.2	14	2	PH1332	Iq heavy chain DJ							
457	2	18.2	14	2	PH1322	Iq heavy chain DJ							
458	2	18.2	14	2	PH1313	Iq heavy chain DJ							
459	2	18.2	14	2	PH1321	Iq heavy chain DJ							
460	2	18.2	14	2	PH1405	Iq heavy chain DJ							
461	2	18.2	14	2	PH1306	Iq heavy chain DJ							
462	2	18.2	14	2	S41601	interferon alpha 1							
463	2	18.2	14	2	PH1757	T cell receptor al							
464	2	18.2	14	2	PH1758	T cell receptor al							
465	2	18.2	14	2	PH1759	T cell receptor al							
466	2	18.2	14	2	PH1766	T cell receptor al							
467	2	18.2	14	2	PH1767	T cell receptor al							

ALIGNMENTS

RESULT 1

B44957 protein I7 - common tobacco (cv. Samsun NN) (fragment)

C:Species: Nicotiana glauca (common tobacco)

C:Date: 01-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 30-Sep-1993

C:Accession: B44957

R:Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.

Plant Cell Physiol. 31: 215-221; 1990

A:Title: Characterization of polypeptides that accumulate in cultured Nicotiana tab

A:Reference number: A44957

A:Accession: B44957

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <TAK>

Query Match 36.4%; Score 4; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAKP 10

DB 7 GAKP 10

RESULT 2

T48890

hypothetical protein ORF-B [imported] - Streptomyces coelicolor (fragment)

C:Species: Streptomyces coelicolor

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 20-Jan-2003

C:Accession: T48890

R:Matsumoto, A.; Honq, S.; Ishizuka, H.; Horinouchi, S.; Beppu, T.

Gene 146, 47-56, 1994

A:Title: Phosphorylation of the AfsR protein involved in secondary metabolism in St

A:Reference number: 224852; MUID:94341568; PMID:8063104

A:Accession: T48890

A:Status: Preliminary; translated from Gb/EMBL/DBs;
 A:Molecule type: DNA
 A:Residues: 1-8 <MAT>
 A:Cross-references: EMBL:DL5022, FIDN:BA840935, 1
 A:Experimental source: strain M10

Query Match 27.3%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 RAL 4
 III
 DB 6 RAL 8

RESULT 3
 155411
 hypothetical histone H2A.X (mistranslated) human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 28-Jan-2000 #sequence_revision 28 Jan 2000 #text_change 28 Jan 2000
 C:Accession: 155411
 R:Avanov, V.S.; Hatch, C.L.; Bonnet, W.M.
 J. Biol. Chem. 269, 24189-24194, 1994
 A:Title: Characterization of the human histone H2A.X gene. Comparison of its promoter with the human histone H2A.X gene.
 A:Reference number: 155411; MUID:95014156; PMID:7929675
 A:Accession: 155411
 A:Status: translation not shown; translated from Gb/EMBL/DBsJ
 A:Molecule type: DNA
 A:Residues: 1-8 <IVA>
 A:Cross-references: GB:S73863; NID:q765293; FIDN:AAH1414.1; FIDN:q4261841
 A:Note: this is a hypothetical translation of a sequence from the promoter region, preceded by a start codon.
 A:Genes: H2A.X

Query Match 27.3%; Score 3; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 ARA 3
 III
 DB 5 ARA 7

RESULT 4
 PT0562
 T cell receptor beta chain V-D-J region (IGH IAK) mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul 1992 #text_change 30-May-1997
 C:Accession: PT0562
 R:Reeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277631; PMID:1711558
 A:Accession: PT0562
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-9 <FEES>
 A:Experimental source: day 18 fetal thymus; strain BALB/c
 C:Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 NWG 7
 III
 DB 6 NWG 8

RESULT 5
 JC1416
 hypertrichosemic hormone I - stick insect (Extatosoma tiaratum)
 N:Alternate names: Cam-HrTH I

A:Status: hypertrichosemic factor II
 C:Species: Carausius morosus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: JC1416; S07157
 R:Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.
 Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992
 A:Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stl
 A:Reference number: JC1416; MUID:93129188; PMID:1482345
 A:Accession: JC1416
 A:Molecule type: protein
 A:Residues: 1-10 <GAEI>
 R:Gaede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 268, 67-75, 1987
 A:Title: Primary structure of the hypertrichosemic factor II from the corpus card
 A:Reference number: S07157; MUID:87157103; PMID:3828078
 A:Accession: S07157
 A:Molecule type: protein
 A:Residues: 1-10 <GAE2>
 C:Comment: hypertrichosemic factor II lacks the tryptophan modification.
 C:Comment: this peptide raises hemolymph levels of trehalose in the cockroach Pe-
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutami
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Binding site: carbohydrate (Trp) (covalent) #status experimental
 F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 27.3%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 NWG 7
 III
 DB 7 NWG 9

RESULT 6
 S09138
 hypertrichosemic hormone II - stick insect (Extatosoma tiaratum)
 N:Alternate names: Cam-HrTH II
 C:Species: Extatosoma tiaratum
 C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
 C:Accession: S09138
 R:Gaede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
 A:Title: Primary structures of hypertrichosemic neuropeptides isolated from the c
 erialis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bo
 A:Reference number: S08995; MUID:90253659; PMID:2340112
 A:Accession: S09138
 A:Molecule type: protein
 A:Residues: 1-10 <GAE>
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 27.3%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 NWG 7
 III
 DB 7 NWG 9

RESULT 7
 JP0072
 ribosomal protein l32 - Lactobacillus plantarum (fragment)
 C:Species: Lactobacillus plantarum
 C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
 C:Accession: JP0072
 R:Ochi, K.
 submitted to JIPB, February 1994

Abstract(s): phylogenetic diversity in the genus *Aspergillus* and comparative ribosomal RNA
 A:Reference number: JP0042
 A:Accession: JP0072
 A:Molecule type: protein
 A:Residues: 1 to 408
 C:Keywords: protein biosynthesis; ribosome

Query Match 27.4% Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKP 10
 DB 4 AKP 6

RESULT 8

A40753
 aldehyde ferredoxin oxidoreductase (EC 1.2.1.2) Pyrococcus furiosus (fragment)
 S:Alternate names: glyceraldehyde:ferredoxin oxidoreductase; red tongs protein (RTP)
 C:Species: Pyrococcus furiosus
 C:Date: 21-Apr-1992 #sequence_revision 21 Apr 1992 #text_change 13 Sep 1996

R:Kukud, S.; Adams, M.W.W.
 J. Biol. Chem. 265, 14208-14216, 1990
 A:Title: The novel, tongs-like iron-sulfur protein of the hyperthermophilic archaeobacterium
 colytic pathway.
 A:Reference number: A40753; MUID:9107766; PMID:1907234

A:Accession: A40753
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1 to 408
 C:Keywords: iron-sulfur protein; oxidoreductase; tongs

Query Match 27.3% Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNW 7
 DB 4 LNW 6

RESULT 9

PT0289
 Ig heavy chain C3b region (Chain 3; 100-91) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30 Sep 1993 #text_change 10 Aug 1994

R:Yamada, M.; Wasserman, K.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 174, 495-507, 1991
 A:Title: Preferential utilization of specific IgG2a subclass in heavy chain diversity and
 A:Reference number: PT0222; MUID:9110810; PMID:1639702

A:Accession: PT0289
 A:Molecule type: DNA
 A:Residues: 1 to 358
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 27.3% Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LNW 6
 DB 2 LNW 4

RESULT 10

PT0164
 chromogranin B, rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 19 Dec 1993 #sequence_revision 19 Nov 1994 #text_change 6 Oct 1995

C:Accession: B49164
 R:Nielsen, E.; Wellander, K.S.; Madsen, O.D.
 Endocrinology 129, 3247-3256, 1992

A:Title: Chromogranin B, a putative precursor of eight novel rat glucagonoma peptide
 A:Reference number: A49164; MUID:92063871; PMID:1954895

A:Accession: B49164

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1 to 481

A:Note: sequence extracted from NBI backbone (NCBIP:66370)

C:Superfamily: chromogranin B precursor

Query Match 27.4% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NMG 7
 DB 7 NMG 9

RESULT 11

S71304
 amine oxidase (copper-containing) (EC 1.4.3.6) 11 - Aspergillus niger (fragment)
 C:Species: Aspergillus niger
 C:Date: 12 Feb 1998 #sequence_revision 01-May-1998 #text_change 07-May-1999

C:Accession: S71304
 R:Reibort, L.; Tamaki, H.; Ishida, H.; Pec, P.; Luhova, L.; Tsuno, H.; Halata, M.;
 Eur. J. Biochem. 237, 255-265, 1996
 A:Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the

A:Reference number: S71303; MUID:96204933; PMID:8620882

A:Accession: S71304

A:Molecule type: protein

A:Residues: 1-114 PRE

C:Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquirone

Query Match 27.4% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALN 5
 DB 5 ALN 7

RESULT 12

PH1343
 Ig heavy chain L3 region (Chain 3; 190-91) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PH1343

R:Wasserman, K.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type JH joining in young children with B precursor

A:Reference number: PH1342; MUID:93094761; PMID:1460419

A:Accession: PH1343

A:Molecule type: DNA

A:Residues: 1 to 114 WAS

C:Keywords: heterotetramer; immunoglobulin

Query Match 27.4% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NMG 7
 DB 6 NMG 8

RESULT 13

S40043
 19 kDa type I alpha chain of rat insulin human (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 22-Nov-1993 #sequence_revision 26-May 1995 #text_change 17-Mar-1999
 C:Accession: S23364
 R:Pluschke, G.; Ricken, G.; Taube, H.; Kronenberg, S.; Meichner, H.H.; Eichman, E.; J. Immunol. 21, 2749-2754, 1991
 A:Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheumatoid arthritis
 A:Reference number: S23364; MUID:92037520; PMID:1657675
 A:Accession: S23364
 A:Status: preliminary; translation: not shown
 A:Molecule type: mRNA
 A:Residues: 1-11 <PDB>
 A:Cross references: EMBL:X58164
 C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALN 5
 DB 8 ALN 10

RESULT 14
 A25169
 phospholipase A2 (EC 3.1.1.4) precursor, sheep (fragment)
 C:Species: ovis orientalis aries, ovis aries (domestic sheep)
 C:Date: 22-Jun-1988 #sequence_revision 02-Jun-1998 #text_change 31-Oct-1997
 C:Accession: A25169
 R:Butlin, C.E.; Van Doren, P.J.; Verheij, F.E.A.M.; Le Baus, G.H.
 Eul. J. Biochem. 53, 91-97, 1975
 A:Title: Isolation and properties of phospholipase A2 from ox and sheep livers
 A:Reference number: A94661
 A:Accession: A25169
 A:Molecule type: protein
 A:Residues: 1-12 <PDB>
 C:Superfamily: phospholipase A2
 C:Keywords: carboxylic ester hydrolase; pyroglutamate and
 F1/Modified site: pyrrolidone carboxylate (Gln) #status: experimental

Query Match 27.3% Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALN 4
 DB 7 ALN 9

RESULT 15
 E58502
 44-2K bile stone protein - unidentified bacterium (fragment)
 C:Species: unidentified bacterium
 C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
 R:Binette, C.P.; Binette, M.B.
 Submitted to the Protein Sequence Database, October 1997
 A:Description: the proteins of kidney and gallbladder stones.
 A:Reference number: E58501
 A:Accession: E58502
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <BIN>
 A:Experimental source: human bile with stones
 A:Note: a secondary sequence DVKISVANS was also found

Query Match 27.3% Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ALN 5
 DB 4 ALN 6

RESULT 16
 A60336
 outer membrane protein ompA homolog - Actinobacillus actinomycetemcomitans (fragment)
 C:Species: Actinobacillus actinomycetemcomitans
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 18-Jun-1993
 C:Accession: A60336
 R:Wilson, M.E.
 Infect. Immun. 59, 2505-2507, 1991
 A:Title: The heat-modifiable outer membrane protein of Actinobacillus actinomycetemcomitans
 A:Reference number: A60336; MUID:91257635; PMID:2050416
 A:Accession: A60336
 A:Molecule type: protein
 A:Residues: 1-19 <WIL>
 C:Superfamily: outer membrane protein A
 C:Keywords: membrane protein

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
 DB 10 GAK 12

RESULT 17
 A60458
 protocatechuate 3,4-dioxygenase (EC 1.13.11.3) alpha chain - Moraxella sp. (strain N)
 A:Alternate names: protocatechuate oxygenase
 C:Species: Moraxella sp.
 C:Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 07-May-1999
 C:Accession: A60458
 R:Storjohannes, R.; Pelmont, J.
 Appl. Environ. Microbiol. 55, 140-147, 1989
 A:Title: Occurrence of two different forms of protocatechuate 3,4-dioxygenase in a
 A:Reference number: A60458; MUID:89245845; PMID:2541659
 A:Accession: A60458
 A:Molecule type: protein
 A:Residues: 1-13 <STE>
 A:Note: two forms P and G of the alpha subunit yielded identical amino terminal seq
 C:Keywords: iron; oxidoreductase

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKP 10
 DB 5 AKP 7

RESULT 18
 A39836
 aggrecan - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 24-Jun-1993
 C:Accession: A39836
 R:Sandy, J.D.; Neame, P.J.; Boynton, R.E.; Flannery, C.R.
 J. Biol. Chem. 265, 8683-8685, 1991
 A:Title: Catabolism of aggrecan in cartilage explants. Identification of a major cl
 A:Reference number: A39836; MUID:91224956; PMID:2026585
 A:Accession: A39836
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <SAN>

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKP 10
 DB 11

A:Accession: PH0804
 A:Molecule type: mRNA
 A:Residues: 1-14 <CAS>
 A:Cross-references: EMBL:X60913
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAL 4
 DB 9 RAL 11

RESULT 25

C48401
 ribosomal protein L1 - Thermus aquaticus (fragment)

C:Species: Thermus aquaticus
 C:Date: 01-Dec-1993 #sequence_revision 18 Nov-1994 #text_change 16-Nov-1994
 C:Accession: C48401
 R:Garber, M.B.; Agalarov, S.C.; Eliseikina, I.A.; Fomenkova, N.P.; Nikonov, S.V.; Sedold
 Biochimie 74, 327-336, 1992
 A:Title: Ribosomal proteins from Thermus thermophilus for structural investigations.
 A:Reference number: A48401; MUID:92345325; PMID:151986
 A:Accession: C48401
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <GAR>
 A:Note: sequence extracted from NCBI backbone (N5516:19994)

Query Match 27.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAL 4
 DB 3 RAL 10

RESULT 26

PT0082

protein G460023 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse cat tissue)
 C:Date: 07-Feb-1996 #sequence_revision 14 Apr-1996 #text_change 06-Jun-1997
 C:Accession: PT0082
 R:Tsugita, A.; Kamo, M.; Kawakami, M.; Otsu, Y.
 submitted to JIPID, December 1995
 A:Description: Two dimensional electrophoresis of plant proteins and standardization of
 A:Reference number: PN0173
 A:Accession: PT0082
 A:Molecule type: protein
 A:Residues: 1-15 <TSU>
 A:Experimental source: leaf

Query Match 27.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
 DB 4 KPK 6

RESULT 27

S41956

Ig mu chain V region (clone 17) - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
 C:Accession: S41956
 R:Waeber, S.D.; Williams, G.T.; Larsen, L.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.
 Nucleic Acids Res. 22, 1389-1393, 1994

A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice
 A:Reference number: S43956; MUID:94248036; PMID:8190629
 A:Accession: S43956
 A:Molecule type: DNA
 A:Residues: 1-15 <WAG>
 C:Keywords: immunoglobulin

Query Match 27.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AKP 10
 DB 3 AKP 5

RESULT 28

PH0136

T-cell receptor beta chain V-D-J region MS18 - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-May-1997
 C:Accession: PH0136
 R:Martin, R.; Howell, M.D.; Jaraquemada, D.; Flierlage, M.; Richert, J.; Brostoff, S.
 J. Exp. Med. 173, 19-24, 1991
 A:Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the c
 A:Reference number: PH0135; MUID:91086843; PMID:1702137
 A:Accession: PH0136
 A:Molecule type: mRNA
 A:Residues: 1-15 <MAR>
 C:Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALN 5
 DB 10 ALN 12

RESULT 29

S03955

acidic fibroblast growth factor - dog (fragment)

N:Alternate names: alpha-endothelial cell growth factor
 C:Species: Canis lupus familiaris (dog)
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
 C:Accession: S03955
 R:Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; S
 Eur. J. Biochem. 181, 67-73, 1989
 A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canin
 A:Reference number: S03953; MUID:89231704; PMID:2714282
 A:Accession: S03955
 A:Molecule type: protein
 A:Residues: 1-15 <QUI>
 C:Keywords: growth factor

Query Match 27.3%; Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
 DB 4 KPK 6

RESULT 30

PH0779

T-cell receptor alpha chain (H83) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PH0779
 R:Casanova, J.L.; Romero, P.; Wildmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 137-148, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex allelic exclusion and antigen-specific repertoire
 A:Reference number: PH0746; MUID:92078846; PMID:184116
 A:Accession: PH0779
 A:Molecule type: mRNA
 A:Residues: 1-15 <CAS>
 A:Cross references: EMBL:X60677
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 27.4% Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALN 5
 II
 II
 DB 2 ALN 4

RESULT 31
 PH0031
 mixed lymphocyte reaction inhibitor - rat (Hagedoorn)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31 Dec-1990 #sequence_revision 31; Dec-1990 #text_change 24-Feb-1995
 C:Accession: PH0031
 R:Shizomiya, T.; Ohara, T.; Wada, N.; Ohnishi, A.; Kanada, N.
 J. Biochem. 127, 435-439, 1990
 A:Title: Rat liver arabinase suppresses mixed lymphocyte reaction.
 A:Reference number: PH0031; MUID:90256720; PMID:2141356
 A:Accession: PH0031
 A:Molecule type: protein
 A:Residues: 1-15 <SR1>
 A:Experimental source: liver
 C:Keywords: lymphocyte

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KFK 11
 III
 DB 10 KFK 12

RESULT 32
 A61348
 red pigment-concentrating hormone - northern shrew
 N:Alternate names: blanching hormone
 C:Species: Pandanus borealis (northern shrew)
 C:Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
 C:Accession: A61348; S07139
 R:Perlund, P.; Josefsson, L.
 Science 177, 173-175, 1972
 A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
 A:Reference number: A61348; MUID:7228758; PMID:564704
 A:Accession: A61348
 A:Molecule type: protein
 A:Residues: 1-8 <PER1>
 R:Perlund, P.
 Biochim. Biophys. Acta 371, 304-311, 1974
 A:Title: Structure of the red-pigment concentrating hormone of the shrimp, *Pandalus borealis*
 A:Reference number: S07139; MUID:75054965; PMID:441643
 A:Accession: S07139
 A:Molecule type: protein
 A:Residues: 'E', 2-8 <PER2>
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C:Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pig-
 ment containing cells.
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyrrolidone
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 II
 II
 DB 2 LN 3

RESULT 33
 S08995
 hypertrehalosemic hormone I - oriental cockroach
 N:Alternate names: Psa-GAH I
 C:Species: Blatta orientalis (oriental cockroach)
 C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
 C:Accession: S08995
 R:Gaede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
 A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the or-
 entalis and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bon
 A:Reference number: S08995; MUID:90253659; PMID:2340112
 A:Accession: S08995
 A:Molecule type: protein
 A:Residues: 1-8 <GAE>
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyrrolidone carboxylic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NW 6
 II
 II
 DB 7 NW 8

RESULT 34
 S08996
 hypertrehalosemic hormone II - oriental cockroach
 N:Alternate names: Psa-GAH II
 C:Species: Blatta orientalis (oriental cockroach)
 C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
 C:Accession: S08996
 R:Gaede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
 A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the or-
 entalis and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bon
 A:Reference number: S08995; MUID:90253659; PMID:2340112
 A:Accession: S08996
 A:Molecule type: protein
 A:Residues: 1-8 <GAE>
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyrrolidone carboxylic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NW 6
 II
 II
 DB 7 NW 8

RESULT 35
 A49823
 adipokinetic hormone I - American cockroach
 N:Alternate names: periplanetic CC-1

C:Keywords: Periplaneta americana (American cockroach)
 C:Date: 03-May-1994 #sequence_revision 03-May 1994 #text_change 07-May 1999
 C:Accession: A49623
 R:Scarthrough, R.M.; Jamieson, G.C.; Kallish, F.; Kramer, S.J.; McEntee, J.A.; Miller, C.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
 A:Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp
 A:Reference number: A49823; M01D:84298179; PMID:6591205
 A:Accession: A49823
 A:Molecule type: protein
 A:Residues: 1-8 <SCA>
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglut
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NW 6
 II
 DB 7 NW 8

RESULT 36
 B49823
 adipokinetic hormone II - American cockroach
 N:Alternative names: neuropeptide M-II; periplaneta M-II
 C:Species: Periplaneta americana (American cockroach)
 C:Date: 03-May 1994 #sequence_revision 03-May 1994 #text_change 07-May 1999
 C:Accession: B49823; A05170
 R:Scarthrough, R.M.; Jamieson, G.C.; Kallish, F.; Kramer, S.J.; McEntee, J.A.; Miller, C.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
 A:Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp
 A:Reference number: A49823; M01D:84298179; PMID:6591205
 A:Accession: B49823
 A:Molecule type: protein
 A:Residues: 1-8 <SCA>
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglut
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NW 6
 II
 DB 7 NW 8

RESULT 37
 A44960
 neuropeptide Leu-QC-11 - Colorado potato beetle
 C:Species: Leptinotarsa decemlineata (Colorado potato beetle)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: A44960
 R:Gaede, G.; Kellner, R.
 Peptides 10, 1287-1289, 1989
 A:Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle
 A:Reference number: A44960; M01D:90160053; PMID:2576128
 A:Accession: A44960
 A:Molecule type: protein
 A:Residues: 1-8 <GAE>
 C:Superfamily: adipokinetic hormone
 C:Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglut
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimen

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NW 6
 II
 DB 7 NW 8

RESULT 39
 S15422
 adipokinetic hormone - cockchafer
 C:Species: Melolontha melolontha (cockchafer)
 C:Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
 C:Accession: S15422
 R:Gaede, G.
 Biochem. J. 275, 671-677, 1991
 A:Title: A unique charged tyrosine containing member of the adipokinetic hormone/ r
 A:Reference number: S15422; M01D:91248100; PMID:2039445
 A:Accession: S15422
 A:Molecule type: protein
 A:Residues: 1-8 <HIO>
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 I
 DB 2 LN 3

RESULT 40
 A43976
 hypotetradecosec hormone - yellow mealworm
 C:Species: Tenebrio molitor (yellow mealworm)
 C:Date: 03-Feb-1999 #sequence_revision 03-Feb 1999 #text_change 07-May 1999
 C:Accession: A43976

Rigaud, G.; Rosinski, G.
Peptides 11: 455-459, 1990
A:Title: The primary structure of the hypothalamic secretory peptide from *Zophobas rugipes*
A:Reference number: A43976; PMID:9341081; PMID:266421

A:Accession: A43976
A:Molecule type: protein
A:Residues: 1-8 <GAP>
A:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; fat body; neurohypophyseal peptide; pyroglutamate
F1/Modified site: pyrrolidone carboxylic acid (C16) #status experimental
F1B/Modified site: amidated carboxyl end (C16) #status experimental

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
1
DB 2 LN 3

RESULT 41
B43976
hypotrichalomic hormone - beetle (*Zophobas rugipes*)
C:Species: *Zophobas rugipes*
C:Date: 03 Feb 1993 #sequence_revision 01 #text_change 01 May 1993
C:Accession: B43976

Rigaud, G.; Rosinski, G.
Peptides 11: 455-459, 1990
A:Title: The primary structure of the hypothalamic secretory peptide from *Zophobas rugipes*
A:Reference number: A43976; PMID:9341081; PMID:266421

A:Accession: B43976
A:Molecule type: protein
A:Residues: 1-8 <GAP>
A:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; corpora cardiaca; fat body; neurohypophyseal peptide; pyroglutamate
F1/Modified site: pyrrolidone carboxylic acid (C16) #status experimental
F1B/Modified site: amidated carboxyl end (C16) #status experimental

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
1
DB 2 LN 3

RESULT 42
A58641
adipokinetic hormone - dor beetle
C:Species: *Geotrupes stercorarius* (dor beetle)
C:Date: 26 Oct 1997 #sequence_revision 01 #text_change 01 Oct 1997
C:Accession: A58641

Rigaud, G.
Biochem. G. 27% 671-677, 1991
A:Title: A unique charged tyrosine-containing member of the adipokinetic hormone/ red pig
A:Reference number: S15422; PMID:9148100; PMID:266421

A:Accession: A58641
A:Molecule type: protein
A:Residues: 1-8 <BIO>
A:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neurohypophyseal peptide; pyroglutamate; acid
F1/Modified site: pyrrolidone carboxylic acid (C16) #status experimental
F1B/Modified site: amidated carboxyl end (C16) #status experimental

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
1
DB 2 LN 4

RESULT 43
P01437
1a heavy chain V region (clone micro m 46-6 PCR) - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C:Date: 31 Dec 1993 #sequence_revision 01 Dec 1993 #text_change 17-Mar-1999
C:Accession: P01407
Kishikawa, T.; Miyazawa, T.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.
J. Exp. Med. 176: 1269-1274, 1992
A:Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in virus.
A:Reference number: P01407; PMID:9401887; PMID:1402663
A:Accession: P01407
A:Molecule type: DNA
A:Residues: 1-8 <SH1>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AL 2
1
DB 3 AL 4

RESULT 44
P60588
sperm-activating peptide a - sea urchin (*Pseudoboletia maculata*)
A:Alternate names: speract homolog
C:Species: *Pseudoboletia maculata*
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: P60588
R.Yoshino, K.I.; Kajitani, H.; Nakura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yai
Comp. Biochem. Physiol. B 94: 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its relat
ous nudus, *Echinometra mathaei* and *Heterocentrotus mamillatus*.
A:Reference number: A60527
A:Accession: P60588
A:Molecule type: protein
A:Residues: 1-8 <YOS>
C:Superfamily: unassigned animal peptides

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AL 4
1
DB 3 AL 4

RESULT 45
P60588
sperm-activating peptide b - sea urchin (*Pseudoboletia maculata*)
A:Alternate names: speract homolog
C:Species: *Pseudoboletia maculata*
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: P60588
R.Yoshino, K.I.; Kajitani, H.; Nakura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yai
Comp. Biochem. Physiol. B 94: 739-751, 1989
A:Title: A halogenated amino acid containing sperm activating peptide and its relat
ous nudus, *Echinometra mathaei* and *Heterocentrotus mamillatus*.
A:Reference number: A60527
A:Accession: P60588
A:Molecule type: protein
A:Residues: 1-8 <YOS>
C:Superfamily: unassigned animal peptides

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY <AL 4
II
3 AL 4

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 46
Q60586
sperm activating peptide c - sea urchin (Pandalus) (Pandalus)

N.A. Interact. Cases: speract homolog
C: Species: pseudoboletia maculata
C: Date: 17-Apr-1993 #sequence_revision 17 Apr-1993 #text_change 18 Aug-2000
C: Accession: G60586

K. Yoshino, K. I. Kajiwara, H. Nomura, K. Takao, I. Shigenishi, Y. J. Kurita, M. Yamaoka
Comp. Biochem. Physiol. B 94, 739-751, 1989

A: Title: A halogenated amino acid-containing sperm activating peptide and its related pe
opus nudus, Echinometra mathaei and heterocentrotus mamillatus.

A: Reference number: A60527

A: Accession: G60586

A: Molecule type: protein

A: Residues: 1-8 <YOS>

C: Superfamily: unassigned animal peptides

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AL 4
II
3 AL 4

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 47
XGROED
urine glycopeptide - human
C: Species: homo sapiens (man)
C: Date: 29-Jun-2000 #sequence_revision 20 Jun-2000 #text_change 29-Jun-2000
C: Accession: A01188

R. Klotz, G. J. Weiss, J. B.
Biochem. J. 123, 25P, 1971

A: Title: Identification in urine of a low-molecular-weight polar glycopeptide containing
A: Reference number: A01188; MUID: 7206238; PMID: 5120885

A: Accession: A01188

A: Molecule type: protein

A: Residues: 1-8 <GPE>

C: Comment: The identity of the glycopeptide in human urine as a sperm activating peptide is unknown
it has also been found (see PIR XGROED).

C: Superfamily: unassigned animal peptides

C: Keywords: glycoprotein
F1/Binding site: carbohydrate (Cys) (oxidized) addition experimental

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CA 8
II
7 CA 5

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 48
A41570
angiotensin-converting enzyme inhibitor yellowfin tuna
C: Species: Thunnus albacares (yellowfin tuna)
C: Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000
C: Accession: A41570

K. Kohama, Y. Matsumoto, S. Oka, H. Teramachi, I. Okabe, M. Misura, T.
Biochem. Biophys. Res. Commun. 155, 342-347, 1988

A: Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.
A: Reference number: A31570; MUID: 88426422; PMID: 3415688

A: Accession: A31570

A: Molecule type: protein

A: Residues: 1-8 <KOH>

A: Note: the source is designated as Neothunnus macropterus

C: Superfamily: unassigned animal peptides

C: Keywords: angiotensin-converting enzyme inhibitor

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WG 7
II
6 WG 7

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 49
S37141
rpsA protein - Erwinia chrysanthemi
C: Species: Erwinia chrysanthemi
C: Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
C: Accession: S37141

R. Doullie, A. Toussaint, A. J. Paelen, M.
submitted to the EMBL Data Library, August 1993

A: Description: Identification of the integration host factor genes of E. chrysanthemi

A: Reference number: S37149

A: Accession: S37141

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-8 <DOD>

A: Cross-references: EMBL: X74750; NID: q399669; PID: CAA52769.1; PID: q581108

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AK 9
II
5 AK 6

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 50
A39308
glycine reductase (EC 1.4.99.-) sulphydryl protein C, alpha chain - Clostridium stru
C: Species: Clostridium sticklandii
C: Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 15-Aug-1997
C: Accession: A39308

R. Stadman, T. C. J. Davis, J. N.
J. Biol. Chem. 266, 22147-22153, 1991

A: Title: Glycine reductase protein C, Properties and characterization of its role i
A: Reference number: A39308; MUID: 92042141; PMID: 1919235

A: Accession: A39308

A: Status: preliminary

A: Molecule type: protein

A: Residues: 1-8 <STA>

C: Function:
A: Description: glycine reductase complex catalyzes the reductive deamination of gly
C: Keywords: ATP; oxidoreductase

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KP 10
II
2 KP 3

Search completed: September 30, 2003, 10:09:43
Job time : 13.4167 secs

GenCore version 5.1.6
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OM protein : protein search, using sw mode.

Run on: September 30, 2003, 11:07:05 : Search time 11.8433 Seconds
(without alignment)
39.341 Million cell updates/sec

Title: US-09-787-443-3

Perfect score: 11

Sequence: 1 ARALNWCAPK 11

Scoring table:

Gapop 60.0 , Gapext 50.0

Searched: 328717 seqs, 4231058 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75359

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database :
1: /cgn2_6/ptodata/1/iaa/5A_Comb.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_Comb.pep.*
3: /cgn2_6/ptodata/1/iaa/5A_Comb.pep.*
4: /cgn2_6/ptodata/1/iaa/5B_Comb.pep.*
5: /cgn2_6/ptodata/1/iaa/ptous_Comb.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4	36.4	9	4	US-09-387-7-5-1
4	4	36.4	10	1	US-08-144-195A-21
5	4	36.4	10	1	US-08-166-195A-22
6	4	36.4	10	1	US-08-378-761A-52
7	4	36.4	10	1	US-08-485-286-52
8	4	36.4	10	2	US-08-436-772-21
9	4	36.4	10	2	US-08-436-772-22
10	4	36.4	10	2	US-08-436-8845-25
11	4	36.4	10	2	US-08-436-8845-22
12	4	36.4	10	2	US-08-536-597-129
13	4	36.4	10	2	US-08-556-597-140
14	4	36.4	10	6	5248606-37
15	4	36.4	11	3	US-08-844-978-42
16	4	36.4	11	3	US-08-844-978-45
17	4	36.4	12	2	US-08-461-990B-27
18	4	36.4	13	1	US-08-248-819A-44
19	4	36.4	13	2	US-08-337-646A-62
20	4	36.4	13	3	US-09-041-889-47
21	4	36.4	13	3	US-08-940-589A-20
22	4	36.4	13	3	US-08-927-326-62
23	4	36.4	13	4	US-09-595-781-26
24	4	36.4	13	4	US-09-417-264-37
25	4	36.4	14	1	US-08-232-453A-23
26	4	36.4	14	1	US-08-232-453A-28
27	4	36.4	14	1	US-08-242-453A-41
28	4	36.4	14	2	US-08-482-228-13
29	4	36.4	14	3	US-08-482-528-13
30	4	36.4	14	4	US-09-400-653A-13
31	4	36.4	14	4	US-09-248-061B-31
32	4	36.4	15	1	US-08-467-083-48
33	4	36.4	15	1	US-08-414-417B-48
34	4	36.4	15	2	US-08-486-348A-48
35	4	36.4	15	2	US-08-710-249-18
36	4	36.4	15	2	US-08-468-545B-48
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39	4	36.4	15	3	US-09-041-889-22
40	4	36.4	15	3	US-09-041-889-24
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49	4	36.4	15	4	US-09-220-157A-18
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61	3	27.3	8	1	US-08-246-941-3
62	3	27.3	8	1	US-08-480-367B-23
63	3	27.3	8	1	US-08-002-466-10
64	3	27.3	8	1	US-08-487-221A-23
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66	3	27.3	8	1	US-08-526-710-24
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72	3	27.3	8	1	US-08-463-052-2
73	3	27.3	8	1	US-08-290-301-44
74	3	27.3	8	1	US-08-633-760-3
75	3	27.3	8	2	US-08-612-302A-39
76	3	27.3	8	2	US-08-480-551-2
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97	3	27.3	8	2	US-08-687-219B-2
98	3	27.3	8	2	US-08-687-219B-3
99	3	27.3	8	2	US-08-687-219B-14
100	3	27.3	8	2	US-08-687-219B-15

Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 31, Appl
Sequence 48, Appl
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Sequence 15, Appl
Sequence 16, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 35, Appl
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Sequence 16, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 33, Appl
Sequence 18, Appl
Sequence 33, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 22, Appl
Sequence 24, Appl
Sequence 36, Appl
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Sequence 2, Appl
Sequence 23, Appl
Sequence 42, Appl
Sequence 3, Appl
Sequence 23, Appl
Sequence 10, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 39, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 44, Appl
Sequence 3, Appl
Sequence 39, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 39, Appl
Sequence 48, Appl
Sequence 7, Appl
Sequence 260, App
Sequence 163, App
Sequence 453, App
Sequence 460, App
Sequence 515, App
Sequence 520, App
Sequence 39, Appl
Sequence 48, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 29, Appl
Sequence 68, Appl
Sequence 59, Appl
Sequence 3, Appl
Sequence 7, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 14, Appl
Sequence 15, Appl

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102	3	27.3	8	2	US-08-687-219B-17	Sequence 17, Appl	175	3	27.3	3	US-08-156-552A-14	Sequence 14, Appl
103	3	27.3	8	2	US-08-687-219B-18	Sequence 18, Appl	176	3	27.3	3	US-08-445-042-11	Sequence 11, Appl
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111	3	27.3	8	3	US-08-350-215-19	Sequence 45, Appl	184	3	27.3	3	US-08-615-181-78	Sequence 78, Appl
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116	3	27.3	8	3	US-08-350-215-19	Sequence 50, Appl	189	3	27.3	3	US-08-397-633A-6	Sequence 6, Appl1
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119	3	27.3	8	3	US-08-350-215-19	Sequence 53, Appl	192	3	27.3	3	US-08-468-975-5	Sequence 5, Appl1
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125	3	27.3	8	3	US-08-350-215-19	Sequence 59, Appl	198	3	27.3	3	US-08-787-547-47	Sequence 47, Appl
126	3	27.3	8	3	US-08-350-215-19	Sequence 60, Appl	199	3	27.3	3	US-08-787-547-52	Sequence 52, Appl
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128	3	27.3	8	3	US-08-350-215-19	Sequence 62, Appl	201	3	27.3	3	US-08-414-417B-17	Sequence 17, Appl
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131	3	27.3	8	3	US-08-350-215-19	Sequence 65, Appl	204	3	27.3	3	US-08-700-035A-13	Sequence 13, Appl
132	3	27.3	8	3	US-08-350-215-19	Sequence 66, Appl	205	3	27.3	3	US-08-486-348A-17	Sequence 17, Appl
133	3	27.3	8	3	US-08-350-215-19	Sequence 67, Appl	206	3	27.3	3	US-08-471-341-5	Sequence 5, Appl1
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136	3	27.3	8	3	US-08-350-215-19	Sequence 70, Appl	209	3	27.3	3	US-08-751-965-10	Sequence 10, Appl
137	3	27.3	8	3	US-08-350-215-19	Sequence 71, Appl	210	3	27.3	3	US-08-474-661-5	Sequence 5, Appl
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139	3	27.3	8	3	US-08-350-215-19	Sequence 73, Appl	212	3	27.3	3	US-08-185-949B-51	Sequence 51, Appl
140	3	27.3	8	3	US-08-350-215-19	Sequence 74, Appl	213	3	27.3	3	US-08-185-949B-56	Sequence 56, Appl
141	3	27.3	8	3	US-08-350-215-19	Sequence 75, Appl	214	3	27.3	3	US-08-468-545B-17	Sequence 17, Appl
142	3	27.3	8	3	US-08-350-215-19	Sequence 76, Appl	215	3	27.3	3	US-08-389-360-3	Sequence 3, Appl1
143	3	27.3	8	3	US-08-350-215-19	Sequence 77, Appl	216	3	27.3	3	US-08-389-360-4	Sequence 4, Appl1
144	3	27.3	8	3	US-08-350-215-19	Sequence 78, Appl	217	3	27.3	3	US-08-389-360-5	Sequence 5, Appl1
145	3	27.3	8	3	US-08-350-215-19	Sequence 79, Appl	218	3	27.3	3	US-08-738-975-10	Sequence 10, Appl
146	3	27.3	8	3	US-08-350-215-19	Sequence 80, Appl	219	3	27.3	3	US-08-902-516-24	Sequence 24, Appl
147	3	27.3	8	3	US-08-350-215-19	Sequence 81, Appl	220	3	27.3	3	US-08-902-516-25	Sequence 25, Appl
148	3	27.3	8	3	US-08-350-215-19	Sequence 82, Appl	221	3	27.3	3	US-08-728-626-10	Sequence 10, Appl
149	3	27.3	8	3	US-08-350-215-19	Sequence 83, Appl	222	3	27.3	3	US-08-625-695A-6	Sequence 6, Appl1
150	3	27.3	8	3	US-08-350-215-19	Sequence 84, Appl	223	3	27.3	3	US-08-968-676-13	Sequence 13, Appl
151	3	27.3	8	3	US-08-350-215-19	Sequence 85, Appl	224	3	27.3	3	US-08-468-964B-6	Sequence 6, Appl1
152	3	27.3	8	3	US-08-350-215-19	Sequence 86, Appl	225	3	27.3	3	US-08-993-738A-1	Sequence 1, Appl1
153	3	27.3	8	3	US-08-350-215-19	Sequence 87, Appl	226	3	27.3	3	US-08-772-113-5	Sequence 5, Appl1
154	3	27.3	8	3	US-08-350-215-19	Sequence 88, Appl	227	3	27.3	3	US-08-735-253-17	Sequence 17, Appl
155	3	27.3	8	3	US-08-350-215-19	Sequence 89, Appl	228	3	27.3	3	US-08-747-137-98	Sequence 98, Appl
156	3	27.3	8	3	US-08-350-215-19	Sequence 90, Appl	229	3	27.3	3	US-08-747-137-132	Sequence 132, Appl
157	3	27.3	8	3	US-08-350-215-19	Sequence 91, Appl	230	3	27.3	3	US-08-469-692-5	Sequence 5, Appl1
158	3	27.3	8	3	US-08-350-215-19	Sequence 92, Appl	231	3	27.3	3	US-08-433-133-54	Sequence 54, Appl
159	3	27.3	8	3	US-08-350-215-19	Sequence 93, Appl	232	3	27.3	3	US-08-433-133-102	Sequence 102, Appl
160	3	27.3	8	3	US-08-350-215-19	Sequence 94, Appl	233	3	27.3	3	US-07-871-282A-6	Sequence 6, Appl1
161	3	27.3	8	3	US-08-350-215-19	Sequence 95, Appl	234	3	27.3	3	US-09-036-582-4	Sequence 4, Appl1
162	3	27.3	8	3	US-08-350-215-19	Sequence 96, Appl	235	3	27.3	3	US-09-036-582-6	Sequence 6, Appl1
163	3	27.3	8	3	US-08-350-215-19	Sequence 97, Appl	236	3	27.3	3	US-09-064-839-12	Sequence 12, Appl
164	3	27.3	8	3	US-08-350-215-19	Sequence 98, Appl	237	3	27.3	3	US-08-318-856A-14	Sequence 14, Appl
165	3	27.3	8	3	US-08-350-215-19	Sequence 99, Appl	238	3	27.3	3	US-08-318-856A-19	Sequence 19, Appl
166	3	27.3	8	3	US-08-350-215-19	Sequence 100, Appl	239	3	27.3	3	US-08-318-856A-20	Sequence 20, Appl
167	3	27.3	8	3	US-08-350-215-19	Sequence 101, Appl	240	3	27.3	3	US-08-318-856A-25	Sequence 25, Appl
168	3	27.3	8	3	US-08-350-215-19	Sequence 102, Appl	241	3	27.3	3	US-08-318-856A-26	Sequence 26, Appl
169	3	27.3	8	3	US-08-350-215-19	Sequence 103, Appl	242	3	27.3	3	US-08-318-856A-27	Sequence 27, Appl
170	3	27.3	8	3	US-08-350-215-19	Sequence 104, Appl	243	3	27.3	3	US-08-318-856A-28	Sequence 28, Appl
171	3	27.3	8	3	US-08-350-215-19	Sequence 105, Appl	244	3	27.3	3	US-08-611-977-5	Sequence 5, Appl1
172	3	27.3	8	3	US-08-350-215-19	Sequence 106, Appl	245	3	27.3	3	US-08-198-046-5	Sequence 5, Appl1
173	3	27.3	8	3	US-08-350-215-19	Sequence 107, Appl	246	3	27.3	3	US-08-612-842-2	Sequence 2, Appl1

247	3	27.3	9	2	US-08-251-678A-6	Sequence 6, Appl	320	3	27.3	4	US-09-705-160-35	Sequence 35, Appl
248	3	27.3	9	3	US-07-792-600-43	Sequence 34, Appl	321	3	27.3	4	US-09-705-160-38	Sequence 38, Appl
249	3	27.3	9	3	US-08-481-985B-128	Sequence 128, App	322	3	27.3	4	US-09-705-160-39	Sequence 39, Appl
250	3	27.3	9	3	US-08-828-712-1	Sequence 15, Appl	323	3	27.3	4	US-09-165-863-4	Sequence 4, Appl
251	3	27.3	9	3	US-09-351-438-12	Sequence 12, Appl	324	3	27.3	4	US-09-165-863-6	Sequence 6, Appl
252	3	27.3	9	3	US-08-880-963-14	Sequence 19, Appl	325	3	27.3	4	US-09-561-526-17	Sequence 17, Appl
253	3	27.3	9	3	US-08-159-349A-133	Sequence 191, App	326	3	27.3	4	US-08-197-484-88	Sequence 88, Appl
254	3	27.3	9	3	US-08-159-349A-638	Sequence 608, App	327	3	27.3	4	US-08-197-484-94	Sequence 94, Appl
255	3	27.3	9	3	US-08-159-349A-742	Sequence 742, App	328	3	27.3	4	US-08-197-484-116	Sequence 116, App
256	3	27.3	9	3	US-08-159-349A-741	Sequence 791, App	329	3	27.3	4	US-08-197-484-147	Sequence 147, App
257	3	27.3	9	3	US-08-159-349A-798	Sequence 798, App	330	3	27.3	4	US-08-197-484-153	Sequence 153, App
258	3	27.3	9	3	US-08-159-349A-822	Sequence 822, App	331	3	27.3	4	US-09-697-884-48	Sequence 48, Appl
259	3	27.3	9	3	US-08-159-349A-1078	Sequence 1078, App	332	3	27.3	4	US-09-697-884-50	Sequence 50, Appl
260	3	27.3	9	3	US-08-657-725B-47	Sequence 47, Appl	333	3	27.3	4	US-09-495-562-1	Sequence 1, Appl
261	3	27.3	9	3	US-08-592-743B-6	Sequence 6, Appl	334	3	27.3	4	US-09-324-782-15	Sequence 15, Appl
262	3	27.3	9	3	US-08-426-680B-17	Sequence 17, Appl	335	3	27.3	4	US-08-469-260A-184	Sequence 184, App
263	3	27.3	9	3	US-08-785-831-47	Sequence 47, Appl	336	3	27.3	4	US-09-668-143-15	Sequence 15, Appl
264	3	27.3	9	3	US-09-064-904-9	Sequence 9, Appl	337	3	27.3	4	US-08-627-820-5	Sequence 5, Appl
265	3	27.3	9	3	US-08-170-299-5	Sequence 6, Appl	338	3	27.3	4	US-09-435-524-3	Sequence 3, Appl
266	3	27.3	9	3	US-08-467-791-5	Sequence 5, Appl	339	3	27.3	4	US-09-435-524-4	Sequence 4, Appl
267	3	27.3	9	3	US-09-157-021-34	Sequence 34, Appl	340	3	27.3	4	US-09-435-524-5	Sequence 5, Appl
268	3	27.3	9	3	US-09-156-842-43	Sequence 34, Appl	341	3	27.3	4	US-09-259-478A-5	Sequence 5, Appl
269	3	27.3	9	3	US-09-048-328-3	Sequence 3, Appl	342	3	27.3	4	US-09-023-905A-19	Sequence 19, Appl
270	3	27.3	9	3	US-09-048-328-5	Sequence 4, Appl	343	3	27.3	4	US-09-847-185-24	Sequence 24, Appl
271	3	27.3	9	3	US-09-038-328-5	Sequence 5, Appl	344	3	27.3	4	US-09-847-185-25	Sequence 25, Appl
272	3	27.3	9	3	US-08-8-8-599A-30	Sequence 10, Appl	345	3	27.3	4	US-09-659-786-182	Sequence 182, App
273	3	27.3	9	3	US-09-035-276-15	Sequence 15, Appl	346	3	27.3	4	US-09-515-514-18	Sequence 18, Appl
274	3	27.3	9	3	US-09-037-749-47	Sequence 47, Appl	347	3	27.3	4	US-09-861-966-134	Sequence 134, App
275	3	27.3	9	3	US-08-924-002-6	Sequence 6, Appl	348	3	27.3	4	US-09-861-966-155	Sequence 155, App
276	3	27.3	9	3	US-09-139-804-182	Sequence 182, App	349	3	27.3	4	US-09-861-966-169	Sequence 169, App
277	3	27.3	9	3	US-09-135-235A-34	Sequence 14, Appl	350	3	27.3	4	US-09-561-499-17	Sequence 17, Appl
278	3	27.3	9	3	US-09-414-742-4	Sequence 4, Appl	351	3	27.3	4	US-09-144-280-18	Sequence 18, Appl
279	3	27.3	9	3	US-09-183-941-28	Sequence 28, Appl	352	3	27.3	4	US-09-289-350-4	Sequence 4, Appl
280	3	27.3	9	3	US-09-183-941-35	Sequence 35, Appl	353	3	27.3	4	US-09-289-350-6	Sequence 6, Appl
281	3	27.3	9	3	US-09-183-941-38	Sequence 38, Appl	354	3	27.3	4	US-09-311-784A-326	Sequence 326, App
282	3	27.3	9	3	US-09-183-941-39	Sequence 39, Appl	355	3	27.3	4	US-09-311-784A-463	Sequence 463, App
283	3	27.3	9	3	US-09-199-142-5	Sequence 5, Appl	356	3	27.3	4	US-09-574-749B-4	Sequence 4, Appl
284	3	27.3	9	3	US-09-531-511-4	Sequence 4, Appl	357	3	27.3	4	US-09-574-749B-8	Sequence 8, Appl
285	3	27.3	9	3	US-09-177-231-261	Sequence 260, App	358	3	27.3	4	US-09-341-982-91	Sequence 91, Appl
286	3	27.3	9	3	US-09-183-726-7	Sequence 7, Appl	359	3	27.3	4	US-09-341-982-92	Sequence 92, Appl
287	3	27.3	9	3	US-09-183-726-9	Sequence 9, Appl	360	3	27.3	4	US-08-488-446-184	Sequence 184, App
288	3	27.3	9	3	US-08-960-944A-25	Sequence 26, Appl	361	3	27.3	4	US-09-880-132-19	Sequence 19, Appl
289	3	27.3	9	3	US-08-958-944A-26	Sequence 1, Appl	362	3	27.3	4	US-08-926-914-182	Sequence 182, App
290	3	27.3	9	3	US-08-713-354-1	Sequence 134, App	363	3	27.3	4	US-09-534-943-1	Sequence 1, Appl
291	3	27.3	9	3	US-08-657-896A-34	Sequence 18, Appl	364	3	27.3	4	US-08-467-344A-184	Sequence 184, App
292	3	27.3	9	3	US-09-10-388A-34	Sequence 153, App	365	3	27.3	4	US-09-311-784A-326	Sequence 326, App
293	3	27.3	9	3	US-09-510-388A-34	Sequence 169, App	366	3	27.3	4	US-09-574-749B-4	Sequence 4, Appl
294	3	27.3	9	3	US-09-510-388A-34	Sequence 19, App	367	3	27.3	4	US-09-574-749B-8	Sequence 8, Appl
295	3	27.3	9	3	US-09-061-554-3	Sequence 48, Appl	368	3	27.3	4	US-09-341-982-91	Sequence 91, Appl
296	3	27.3	9	3	US-09-104-528-48	Sequence 50, Appl	369	3	27.3	4	US-09-341-982-92	Sequence 92, Appl
297	3	27.3	9	3	US-09-104-528-48	Sequence 86, Appl	370	3	27.3	4	US-08-488-446-184	Sequence 184, App
298	3	27.3	9	3	US-09-518-436-83	Sequence 109, App	371	3	27.3	4	US-09-880-132-19	Sequence 19, Appl
299	3	27.3	9	3	US-09-518-436-133	Sequence 112, App	372	3	27.3	4	US-08-926-914-182	Sequence 182, App
300	3	27.3	9	4	US-09-518-436-112	Sequence 7, Appl	373	3	27.3	4	US-09-534-943-1	Sequence 1, Appl
301	3	27.3	9	4	US-09-567-995A-3	Sequence 9, Appl	374	3	27.3	4	US-08-467-344A-184	Sequence 184, App
302	3	27.3	9	4	US-09-567-995A-3	Sequence 19, App	375	3	27.3	4	US-09-574-749B-4	Sequence 4, Appl
303	3	27.3	9	4	US-09-436-781-14	Sequence 39, Appl	376	3	27.3	4	US-09-574-749B-8	Sequence 8, Appl
304	3	27.3	9	4	US-09-436-781-14	Sequence 134, Appl	377	3	27.3	4	US-09-341-982-91	Sequence 91, Appl
305	3	27.3	9	4	US-09-436-781-14	Sequence 153, App	378	3	27.3	4	US-09-341-982-92	Sequence 92, Appl
306	3	27.3	9	4	US-09-436-781-14	Sequence 169, App	379	3	27.3	4	US-08-488-446-184	Sequence 184, App
307	3	27.3	9	4	US-09-436-781-14	Sequence 19, App	380	3	27.3	4	US-09-880-132-19	Sequence 19, Appl
308	3	27.3	9	4	US-08-464-496-37	Sequence 37, Appl	381	3	27.3	4	US-08-926-914-182	Sequence 182, App
309	3	27.3	9	4	US-08-441-268-1	Sequence 1, Appl	382	3	27.3	4	US-09-534-943-1	Sequence 1, Appl
310	3	27.3	9	4	US-08-457-648A-1	Sequence 10, Appl	383	3	27.3	4	US-08-467-344A-184	Sequence 184, App
311	3	27.3	9	4	US-09-099-543B-14	Sequence 29, Appl	384	3	27.3	4	US-09-574-749B-4	Sequence 4, Appl
312	3	27.3	9	4	US-08-492-492B-3	Sequence 5, Appl	385	3	27.3	4	US-09-574-749B-8	Sequence 8, Appl
313	3	27.3	9	4	US-08-959-496A-22	Sequence 22, Appl	386	3	27.3	4	US-09-341-982-91	Sequence 91, Appl
314	3	27.3	9	4	US-09-057-052-9	Sequence 9, Appl	387	3	27.3	4	US-09-341-982-92	Sequence 92, Appl
315	3	27.3	9	4	US-09-561-560-17	Sequence 17, Appl	388	3	27.3	4	US-08-488-446-184	Sequence 184, App
316	3	27.3	9	4	US-09-561-560-17	Sequence 17, Appl	389	3	27.3	4	US-09-880-132-19	Sequence 19, Appl
317	3	27.3	9	4	US-09-412-928-14	Sequence 19, Appl	390	3	27.3	4	US-08-926-914-182	Sequence 182, App
318	3	27.3	9	4	US-09-412-928-14	Sequence 19, Appl	391	3	27.3	4	US-09-534-943-1	Sequence 1, Appl
319	3	27.3	9	4	US-09-705-160-35	Sequence 35, Appl	392	3	27.3	4	US-08-467-344A-184	Sequence 184, App

434	3	27.3	10	1	US-08-483-144B-241	Sequence 241, App	465	3	27.3	10	4	US-09-490-702B-45	Sequence 45, Appl
435	3	27.3	10	1	US-07-869-943-17	Sequence 19, Appl	466	3	27.3	10	4	US-08-983-157B-13	Sequence 13, Appl
436	3	27.3	10	1	US-08-477-539B-2	Sequence 2, Appl	467	3	27.3	10	4	US-08-983-157B-14	Sequence 14, Appl
437	3	27.3	10	1	US-08-218-526-24	Sequence 24, Appl	468	3	27.3	10	4	US-08-983-157B-15	Sequence 15, Appl
438	3	27.3	10	1	US-08-218-526-25	Sequence 25, Appl	469	3	27.3	10	4	US-08-983-157B-16	Sequence 16, Appl
439	3	27.3	10	1	US-08-218-526-26	Sequence 26, Appl	470	3	27.3	10	4	US-08-983-157B-17	Sequence 17, Appl
440	3	27.3	10	1	US-08-218-526-27	Sequence 27, Appl	471	3	27.3	10	4	US-08-983-157B-18	Sequence 18, Appl
441	3	27.3	10	1	US-08-218-526-28	Sequence 28, Appl	472	3	27.3	10	4	US-08-983-157B-19	Sequence 19, Appl
442	3	27.3	10	1	US-08-218-526-29	Sequence 29, Appl	473	3	27.3	10	4	US-08-983-157B-20	Sequence 20, Appl
443	3	27.3	10	1	US-08-218-526-30	Sequence 30, Appl	474	3	27.3	10	4	US-08-983-157B-21	Sequence 21, Appl
444	3	27.3	10	1	US-08-218-526-31	Sequence 31, Appl	475	3	27.3	10	4	US-08-983-157B-22	Sequence 22, Appl
445	3	27.3	10	1	US-08-218-526-32	Sequence 32, Appl	476	3	27.3	10	4	US-08-983-157B-23	Sequence 23, Appl
446	3	27.3	10	1	US-08-218-526-33	Sequence 33, Appl	477	3	27.3	10	4	US-08-983-157B-24	Sequence 24, Appl
447	3	27.3	10	1	US-08-218-526-34	Sequence 34, Appl	478	3	27.3	10	4	US-08-983-157B-25	Sequence 25, Appl
448	3	27.3	10	1	US-08-218-526-35	Sequence 35, Appl	479	3	27.3	10	4	US-08-983-157B-26	Sequence 26, Appl
449	3	27.3	10	1	US-08-218-526-36	Sequence 36, Appl	480	3	27.3	10	4	US-08-983-157B-27	Sequence 27, Appl
450	3	27.3	10	1	US-08-218-526-37	Sequence 37, Appl	481	3	27.3	10	4	US-08-983-157B-28	Sequence 28, Appl
451	3	27.3	10	1	US-08-218-526-38	Sequence 38, Appl	482	3	27.3	10	4	US-08-983-157B-29	Sequence 29, Appl
452	3	27.3	10	1	US-08-218-526-39	Sequence 39, Appl	483	3	27.3	10	4	US-08-983-157B-30	Sequence 30, Appl
453	3	27.3	10	1	US-08-218-526-40	Sequence 40, Appl	484	3	27.3	10	4	US-08-983-157B-31	Sequence 31, Appl
454	3	27.3	10	1	US-08-218-526-41	Sequence 41, Appl	485	3	27.3	10	4	US-08-983-157B-32	Sequence 32, Appl
455	3	27.3	10	1	US-08-218-526-42	Sequence 42, Appl	486	3	27.3	10	4	US-08-983-157B-33	Sequence 33, Appl
456	3	27.3	10	1	US-08-218-526-43	Sequence 43, Appl	487	3	27.3	10	4	US-08-983-157B-34	Sequence 34, Appl
457	3	27.3	10	1	US-08-218-526-44	Sequence 44, Appl	488	3	27.3	10	4	US-08-983-157B-35	Sequence 35, Appl
458	3	27.3	10	1	US-08-218-526-45	Sequence 45, Appl	489	3	27.3	10	4	US-08-983-157B-36	Sequence 36, Appl
459	3	27.3	10	1	US-08-218-526-46	Sequence 46, Appl	490	3	27.3	10	4	US-08-983-157B-37	Sequence 37, Appl
460	3	27.3	10	1	US-08-218-526-47	Sequence 47, Appl	491	3	27.3	10	4	US-08-983-157B-38	Sequence 38, Appl
461	3	27.3	10	1	US-08-218-526-48	Sequence 48, Appl	492	3	27.3	10	4	US-08-983-157B-39	Sequence 39, Appl
462	3	27.3	10	1	US-08-218-526-49	Sequence 49, Appl	493	3	27.3	10	4	US-08-983-157B-40	Sequence 40, Appl
463	3	27.3	10	1	US-08-218-526-50	Sequence 50, Appl	494	3	27.3	10	4	US-08-983-157B-41	Sequence 41, Appl
464	3	27.3	10	1	US-08-218-526-51	Sequence 51, Appl	495	3	27.3	10	4	US-08-983-157B-42	Sequence 42, Appl
465	3	27.3	10	1	US-08-218-526-52	Sequence 52, Appl	496	3	27.3	10	4	US-08-983-157B-43	Sequence 43, Appl
466	3	27.3	10	1	US-08-218-526-53	Sequence 53, Appl	497	3	27.3	10	4	US-08-983-157B-44	Sequence 44, Appl
467	3	27.3	10	1	US-08-218-526-54	Sequence 54, Appl	498	3	27.3	10	4	US-08-983-157B-45	Sequence 45, Appl
468	3	27.3	10	1	US-08-218-526-55	Sequence 55, Appl	499	3	27.3	10	4	US-08-983-157B-46	Sequence 46, Appl
469	3	27.3	10	1	US-08-218-526-56	Sequence 56, Appl	500	3	27.3	10	4	US-08-983-157B-47	Sequence 47, Appl
470	3	27.3	10	1	US-08-218-526-57	Sequence 57, Appl							
471	3	27.3	10	1	US-08-218-526-58	Sequence 58, Appl							
472	3	27.3	10	1	US-08-218-526-59	Sequence 59, Appl							
473	3	27.3	10	1	US-08-218-526-60	Sequence 60, Appl							
474	3	27.3	10	1	US-08-218-526-61	Sequence 61, Appl							
475	3	27.3	10	1	US-08-218-526-62	Sequence 62, Appl							
476	3	27.3	10	1	US-08-218-526-63	Sequence 63, Appl							
477	3	27.3	10	1	US-08-218-526-64	Sequence 64, Appl							
478	3	27.3	10	1	US-08-218-526-65	Sequence 65, Appl							
479	3	27.3	10	1	US-08-218-526-66	Sequence 66, Appl							
480	3	27.3	10	1	US-08-218-526-67	Sequence 67, Appl							
481	3	27.3	10	1	US-08-218-526-68	Sequence 68, Appl							
482	3	27.3	10	1	US-08-218-526-69	Sequence 69, Appl							
483	3	27.3	10	1	US-08-218-526-70	Sequence 70, Appl							
484	3	27.3	10	1	US-08-218-526-71	Sequence 71, Appl							
485	3	27.3	10	1	US-08-218-526-72	Sequence 72, Appl							
486	3	27.3	10	1	US-08-218-526-73	Sequence 73, Appl							
487	3	27.3	10	1	US-08-218-526-74	Sequence 74, Appl							
488	3	27.3	10	1	US-08-218-526-75	Sequence 75, Appl							
489	3	27.3	10	1	US-08-218-526-76	Sequence 76, Appl							
490	3	27.3	10	1	US-08-218-526-77	Sequence 77, Appl							
491	3	27.3	10	1	US-08-218-526-78	Sequence 78, Appl							
492	3	27.3	10	1	US-08-218-526-79	Sequence 79, Appl							
493	3	27.3	10	1	US-08-218-526-80	Sequence 80, Appl							
494	3	27.3	10	1	US-08-218-526-81	Sequence 81, Appl							
495	3	27.3	10	1	US-08-218-526-82	Sequence 82, Appl							
496	3	27.3	10	1	US-08-218-526-83	Sequence 83, Appl							
497	3	27.3	10	1	US-08-218-526-84	Sequence 84, Appl							
498	3	27.3	10	1	US-08-218-526-85	Sequence 85, Appl							
499	3	27.3	10	1	US-08-218-526-86	Sequence 86, Appl							
500	3	27.3	10	1	US-08-218-526-87	Sequence 87, Appl							

ALIGNMENTS

RESULT 1
US-09-016-366A-44
Sequence 44, Application US/39016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
ATTORNEY: Howard, Chitt.
TITLE OF INVENTION: FAST CELL PROTEASE PEPTIDE
INVENTOR: STEVENS, RICHARD L.
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolff, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 53C
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 69/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pinner, Elizabeth K.
REGISTRATION NUMBER: 36,647
REFERENCE/KEY NUMBER: H00117093

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-016-366A-44

Query Match 36.4%: Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
Db 4 ARAL 7

RESULT 2

US-09-256-194-13
Sequence 13, Application US/09256194
Patent No. 6395714
GENERAL INFORMATION:
APPLICANT: Sia, Charles D.Y.
APPLICANT: Gao, Shi Xian
APPLICANT: Persson, Roy
APPLICANT: Kovinski, Benjamin
TITLE OF INVENTION: EXPRESSING GP140 FRAGMENT OF PRIMARY HIV-1 ISOLATE
FILE REFERENCE: 1038-920
CURRENT APPLICATION NUMBER: US/09/256-194
CURRENT FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 9
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-256-194-13

Query Match 36.4%: Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
Db 6 ARAL 9

RESULT 3

US-09-387-715-10
Sequence 10, Application US/09387715
Patent No. 6551574
GENERAL INFORMATION:
APPLICANT: Sharma, Shubh
TITLE OF INVENTION: Tuftsin Metallopeptides Analogs and Uses Thereof
FILE REFERENCE: 1173/1D794US1
CURRENT APPLICATION NUMBER: US/09/387-715
CURRENT FILING DATE: 1999-08-30
PRIOR APPLICATION NUMBER: PCT/US99/05654
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

NAME/KEY: modified residue
LOCATION: 3,6,8
OTHER INFORMATION: D-amino acid
US-09-387-715-10

Query Match 36.4%: Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
Db 3 AKPK 6

RESULT 4

US-08-166-195A-21
Sequence 21, Application US/08166195A
Patent No. 5480799
GENERAL INFORMATION:
APPLICANT: O'Rand, Michael G.
APPLICANT: Widgren, Esther E.
APPLICANT: Richardson, Richard T.
APPLICANT: Lea, Isabel
TITLE OF INVENTION: Sperm Antigen Corresponding to a
TITLE OF INVENTION: Sperm Zona Binding Protein Autoantigenic Epitope
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Box 34009
CITY: Charlotte
STATE: No. 5480799th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/166,195A
FILING DATE: 10 DEC 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470/73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-166-195A-21

Query Match 36.4%: Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WGAK 4
Db 6 WGAK 9

RESULT 5

US-08-166-195A-22
Sequence 22, Application US/08166195A
Patent No. 5480799
GENERAL INFORMATION:
APPLICANT: O'Rand, Michael G.


```

1  APPLICANT:  Widdgren, Esther E.
2  APPLICANT:  Richardson, Richard E.
3  APPLICANT:  Lea, Isabel
4  TITLE OF INVENTION:  Sperm Antigen Corresponding to a
5  NUMBER OF SEQUENCES:  51
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE:  Kenneth D. Sibbey
8  STREET:  P.O. Box 34009
9  CITY:  Charlotte
10 STATE:  No. 5480799th Carolina
11 COUNTRY:  USA
12 ZIP:  28234
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE:  Floppy disk
15 OPERATING SYSTEM:  PC-DOS/MS-DOS
16 SOFTWARE:  Patent In Release #1.0, Version #1.25
17 CURRENT APPLICATION DATA:
18 FILING DATE:  10 DEC 1994
19 CLASSIFICATION:  435
20 ATTORNEY/AGENT INFORMATION:
21 NAME:  Sibbey, Kenneth E.
22 REGISTRATION NUMBER:  31,665
23 REFERENCE/DOCKET NUMBER:  5476/7
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE:  919-881-3140
26 TELEFAX:  919-881-3175
27 INFORMATION FOR SEQ ID NO:  22:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH:  10 amino acids
30 TYPE:  amino acid
31 STRANDEDNESS:  single
32 TOPOLOGY:  linear
33 MOLECULE TYPE:  polypeptide
34 US 08-155-195A-22
35
36 Query Match          36.4%  Score 4:  DB 1:  Length 10:
37 Best Local Similarity 100.0%  Pred. No. 1.7e+02:
38 Matches      4:  Conservative  0:  Mismatches  0:  Indels  0:  Gaps  0:
39
40 QY      6  WGAK 5
41      1  1  1
42      3  WCAK 6
43
44 RESULT 6:
45 US-08-478-761A-52
46 : Sequence 52, Application US/08478761A
47 : Patent No. 5645384
48 : GENERAL INFORMATION:
49 : APPLICANT:  WALSH, TERENCE A
50 : APPLICANT:  HEY, TIMOTHY D
51 : APPLICANT:  MORGAN, ALICE EK
52 : TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
53 : TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
54 : NUMBER OF SEQUENCES:  81
55 : CORRESPONDENCE ADDRESS:
56 : ADDRESSEE:  ANDREA T. BORUCKI
57 : STREET:  9330 ZIONSVILLE ROAD
58 : CITY:  INDIANAPOLIS
59 : STATE:  IN
60 : COUNTRY:  US
61 : ZIP:  46268
62 : COMPUTER READABLE FORM:
63 : MEDIUM TYPE:  Floppy disk
64 : COMPUTER:  IBM PC compatible
65 : OPERATING SYSTEM:  PC-DOS/MS-DOS
66 : SOFTWARE:  Patent In Release #1.0, Version #1.25
67 : CURRENT APPLICATION DATA:
68 : APPLICATION NUMBER:  US/08/378,761A
69 : FILING DATE:
70 : CLASSIFICATION:  435
71 : PRIOR APPLICATION DATA:
72 : APPLICATION NUMBER:  US 08/378761
73 : FILING DATE:  26-JAN-1995
74 : ATTORNEY/AGENT INFORMATION:
75 : NAME:  BORUCKI, ANDREA T
76 : REGISTRATION NUMBER:  33651
77 : REFERENCE/DOCKET NUMBER:  38272B
78 : TELECOMMUNICATION INFORMATION:
79 : TELEPHONE:  (317) 337-4846
80 : INFORMATION FOR SEQ ID NO:  52:
81 SEQUENCE CHARACTERISTICS:
82 LENGTH:  10 amino acids
83 TYPE:  amino acid
84 STRANDEDNESS:  single
85 TOPOLOGY:  linear
86 MOLECULE TYPE:  protein
87 US-08-485-286-52

```

```

1  FILING DATE:  26-JAN-1995
2  CLASSIFICATION:  435
3  ATTORNEY/AGENT INFORMATION:
4  NAME:  BORUCKI, ANDREA T
5  REGISTRATION NUMBER:  33651
6  REFERENCE/DOCKET NUMBER:  38272B
7  TELECOMMUNICATION INFORMATION:
8  TELEPHONE:  (317) 337-4846
9  INFORMATION FOR SEQ ID NO:  52:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH:  10 amino acids
12 TYPE:  amino acid
13 STRANDEDNESS:  single
14 TOPOLOGY:  linear
15 MOLECULE TYPE:  protein
16 US-08-378-761A-52
17
18 Query Match          36.4%  Score 4:  DB 1:  Length 10:
19 Best Local Similarity 100.0%  Pred. No. 1.7e+02:
20 Matches      4:  Conservative  0:  Mismatches  0:  Indels  0:  Gaps  0:
21
22 QY      4  LNWG 7
23      1  1  1  1
24      2  LNWG 5
25
26 RESULT 7:
27 US-08-485-286-52
28 : Sequence 52, Application US/08485286
29 : Patent No. 5646026
30 : Patent No. 5646026 5646119
31 : GENERAL INFORMATION:
32 : APPLICANT:  WALSH, TERENCE A
33 : APPLICANT:  HEY, TIMOTHY D
34 : APPLICANT:  MORGAN, ALICE EK
35 : TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
36 : TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
37 : NUMBER OF SEQUENCES:  81
38 : CORRESPONDENCE ADDRESS:
39 : ADDRESSEE:  ANDREA T. BORUCKI
40 : STREET:  9330 ZIONSVILLE ROAD
41 : CITY:  INDIANAPOLIS
42 : STATE:  IN
43 : COUNTRY:  US
44 : ZIP:  46268
45 : COMPUTER READABLE FORM:
46 : MEDIUM TYPE:  Floppy disk
47 : COMPUTER:  IBM PC compatible
48 : OPERATING SYSTEM:  PC-DOS/MS-DOS
49 : SOFTWARE:  Patent In Release #1.0, Version #1.25
50 : CURRENT APPLICATION DATA:
51 : APPLICATION NUMBER:  US/08/485,286
52 : FILING DATE:
53 : CLASSIFICATION:  435
54 : PRIOR APPLICATION DATA:
55 : APPLICATION NUMBER:  US 08/378761
56 : FILING DATE:  26-JAN-1995
57 : ATTORNEY/AGENT INFORMATION:
58 : NAME:  BORUCKI, ANDREA T
59 : REGISTRATION NUMBER:  33651
60 : REFERENCE/DOCKET NUMBER:  38272B
61 : TELECOMMUNICATION INFORMATION:
62 : TELEPHONE:  (317) 337-4846
63 : INFORMATION FOR SEQ ID NO:  52:
64 SEQUENCE CHARACTERISTICS:
65 LENGTH:  10 amino acids
66 TYPE:  amino acid
67 STRANDEDNESS:  single
68 TOPOLOGY:  linear
69 MOLECULE TYPE:  protein
70 US-08-485-286-52

```

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Query Match          36.4%, Score 4, DB 2, Length 10;
Best Local Similarity 100.0%, Pred. No. 1.7e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LNWG 7
Db 2 LNWG 5

RESULT 8
US-08-436-772-21
: Sequence 21, Application US/08436772
: Patent No. 5814456
: GENERAL INFORMATION:
: APPLICANT: O'Rand, Michael G.
: APPLICANT: Widgren, Esther E.
: APPLICANT: Richardson, Richard T.
: APPLICANT: Lea, Isabel
: TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
: TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kenneth D. Sibley
: STREET: P.O. Box 34009
: CITY: Charlotte
: STATE: No. 5814456th Carolina
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/436,772
: FILING DATE: 08-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sibley, Kenneth D.
: REGISTRATION NUMBER: 31,665
: REFERENCE/DOCKET NUMBER: 5470-73B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-881-3140
: TELEFAX: 919-881-3175
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-436-772-21

Query Match          36.4%, Score 4, DB 2, Length 10;
Best Local Similarity 100.0%, Pred. No. 1.7e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WCAK 9
Db 6 WCAK 9

RESULT 9
US-08-436-772-22
: Sequence 22, Application US/08436772
: Patent No. 5814456
: GENERAL INFORMATION:
: APPLICANT: O'Rand, Michael G.
: APPLICANT: Widgren, Esther E.
: APPLICANT: Richardson, Richard T.
: APPLICANT: Lea, Isabel
: TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
: TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope

```

```

: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kenneth D. Sibley
: STREET: P.O. Box 34009
: CITY: Charlotte
: STATE: No. 5814456th Carolina
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/436,772
: FILING DATE: 08-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sibley, Kenneth D.
: REGISTRATION NUMBER: 31,665
: REFERENCE/DOCKET NUMBER: 5470-73B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-881-3140
: TELEFAX: 919-881-3175
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-436-772-22

Query Match          36.4%, Score 4, DB 2, Length 10;
Best Local Similarity 100.0%, Pred. No. 1.7e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WCAK 9
Db 3 WCAK 6

RESULT 10
US-08-436-883B-21
: Sequence 21, Application US/084368484
: Patent No. 5823861
: GENERAL INFORMATION:
: APPLICANT: O'Rand, Michael G.
: APPLICANT: Widgren, Esther E.
: APPLICANT: Richardson, Richard T.
: APPLICANT: Lea, Isabel
: TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
: TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kenneth D. Sibley
: STREET: P.O. Box 34009
: CITY: Charlotte
: STATE: No. 5820861th Carolina
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/436,883B
: FILING DATE: 08-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sibley, Kenneth D.
: REGISTRATION NUMBER: 31,665

```

1 REFERENCE/LOCKET NUMBER: 5470-730
 2 TELECOMMUNICATION INFORMATION:
 3 TELEPHONE: 919-420-2200
 4 TELEFAX: 919-881-3175
 5 INFORMATION FOR SEQ ID NO: 21:
 6 SEQUENCE CHARACTERISTICS:
 7 LENGTH: 10 amino acids
 8 TYPE: amino acid
 9 STRANDEDNESS: single
 10 TOPOLOGY: linear
 11 MOLECULE TYPE: peptide
 12 US-08-436-883B-21

Query Match 36.4% Score 4 DB 2 Length 10
 Best Local Similarity 100.0% Ident 100%
 Matches 4 Conservative 0 Mismatches 0 Gaps 0

QY 6 WGAK 9
 DB 6 WGAK 9

1 RESULT 11
 2 US-08-436-883B-22
 3 Sequence 22, Application US/08406435
 4 Patent No. 5820861
 5 GENERAL INFORMATION:
 6 APPLICANT: O'Rand, Michael G.
 7 APPLICANT: Widgren, Esther E.
 8 APPLICANT: Richardson, Richard L.
 9 APPLICANT: Lea, Isabel
 10 TITLE OF INVENTION: Serum Antigen Corresponding to a Specific
 11 NUMBER OF SEQUENCES: 60
 12 CORRESPONDENCE ADDRESS:
 13 ADDRESSEE: Kenneth G. Sibley
 14 STREET: P.O. Box 34009
 15 CITY: Charlotte
 16 STATE: NC 28208
 17 COUNTRY: USA
 18 ZIP: 28284

19 COMPUTER READABLE FORM:
 20 MEDIUM TYPE: Floppy disk
 21 COMPUTER: IBM PC Compatible
 22 OPERATING SYSTEM: PC-DOS/MS-DOS
 23 SOFTWARE: Patent In Release #1.0, Version #1.0
 24 CURRENT APPLICATION DATA:
 25 APPLICATION NUMBER: US/08/436-883B-22
 26 FILING DATE: 08-MAY-1995
 27 CLASSIFICATION: 435
 28 ATTORNEY/AGENT INFORMATION:
 29 NAME: Sibley, Kenneth G.
 30 REGISTRATION NUMBER: 31,640
 31 REFERENCE/LOCKET NUMBER: 5470-730
 32 TELECOMMUNICATION INFORMATION:
 33 TELEPHONE: 919-420-2200
 34 TELEFAX: 919-881-3175

35 INFORMATION FOR SEQ ID NO: 22:
 36 SEQUENCE CHARACTERISTICS:
 37 LENGTH: 10 amino acids
 38 TYPE: amino acid
 39 STRANDEDNESS: single
 40 TOPOLOGY: linear
 41 MOLECULE TYPE: peptide
 42 US-08-436-883B-22

Query Match 36.4% Score 4 DB 2 Length 10
 Best Local Similarity 100.0% Ident 100%
 Matches 4 Conservative 0 Mismatches 0 Gaps 0

QY 6 WGAK 9
 DB 6 WGAK 9

1 RESULT 12
 2 US-08-556-597-129
 3 Sequence 129, Application US/08556597
 4 Patent No. 5877155
 5 GENERAL INFORMATION:
 6 APPLICANT: Miller, Jonathan L.
 7 APPLICANT: Lytle, Vicki A.
 8 TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
 9 TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
 10 NUMBER OF SEQUENCES: 173
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: Nixon, Hartlage, Levens & Doyle LLP
 13 STREET: Clinton Square, P.O. Box 1051
 14 CITY: Rochester
 15 STATE: New York
 16 COUNTRY: USA
 17 ZIP: 14604

18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: Floppy disk
 20 COMPUTER: IBM PC Compatible
 21 OPERATING SYSTEM: PC-DOS/MS-DOS
 22 SOFTWARE: Patent In Release #1.0, Version #1.30
 23 CURRENT APPLICATION DATA:
 24 APPLICATION NUMBER: US/08/556,597
 25 FILING DATE:
 26 CLASSIFICATION: 530
 27 PRIOR APPLICATION DATA:
 28 APPLICATION NUMBER: US 08/406,430
 29 FILING DATE: 17-MAR-1995
 30 ATTORNEY/AGENT INFORMATION:
 31 NAME: Timlin, Susan J.
 32 REGISTRATION NUMBER: 34,193
 33 REFERENCE/LOCKET NUMBER: 20884/101
 34 TELECOMMUNICATION INFORMATION:
 35 TELEPHONE: (716) 263 1636
 36 TELEFAX: (716) 263 1600

37 INFORMATION FOR SEQ ID NO: 129:
 38 SEQUENCE CHARACTERISTICS:
 39 LENGTH: 10 amino acids
 40 TYPE: amino acid
 41 STRANDEDNESS:
 42 TOPOLOGY: linear
 43 MOLECULE TYPE: peptide
 44 US-08-556-597-129

Query Match 36.4% Score 4 DB 2 Length 10
 Best Local Similarity 100.0% Ident 100%
 Matches 4 Conservative 0 Mismatches 0 Gaps 0

QY 6 WGAK 9
 DB 2 WGAK 5

1 RESULT 13
 2 US-08-556-597-140
 3 Sequence 140, Application US/08556597
 4 Patent No. 5877155
 5 GENERAL INFORMATION:
 6 APPLICANT: Miller, Jonathan L.
 7 APPLICANT: Lytle, Vicki A.
 8 TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
 9 TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
 10 NUMBER OF SEQUENCES: 173
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: Nixon, Hartlage, Levens & Doyle LLP
 13 STREET: Clinton Square, P.O. Box 1051
 14 CITY: Rochester
 15 STATE: New York
 16 COUNTRY: USA
 17 ZIP: 14604

Query Match 36.4% Score 4 DB 2 Length 10
 Best Local Similarity 100.0% Ident 100%
 Matches 4 Conservative 0 Mismatches 0 Gaps 0

QY 6 WGAK 9
 DB 2 WGAK 5

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: Patent In Release #1.0, Version #1.00
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/556,597
8  FILING DATE:
9  CLASSIFICATION: 514
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 08/406,146
12 FILING DATE: 17-MAR-1995
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Tuelan, Susan J.
15 REGISTRATION NUMBER: 34,103
16 REFERENCE/DOCKET NUMBER: 20884/101
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: (716) 263-1636
19 TELEFAX: (716) 263-1600
20 INFORMATION FOR SEQ ID NO: 140:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 10 amino acids
23 TYPE: amino acid
24 STRANDEDNESS:
25 TOPOLOGY: linear
26 MOLECULE TYPE: peptide
27 US 08-556 597-140

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Query Match      36.4%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1,766,942;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

```

```

Cy      2 RAIN 5
Db      4 RAIN 7

```

```

RESULT 14
5248606 37
1 Patent No. 5248606
2 APPLICANT: WALSH, TERENCE A. (BY: TIMOTHY D. MURPHY, Esq.)
3 TITLE: E.R.
4 TITLE OF INVENTION: DNA ENCODING NATIVE PEPTIDES R AND
5 NATIVE FORMS OF MAIZE RIBOSOME INACTIVATOR
6 NUMBER OF SEQUENCES: 49
7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: US/01/ 65,000
9 FILING DATE: 11-JUN-1990
10 SEQ ID NO: 37
11 LENGTH: 10
12 5248606-37

```

```

Query Match      36.4%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1,766,942;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Cy      4 INWG 7
Db      2 INWG 5

```

```

RESULT 15
US 08-844 978-12
1 Sequence 32, Application US/08844978
2 Patent No. 6075004
3 GENERAL INFORMATION:
4 APPLICANT: Benedict, Stephen
5 APPLICANT: Stahaan, Teruna
6 APPLICANT: Chan, Marcia
7 APPLICANT: Tibbets, Scott
8 TITLE OF INVENTION: Peptide Compositions Which Induce Immune
9 NUMBER OF SEQUENCES: 36
10 CORRESPONDENCE ADDRESS:

```

```

1 ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
2 STREET: 2405 Grand Boulevard, Suite 400
3 CITY: Kansas City
4 STATE: MO
5 COUNTRY: USA
6 ZIP: 64108
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Patent In Release #1.0, Version #1.25
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/844,978
14 FILING DATE:
15 CLASSIFICATION: 514
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Collins, John M.
18 REGISTRATION NUMBER: 26262
19 REFERENCE/DOCKET NUMBER: 24769-A
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: (816)474-9050
22 TELEFAX: (816)474-9057
23 TELEX: 434-363
24 INFORMATION FOR SEQ ID NO: 32:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 11 amino acids
27 TYPE: amino acid
28 TOPOLOGY: linear
29 MOLECULE TYPE: peptide
30 US-08-844-978-12

```

```

Query Match      45.4%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1,96-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Cy      2 RAIN 5
Db      6 RAIN 9

```

```

RESULT 16
US-08-844-978-35
1 Sequence 35, Application US/08844978
2 Patent No. 6075004
3 GENERAL INFORMATION:
4 APPLICANT: Benedict, Stephen
5 APPLICANT: Stahaan, Teruna
6 APPLICANT: Chan, Marcia
7 APPLICANT: Tibbets, Scott
8 TITLE OF INVENTION: Peptide Compositions Which Induce Immune
9 NUMBER OF SEQUENCES: 36
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
12 STREET: 2405 Grand Boulevard, Suite 400
13 CITY: Kansas City
14 STATE: MO
15 COUNTRY: USA
16 ZIP: 64108
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: Patent In Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/844,978
24 FILING DATE:
25 CLASSIFICATION: 514
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Collins, John M.
28 REGISTRATION NUMBER: 26262
29 REFERENCE/DOCKET NUMBER: 24769-A
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: (816)474-9050

```

1 TELEFAX: 816(474-9057
 2 TELEX: 434 363
 3 INFORMATION FOR SEQ ID NO: 35:
 4 SEQUENCE CHARACTERISTICS:
 5 LENGTH: 11 amino acids
 6 TYPE: amino acid
 7 TOPOLOGY: circular
 8 MOLECULE TYPE: peptide
 9 US-08 644-976-35

Query Match 36.4%, Score 4; DB 5; Length 11;
 Best Local Similarity 100.0%, Pred. No. 2.le-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 ALNW 5
 11
 10 6 ALNW 9

RESULT 17
 US-08-461 9908-27
 Sequence 27, Application US/084619908
 Patent No. 5851810
 GENERAL INFORMATION:

1 APPLICANT: JOHN S. BLANCHARD
 2 TITLE OF INVENTION: NUCLEIC ACID-ENZYME PHOSPHATASE
 3 NUMBER OF SEQUENCES: 30
 4 CORRESPONDENCE ADDRESS:
 5 ADDRESSEE: AMSTER, ROHSTEIN & BERNSTEIN
 6 STREET: 90 PARK AVENUE
 7 CITY: NEW YORK
 8 STATE: NEW YORK
 9 COUNTRY: U.S.A.
 10 ZIP: 10016

11 COMPUTER READABLE FORM:
 12 MEDIUM TYPE: 3.5 INCH 1.44 MB SOFTWARE DISKETTE
 13 OPERATING SYSTEM: MS-DOS
 14 SOFTWARE: ASCII
 15 CURRENT APPLICATION DATA:
 16 FILING DATE: JUNE 5, 1995
 17 ATTORNEY/AGENT INFORMATION:
 18 NAME: CRAIG J. ARNOLD
 19 REGISTRATION NUMBER: 34,267
 20 REFERENCE/DOCKET NUMBER: 9476/73
 21 TELEPHONE: (212) 697-5995
 22 TELEFAX: (212) 286-0954 OF 286-6002
 23 TELEX: TWX 710-581-4766
 24 INFORMATION FOR SEQ ID NO: 27:
 25 SEQUENCE CHARACTERISTICS:
 26 LENGTH: 12
 27 TYPE: AMINO ACID
 28 TOPOLOGY: LINEAR
 29 MOLECULE TYPE: PEPTIDE
 30 DESCRIPTION: NO
 31 HYPOTHETICAL: NO
 32 ORGANISM: RHODOCOCCUS SP. M4
 33 INDIVIDUAL ISOLATE: PHENYLALANINE DEHYDROGENASE
 34 US-08-461-9908-27

Query Match 36.4%, Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%, Pred. No. 2e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 3 ALNW 5
 11-1
 10 5 ALNW 9

RESULT 18
 US-08-248-819A-44
 Sequence 44, Application US/08248819A
 Patent No. 5700638
 GENERAL INFORMATION:
 1 APPLICANT: KORSMEYER, Stanley J.
 2 TITLE OF INVENTION: CELL DEATH REGULATORS
 3 NUMBER OF SEQUENCES: 60
 4 CORRESPONDENCE ADDRESS:
 5 ADDRESSEE: Townsend and Townsend Kourie and Crew
 6 STREET: 379 Lytton Avenue
 7 CITY: Palo Alto
 8 STATE: California
 9 COUNTRY: US
 10 ZIP: 94301

11 COMPUTER READABLE FORM:
 12 MEDIUM TYPE: Floppy disk
 13 COMPUTER: IBM PC compatible
 14 OPERATING SYSTEM: PC-DOS/MS-DOS
 15 SOFTWARE: Patent In Release #1.0, Version #1.25
 16 CURRENT APPLICATION DATA:
 17 FILING DATE: 25-NOV-1994
 18 APPLICATION NUMBER: US/08/248,819A
 19 CLASSIFICATION: 435
 20 PRIOR APPLICATION DATA:
 21 APPLICATION NUMBER: US 08/112,204
 22 FILING DATE: 26-AUG 1993
 23 ATTORNEY/AGENT INFORMATION:
 24 NAME: Smith, William M.
 25 REGISTRATION NUMBER: 40,224
 26 REFERENCE/DOCKET NUMBER: 15726A-000610
 27 TELEPHONE: (415) 326-2400
 28 TELEFAX: (415) 326-2422
 29 INFORMATION FOR SEQ ID NO: 44:
 30 SEQUENCE CHARACTERISTICS:
 31 LENGTH: 13 amino acids
 32 TYPE: amino acid
 33 STRANDEDNESS: Not relevant
 34 TOPOLOGY: Not relevant
 35 MOLECULE TYPE: peptide
 36 US-08-248 819A-44

Query Match 36.4%, Score 4; DB 1; Length 13;
 Best Local Similarity 100.0%, Pred. No. 2.le-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWGA 8
 11-1
 10 7 NWGA 10

RESULT 19
 US-08-317-646A-62
 Sequence 62, Application US/08317646A
 Patent No. 5856171
 GENERAL INFORMATION:
 1 APPLICANT: KORSMEYER, Stanley J.
 2 TITLE OF INVENTION: CELL DEATH REGULATORS
 3 NUMBER OF SEQUENCES: 78
 4 CORRESPONDENCE ADDRESS:
 5 ADDRESSEE: Townsend and Townsend Kourie and Crew
 6 STREET: 379 Lytton Avenue
 7 CITY: Palo Alto
 8 STATE: California
 9 COUNTRY: US
 10 ZIP: 94301

11 COMPUTER READABLE FORM:
 12 MEDIUM TYPE: Floppy disk
 13 COMPUTER: IBM PC compatible
 14 OPERATING SYSTEM: PC-DOS/MS-DOS
 15 SOFTWARE: Patent In Release #1.0, Version #1.25
 16 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/337,646A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,408
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A 0.1.16.20
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-337-646A-62

Query Match 36.4%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWGA 8
DB 7 NWGA 10

RESULT 26
US-09-041-889-37
Sequence 37, Application US/09-41889
Patent No. 603864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial DC PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 200
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,958
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3036
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-041-889-37

Query Match 36.4%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 10 AKPK 13

RESULT 21
US-08-930-589A-20
Sequence 20, Application US/08930589A
Patent No. 6107087
GENERAL INFORMATION:
APPLICANT: MERCK FROSST CANADA & CO.
APPLICANT: O'NEILL, GARY P.
APPLICANT: MANCINI, JOSEPH A.
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
TITLE OF INVENTION: CYCLOOXYGENASE-2
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,589A
FILING DATE: 28-JUN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coppola, Joseph A
REGISTRATION NUMBER: 38,413
REFERENCE/DOCKET NUMBER: 19029PC
TELEPHONE: 732-594-6734
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-930-589A-20

Query Match 36.4%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 3 ARAL 6

RESULT 22
US-08-927-326-62

```

: Sequence 62, Application US/08927326
: Patent No. 6184202
: GENERAL INFORMATION:
: APPLICANT: KORSMEYER, Stanley J.
: TITLE OF INVENTION: CELL DEATH REGULATORS
: NUMBER OF SEQUENCES: 78
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kleinfelder and Frew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/927,326
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/337,646
: FILING DATE: 10-NOV-1994
: APPLICATION NUMBER: US 08/248,619
: FILING DATE: 25-MAY-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/112,206
: FILING DATE: 26-AUG-1993
: ATTORNEY/AGENCY INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,224
: REFERENCE/DOCKET NUMBER: 157,264 US/09/20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 62:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 13 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
US 08-927-326-62

Query Match 46.4% Score 4: DB 4: Length 12;
Best Local Similarity 100.0% Pred. No. 2.1e+02;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 NWSA 8
DB 7 NWSA 10

RESULT 23
US-09-599-781-20
: Sequence 20, Application US/09599781
: Patent No. 6362327
: GENERAL INFORMATION:
: APPLICANT: MERCK FROSST CANADA S 200
: O'NEILL, GARY P.
: MANCINI, JOSEPH A.
: TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
: CYCLOOXYGENASE-2
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merck & Co., Inc.
: STREET: P.O. Box 2000, 126 E. Lincoln Ave.
: CITY: Rahway
: STATE: NJ
: COUNTRY: USA
: ZIP: 07065-0900

```

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM compatible
: OPERATING SYSTEM: Windows
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/599,781
: FILING DATE: 21 Jun-2000
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/084,033
: FILING DATE: 27-Sep-1993
: ATTORNEY/AGENCY INFORMATION:
: NAME: Coppola, Joseph A
: REGISTRATION NUMBER: 38,413
: REFERENCE/DOCKET NUMBER: 19029PC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 732-594 6734
: TELEFAX: 732-594-4720
: TELEX: <Unknown>
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 13 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-599-781-20

Query Match 46.4% Score 4: DB 4: Length 13;
Best Local Similarity 100.0% Pred. No. 2.1e+02;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ARAL 4
DB 3 ARAL 6

RESULT 24
US-09-417-264-37
: Sequence 37, Application US/09417264
: Patent No. 6537768
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Cohavy, Ofer
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: Microbial UC PANCA antigens
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/417,264
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/041,889
: FILING DATE:
: ATTORNEY/AGENCY INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-PH 3006

```

```

: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 37:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 13 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US 09-417-264 37

Query Match: 36.4%, Score 4, DB 1, Length 13
Best Local Similarity 100.0%, Pred. No. 2, 3e-02
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 8 AKPK 11
DB 10 AKPK 13

RESULT 25
US-08-232-453A-23
: Sequence 23, Application US/08212453A
: Patent No. 5589568
: GENERAL INFORMATION:
: APPLICANT: HIGASHIJIMA, TSUTOMU
: APPLICANT: ROSS, ELLIOTT M.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
: MODULATING G PROTEIN ACTION
: NUMBER OF SEQUENCES: 71
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ARNOLD, WHITE & DORKEE
: STREET: P.O. BOX 4433
: CITY: HOUSTON
: STATE: TX
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:
: MEDIUM TYPE: FLOPPY DISK
: COMPUTER: IBM PC COMPATIBLE
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WORDPERFECT 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/232,453A
: FILING DATE: APRIL 22, 1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/748,319
: FILING DATE: AUGUST 21, 1991
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: PARKER, DAVID L.
: REGISTRATION NUMBER: 32,165
: REFERENCE/DOCKET NUMBER: UTSD:253/PAR
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (512) 418-3000
: TELEFAX: (512) 474-7577
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 14 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
US-08-232-453A-28

Query Match: 36.4%, Score 4, DB 1, Length 14
Best Local Similarity 100.0%, Pred. No. 2, 3e-02
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 1 ARAL 4
DB 10 ARAL 14

RESULT 27
US-08-232-453A-41
: Sequence 41, Application US/08212453A
: Patent No. 5589568
: GENERAL INFORMATION:
: APPLICANT: HIGASHIJIMA, TSUTOMU
: APPLICANT: ROSS, ELLIOTT M.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
: MODULATING G PROTEIN ACTION
: NUMBER OF SEQUENCES: 71
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: ARNOLD, WHITE & DORKEE
: STREET: P.O. BOX 4433
: CITY: HOUSTON
: STATE: TX
: COUNTRY: USA
: ZIP: 77210
: COMPUTER READABLE FORM:

```


MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/482,453A
 FILING DATE: APRIL 22, 1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/748,414
 FILING DATE: AUGUST 23, 1991
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: PARKER, DAVID L.
 REGISTRATION NUMBER: 32,195
 REFERENCE/DOCKET NUMBER: 015145/HAR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 41:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-482-453A 41

Query Match: 36.4% Score 4: DB 1: Length 14:
 Best Local Similarity 100.0% Pred. No. 2.3e+02
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:
 QY 1 ARA 4
 DB 10 WGA 13
 RESULT 28
 US-09-482-428 13
 Sequence 13, Application US/0848228
 Patent No. 5968753
 GENERAL INFORMATION:
 APPLICANT: Tsenq-Law, Janet
 APPLICANT: Kobori, Joan A.
 APPLICANT: Al-Abdaly, Fahad A.
 APPLICANT: Guillermo, Roy
 APPLICANT: Helgerson, Sam L.
 APPLICANT: Deans, Robert J.
 TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
 SELECTION MEDIATED BY PEPTIDE RELEASE
 NUMBER OF SEQUENCES: 215
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Janice Guthrie, Ph.D.
 STREET: P.O. Box 15210
 CITY: Irvine
 STATE: California
 COUNTRY: USA
 ZIP: 92713-5210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/482,428
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Guthrie, Janice
 REGISTRATION NUMBER: 35,170
 REFERENCE/DOCKET NUMBER: IT 4630CIP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (714) 440-5354
 TELEFAX: (714) 553-1952

INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-482-228 13
 Query Match: 36.4% Score 4: DB 2: Length 14:
 Best Local Similarity 100.0% Pred. No. 2.3e+02
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 6 WGA 9
 DB 10 WGA 13

RESULT 29
 US-08-482-528 13
 Sequence 13, Application US/08482528
 Patent No. 6017719
 GENERAL INFORMATION:
 APPLICANT: Tsenq-Law, Janet
 APPLICANT: Kobori, Joan A.
 APPLICANT: Al-Abdaly, Fahad A.
 APPLICANT: Guillermo, Roy
 APPLICANT: Helgerson, Sam L.
 APPLICANT: Deans, Robert J.
 TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
 SELECTION MEDIATED BY PEPTIDE RELEASE
 NUMBER OF SEQUENCES: 215
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Janice Guthrie, Ph.D.
 STREET: P.O. Box 15210
 CITY: Irvine
 STATE: California
 COUNTRY: USA
 ZIP: 92713-5210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,528
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Guthrie, Janice
 REGISTRATION NUMBER: 35,170
 REFERENCE/DOCKET NUMBER: IT 4630CIP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (714) 440-5353
 TELEFAX: (714) 553-1952
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-482-528 13

QY 6 WGA 9
 DB 10 WGA 13

Query Match: 36.4% Score 4: DB 3: Length 14:
 Best Local Similarity 100.0% Pred. No. 2.3e+02
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 6 WGA 9
 DB 10 WGA 13

RESULT 30
 US-09-482-653A 14

```
? Sequence 13, Application US/0940065A
? Patent No. 6348311
? GENERAL INFORMATION:
? APPLICANT: Kastan, Michael
? APPLICANT: Carman, Christine
? APPLICANT: Kim, Seong-Tae
? APPLICANT: Lim, Dae-Sik
? APPLICANT: St. Jude Children's Research Hospital
? TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
? FILE REFERENCE: 2427/0142
? CURRENT APPLICATION NUMBER: US/09/400,653A
? CURRENT FILING DATE: 1999-09-21
? PRIOR APPLICATION NUMBER: 09/246,061
? PRIOR FILING DATE: 1999-02-10
? NUMBER OF SEQ ID NOS: 49
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 13
? LENGTH: 14
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-400-653A-13

Query Match 36.4% Score 47 DB 47 Length 14
Best Local Similarity 100.0% Pred. No. 2.4e+02
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ARAL 4
Db 2 ARAL 5

RESULT 31
US-09-248-061B-31
? Sequence 31, Application US/09248061b
? Patent No. 6987640
? GENERAL INFORMATION:
? APPLICANT: Kastan, M.
? APPLICANT: Carman, C.
? APPLICANT: Kim, S-T.
? APPLICANT: Lim, D-S.
? APPLICANT: St. Jude Children's Research Hospital
? TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
? FILE REFERENCE: 2427/0142
? CURRENT APPLICATION NUMBER: US/09/248,061b
? CURRENT FILING DATE: 1999-02-10
? NUMBER OF SEQ ID NOS: 32
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 31
? LENGTH: 14
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-248-061B-31

Query Match 36.4% Score 47 DB 47 Length 14
Best Local Similarity 100.0% Pred. No. 2.4e+02
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ARAL 4
Db 2 ARAL 5

RESULT 32
US-08-467-083-48
? Sequence 48, Application US/08467083
? Patent No. 5726023
? GENERAL INFORMATION:
? APPLICANT: Cheever, Martin A.
? APPLICANT: Disis, Mary L.
? TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
? TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
? TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
? NUMBER OF SEQUENCES: 68
```

```
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Seed and Berry
? STREET: 6300 Columbia Center, 701 Fifth Avenue
? CITY: Seattle
? STATE: Washington
? COUNTRY: US
? ZIP: 98104-7092
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/467,083
? FILING DATE: 06-JUN-1995
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/414,417
? FILING DATE: 06-JUN-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: Sharkey, Richard G.
? REGISTRATION NUMBER: 32,629
? REFERENCE/DOCKET NUMBER: 920010.448C2
? TELEPHONE: (206) 622 4900
? TELEFAX: (206) 682-6031
? TELEX: 3723836 SEELANDERRY
? INFORMATION FOR SEQ ID NO: 48:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 15 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? US-08-467-083-48

Query Match 36.4% Score 47 DB 17 Length 15
Best Local Similarity 100.0% Pred. No. 2.4e+02
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 GAKP 10
Db 9 GAKP 12

RESULT 33
US-08-414-417B-48
? Sequence 48, Application US/08414417B
? Patent No. 5801005
? GENERAL INFORMATION:
? APPLICANT: Cheever, Martin A.
? APPLICANT: Disis, Mary L.
? TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
? TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
? TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
? NUMBER OF SEQUENCES: 69
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Seed and Berry LLP
? STREET: 6300 Columbia Center, 701 Fifth Avenue
? CITY: Seattle
? STATE: Washington
? COUNTRY: US
? ZIP: 98104-7092
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/414,417B
? FILING DATE: 31-MAR-1995
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Sharkey, Richard G.
? REGISTRATION NUMBER: 32,629
```

```

: REFERENCE/DOCKET NUMBER: 920010.448C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 48:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-414-417B-48

```

```

Query Match: 36.4%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 7 GAKP 10
    ||||
DL 9 GAKP 12

```

```

: RESULT 14
: US-08-486-348A-48
: Sequence 48, Application US/08486348A
: Patent No. 5846538
: GENERAL INFORMATION:
: APPLICANT: Cheever, Martin A.
: APPLICANT: Disis, Mary L.
: TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
: TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
: NUMBER OF SEQUENCES: 69
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed and Berry LLP
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: US
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/486,348A
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Sharkey, Richard G.
: REGISTRATION NUMBER: 32,629
: REFERENCE/DOCKET NUMBER: 920010.448C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 48:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-486-348A-48

```

```

Query Match: 36.4%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 7 GAKP 10
    ||||
DL 9 GAKP 12

```

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: RESULT 35
: US-08-710-249-18
: Sequence 18, Application US/08710249

```

```

: Patent No. 5858777
: GENERAL INFORMATION:
: APPLICANT: Villeponteau, Bryant
: APPLICANT: Feng, Junli
: APPLICANT: Adams, William H.
: APPLICANT: Adams, Robert R.
: TITLE OF INVENTION: Methods and Reagents for Regulating
: TITLE OF INVENTION: Telomere Length and Telomerase Activity
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/710,249
: FILING DATE: 13-SEP-1996
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/583,808
: FILING DATE: 05-JAN-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/003,492
: FILING DATE: 08-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Storella, John R.
: REGISTRATION NUMBER: 32,944
: REFERENCE/DOCKET NUMBER: 015389-0012200S
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-710-249-18

```

```

Query Match: 36.4%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 8 AKPK 11
    ||||
DL 12 AKPK 15

```

```

: RESULT 36

```

```

: US-08-468-545B-48
: Sequence 48, Application US/08468545B
: Patent No. 5876712
: GENERAL INFORMATION:
: APPLICANT: Cheever, Martin A.
: APPLICANT: Disis, Mary L.
: TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
: TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
: NUMBER OF SEQUENCES: 69
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed and Berry LLP
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: US

```



```

1 TITLE OF INVENTION: Diagnosis, Prevention, and Treatment of
2 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
3 TITLE OF INVENTION: Microbial UC PANCA antigens
4 NUMBER OF SEQUENCE ADDRESSES: 41
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Campbell & Flores LLP
7 STREET: 4370 La Jolla Village Drive, Suite 700
8 CITY: San Diego
9 STATE: California
10 COUNTRY: USA
11 ZIP: 92122
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent in Release #1.0, Version #1.25
17 CURRENT APPLICATION NUMBER: US/09/041.889
18 FILING DATE:
19 CLASSIFICATION:
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 08/837,058
22 FILING DATE: 11-APR-1997
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Campbell, Cathryn A.
25 REGISTRATION NUMBER: 31,815
26 REFERENCE/DOCKET NUMBER: P-PM 3006
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (619) 535-9001
29 TELEFAX: (619) 535-8949
30 INFORMATION FOR SEQ ID NO: 24:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 15 amino acids
33 TYPE: amino acid
34 TOPOLOGY: linear
35 US-09-041-889-22
36
37 Query Match 36.4% Score 4: DB 3: Length 15;
38 Best Local Similarity 100.0% Pred. No. 2.4e+02;
39 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
40
41 QY 8 AKPK 11
42 DB 1111
43 6 AKPK 9
44
45 RESULT 43
46 US-09-041-889-24
47 Sequence 24, Application US/09041889
48 Patent No. 6033864
49 GENERAL INFORMATION:
50 APPLICANT: Braun, Jonathan
51 APPLICANT: Cohavy, Ofer
52 TITLE OF INVENTION: Diagnosis, Prevention, and Treatment of
53 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
54 TITLE OF INVENTION: Microbial UC PANCA antigens
55 NUMBER OF SEQUENCES: 41
56 CORRESPONDENCE ADDRESS:
57 ADDRESSEE: Campbell & Flores LLP
58 STREET: 4370 La Jolla Village Drive, Suite 700
59 CITY: San Diego
60 STATE: California
61 COUNTRY: USA
62 ZIP: 92122
63 COMPUTER READABLE FORM:
64 MEDIUM TYPE: Floppy disk
65 COMPUTER: IBM PC compatible
66 OPERATING SYSTEM: PC-DOS/MS-DOS
67 SOFTWARE: Patent in Release #1.0, Version #1.25
68 CURRENT APPLICATION DATA:
69 APPLICATION NUMBER: US/09/041.889
70 FILING DATE:
71 CLASSIFICATION:
72 PRIOR APPLICATION DATA:
73 APPLICATION NUMBER: US 08/837,058
74 FILING DATE: 11-APR-1997
75 ATTORNEY/AGENT INFORMATION:
76 NAME: Campbell, Cathryn A.
77 REGISTRATION NUMBER: 31,815
78 REFERENCE/DOCKET NUMBER: P-PM 3006
79 TELECOMMUNICATION INFORMATION:
80 TELEPHONE: (619) 535-9001
81 TELEFAX: (619) 535-8949
82 INFORMATION FOR SEQ ID NO: 25:
83 SEQUENCE CHARACTERISTICS:
84 LENGTH: 15 amino acids
85 TYPE: amino acid
86 TOPOLOGY: linear
87 MOLECULE TYPE: peptide
88 US-09-041-889-25
89
90 Query Match 36.4% Score 4: DB 3: Length 15;
91 Best Local Similarity 100.0% Pred. No. 2.4e+02;
92 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
93
94 QY 8 AKPK 11
95 DB 1111
96 6 AKPK 9
97
98 RESULT 42
99 US-09-041-889-24
100 Sequence 24, Application US/09041889
101 Patent No. 6033864
102 GENERAL INFORMATION:
103 APPLICANT: Braun, Jonathan
104 APPLICANT: Cohavy, Ofer
105 TITLE OF INVENTION: Diagnosis, Prevention, and Treatment of
106 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
107 TITLE OF INVENTION: Microbial UC PANCA antigens
108 NUMBER OF SEQUENCES: 41
109 CORRESPONDENCE ADDRESS:
110 ADDRESSEE: Campbell & Flores LLP
111 STREET: 4370 La Jolla Village Drive, Suite 700
112 CITY: San Diego
113 STATE: California
114 COUNTRY: USA
115 ZIP: 92122
116 COMPUTER READABLE FORM:
117 MEDIUM TYPE: Floppy disk
118 COMPUTER: IBM PC compatible
119 OPERATING SYSTEM: PC-DOS/MS-DOS
120 SOFTWARE: Patent in Release #1.0, Version #1.25
121 CURRENT APPLICATION DATA:
122 APPLICATION NUMBER: US/09/041.889
123 FILING DATE:
124 CLASSIFICATION:

```

```

Matches      4:  Conservative      0:  Mismatches      6:  Indels      9:  Gaps      0:

QY      8 AKPK 11
      11-1
DB      12 AKPK 15

RESULT: 42
US-09-041-889-36
: Sequence 36, Application US/0904189
: Patent No. 603864
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Cobarr, Olier
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes thereof, Using
: TITLE OF INVENTION: Microbial UC PANDA antigens
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/041-889
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/837-058
: FILING DATE: 11-APR-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-PM 3609
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-09-041-889-36

Query Match: 36.4%, Score 4: DB 3: Length 15:
Best Local Similarity 100.0%, Pred. No. 2.4e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY      8 AKPK 11
      11-1
DB      12 AKPK 15

RESULT: 43
US-09-837-058-15
: Sequence 15, Application US/09847058
: Patent No. 6074835
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Targan, Stephan R.
: APPLICANT: Eggens, Mark
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes thereof, Using
: TITLE OF INVENTION: Histone H1
: NUMBER OF SEQUENCES: 26

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847-058
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 2438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-837-058-15

Query Match: 36.4%, Score 4: DB 3: Length 15:
Best Local Similarity 100.0%, Pred. No. 2.4e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY      8 AKPK 11
      11-1
DB      12 AKPK 15

RESULT: 44
US-08-837-058-15
: Sequence 16, Application US/08847058
: Patent No. 6074835
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Targan, Stephan R.
: APPLICANT: Eggens, Mark
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes thereof, Using
: TITLE OF INVENTION: Histone H1
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/847-058
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-PM 2438
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001

```

```

: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-837-058-16

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DL 2 AKPK 5

RESULT 45
US-08-837-058-22
: Sequence 22, Application US/08847058
: Patent No. 6074835
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Targan, Stephan R.
: APPLICANT: Eggena, Mark
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis and Related Subtypes Thereof, Using
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/837-058
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-PM 2438
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-837-058-24

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DL 4 AKPK 7

RESULT 47
US-08-466-680H-48
: Sequence 48, Application US/0846680H
: Patent No. 6075122
: GENERAL INFORMATION:
: APPLICANT: Cheever, Martin A.
: APPLICANT: Disis, Mary L.
: TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
: TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
: TITLE OF INVENTION: HER 2/neu ONCOGENE IS ASSOCIATED
: NUMBER OF SEQUENCES: 69
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed and Berry LLP
: STREET: 6800 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: US
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466-680H
: FILING DATE: 06 JUN 1995
: CLASSIFICATION: 424

```

```

: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-837-058-16

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DL 2 AKPK 5

RESULT 45
US-08-837-058-22
: Sequence 22, Application US/08847058
: Patent No. 6074835
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Targan, Stephan R.
: APPLICANT: Eggena, Mark
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis and Related Subtypes Thereof, Using
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/837-058
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-PM 2438
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-837-058-24

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DL 6 AKPK 9

RESULT 46
US-08-837-058-24
: Sequence 24, Application US/08847058
: Patent No. 6074835
: GENERAL INFORMATION:

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: APPLICANT: Braun, Jonathan
: APPLICANT: Targan, Stephan R.
: APPLICANT: Eggena, Mark
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/837-058
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-PM 2438
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-09-837-058-24

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DL 4 AKPK 7

RESULT 47
US-08-466-680H-48
: Sequence 48, Application US/0846680H
: Patent No. 6075122
: GENERAL INFORMATION:
: APPLICANT: Cheever, Martin A.
: APPLICANT: Disis, Mary L.
: TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
: TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
: TITLE OF INVENTION: HER 2/neu ONCOGENE IS ASSOCIATED
: NUMBER OF SEQUENCES: 69
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed and Berry LLP
: STREET: 6800 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: US
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466-680H
: FILING DATE: 06 JUN 1995
: CLASSIFICATION: 424

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ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920510.448C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US 08-466-680B-48

Query Match 36.4%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 7 GAKP 10
Db 9 GAKP 12

RESULT 48
US-08-602-999A-333
Sequence 333, Application US/0860299A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OJILLIAM, Lawrence A.
APPLICANT: DEK, Channing J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDGER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.00
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1:01 202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 333:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-333

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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 4 ARAL 4
Db 4 ARAL 7

RESULT 49
US-09-220-157A-18
Sequence 18, Application US/09220157A
Patent No. 6300110
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Sunli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,157A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-00122005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-220-157A-18

Query Match 36.4%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 AKPK 11
Db 12 AKPK 15

RESULT 50
US-09-500-124-333
Sequence 333, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.


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1  APPLICANT: KAY, Brian K.
2  APPLICANT: THORN, Judith M.
3  APPLICANT: QUILLIAM, Lawrence A.
4  APPLICANT: DER, Channing J.
5  APPLICANT: FOWLKES, Dana M.
6  APPLICANT: RIDER, James E.
7  TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
8  TITLE OF INVENTION: ISOLATING AND USING SAME
9  NUMBER OF SEQUENCES: 467
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Pennile & Edmonds
12 STREET: 1155 Avenue of the Americas
13 CITY: New York
14 STATE: New York
15 COUNTRY: U.S.A.
16 ZIP: 10016-2711
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: PatentIn Release #1.0, Version #1.3.0
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/09/500,124
24 FILING DATE:
25 CLASSIFICATION:
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 08/602,999
28 FILING DATE: 16-FEB-1996
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Mistrock, S. Leslie
31 REGISTRATION NUMBER: 18,872
32 REFERENCE/DOCKET NUMBER: 1101-262
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (212) 790-9093
35 TELEFAX: (212) 869-9741/8864
36 TELEX: 66141 PENNIE
37 INFORMATION FOR SEQ ID NO: 333:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 15 amino acids
40 TYPE: amino acid
41 TOPOLOGY: unknown
42 MOLECULE TYPE: peptide
43 US-09-500-124-333

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Query Match: 36.4%; Score: 4; Pos: 4; Length: 15;
Best Local Similarity: 100.0%; Pos: 2; Length: 15;
Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0;

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01 1111
02 4 ARAL 7

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Job time : 18.9167 secs

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EM protein - protein search, using sw model

Run on: September 30, 2003, 10:10:04 - Search time 21.5 seconds
(without alignments)
77.413 Million cell updates/sec

Title: US-09-787-443-3

Perfect score: 11

Sequence: 1 ARALNWGAKPK 11

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Gap 60.0, Gapext 60.0

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Post-processing: Listing first 500 summaries

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Fired No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	4	36.4	10	11	US-09-572-404B-1882 Sequence 1882, Ap
6	4	36.4	10	11	US-09-572-404B-1156 Sequence 3136, Ap
7	4	36.4	10	12	US-09-572-270A-291 Sequence 891, App
8	4	36.4	10	12	US-09-572-270A-293 Sequence 893, App
9	4	36.4	10	12	US-10-239-53A-480 Sequence 280, App
10	4	36.4	12	10	US-09-810-481-26 Sequence 46, Appl
11	4	36.4	12	12	US-10-050-260-59 Sequence 59, Appl
12	4	36.4	13	10	US-10-050-126-86 Sequence 85, Appl
13	4	36.4	13	11	US-09-896-896A-49 Sequence 49, Appl
14	4	36.4	13	15	US-09-847-185-25 Sequence 25, Appl
15	4	36.4	13	15	US-10-024-123-13 Sequence 13, Appl

16	4	36.4	14	15	US-10-024-123-13 Sequence 13, Appl
17	4	36.4	15	9	US-09-873-409-17 Sequence 17, Appl
18	4	36.4	15	12	US-10-268-561-16 Sequence 16, Appl
19	4	36.4	15	12	US-10-268-569-16 Sequence 16, Appl
20	4	36.4	15	12	US-10-014-322A-11 Sequence 11, Appl
21	4	36.4	15	15	US-10-174-105A-94 Sequence 94, Appl
22	4	36.4	15	15	US-10-174-105A-95 Sequence 95, Appl
23	4	36.4	15	15	US-10-229-567-15 Sequence 15, Appl
24	4	36.4	15	15	US-10-229-567-16 Sequence 16, Appl
25	4	36.4	15	15	US-10-229-567-22 Sequence 22, Appl
26	4	36.4	15	15	US-10-229-567-24 Sequence 24, Appl
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28	4	36.4	15	15	US-10-229-567-36 Sequence 36, Appl
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34	3	27.3	8	10	US-09-910-552-43 Sequence 43, Appl
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61	3	27.3	8	15	US-10-052-942-73 Sequence 73, Appl
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68	3	27.3	9	7	US-08-344-824-273 Sequence 273, App
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92	3	27.3	9	10	US-09-780-055-255	Sequence 255, App	Sequence 255, App	3	27.3	9	12	US-10-226-872-32	Sequence 32, Appl
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118	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	14	US-10-044-034-7	Sequence 7, Appl
119	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-113-085-6	Sequence 6, Appl
120	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-102-283-134	Sequence 134, App
121	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-102-283-155	Sequence 155, App
122	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-165-015-4	Sequence 4, Appl
123	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-094-699-48	Sequence 48, Appl
124	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-094-699-57	Sequence 57, Appl
125	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-062-710-139	Sequence 139, App
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127	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-193-934-1	Sequence 1, Appl
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129	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-158-596A-84	Sequence 84, Appl
130	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-157-775B-35	Sequence 35, Appl
131	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-157-775B-84	Sequence 84, Appl
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142	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-128-711-147	Sequence 147, App
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145	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-224-286-24	Sequence 24, Appl
146	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-224-286-25	Sequence 25, Appl
147	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-213-512-260	Sequence 260, App
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149	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-254-446A-35	Sequence 35, Appl
150	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-254-446A-84	Sequence 84, Appl
151	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-219-850-12	Sequence 12, Appl
152	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	9	15	US-10-301-644-18	Sequence 18, Appl
153	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	10	7	US-08-344-824-210	Sequence 210, App
154	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	10	7	US-08-344-824-245	Sequence 245, App
155	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	10	7	US-08-344-824-250	Sequence 250, App
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158	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	10	8	US-08-854-825-5	Sequence 5, Appl
159	3	27.3	9	10	US-09-934-148-116	Sequence 148, App	Sequence 148, App	3	27.3	10	9	US-09-767-460-45	Sequence 45, Appl
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393	3	27.3	10	12	US-09-572-270A-85	Sequence 85, Appl	466	3	27.3	11	10	US-09-017-743C-125	Sequence 125, App
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395	3	27.3	10	12	US-09-572-270A-150	Sequence 150, App	468	3	27.3	11	10	US-09-758-198-40	Sequence 40, Appl
396	3	27.3	10	12	US-09-572-270A-291	Sequence 291, App	469	3	27.3	11	10	US-09-879-572A-23	Sequence 23, Appl
397	3	27.3	10	14	US-09-572-270A-420	Sequence 320, App	470	3	27.3	11	10	US-09-879-572A-25	Sequence 25, Appl
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399	3	27.3	10	12	US-09-572-270A-410	Sequence 410, App	472	3	27.3	11	11	US-09-956-940-53	Sequence 53, Appl
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401	3	27.3	10	12	US-09-572-270A-449	Sequence 449, App	474	3	27.3	11	11	US-09-791-389-187	Sequence 187, App
402	3	27.3	10	12	US-09-572-270A-738	Sequence 738, App	475	3	27.3	11	11	US-09-906-393A-7	Sequence 7, Appl
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412	3	27.3	10	12	US-10-672-419-1	Sequence 1, Appl	485	3	27.3	11	11	US-09-775-052-40	Sequence 40, Appl
413	3	27.3	10	12	US-10-672-419-44	Sequence 34, Appl	486	3	27.3	11	11	US-09-775-052-41	Sequence 41, Appl
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416	3	27.3	10	12	US-10-156-212-6	Sequence 5, Appl	489	3	27.3	11	11	US-09-775-052-57	Sequence 57, Appl
417	3	27.3	10	12	US-10-265-485-17	Sequence 17, Appl	490	3	27.3	11	11	US-09-847-946A-128	Sequence 128, App
418	3	27.3	10	12	US-10-606-173-15	Sequence 15, Appl	491	3	27.3	11	11	US-09-847-946A-129	Sequence 129, App
419	3	27.3	10	12	US-10-219-563-14	Sequence 13, Appl	492	3	27.3	11	11	US-09-876-904A-531	Sequence 531, App
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421	3	27.3	10	12	US-10-224-990A-1337	Sequence 1337, Ap	494	3	27.3	11	11	US-09-876-904A-597	Sequence 597, App
422	3	27.3	10	12	US-10-224-990A-1438	Sequence 1338, Ap	495	3	27.3	11	11	US-09-876-904A-622	Sequence 622, App
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424	3	27.3	10	12	US-10-308-444-94	Sequence 94, Appl	497	3	27.3	11	11	US-09-992-665-12	Sequence 12, Appl
425	3	27.3	10	12	US-10-368-445-61	Sequence 67, Appl	498	3	27.3	11	11	US-09-852-910-248	Sequence 248, App
426	3	27.3	10	12	US-10-239-316A-176	Sequence 176, App	499	3	27.3	11	11	US-09-848-781-3	Sequence 3, Appl
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448	3	27.3	10	15	US-10-219-329-13	Sequence 13, Appl							
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452	3	27.3	11	10	US-09-900-147-3	Sequence 9, Appl							
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ALIGNMENTS

RESULTS :
US-09-387 715-10
: Sequence 10, Application US/09487715
: Publication NO. US20030059422A1
: GENERAL INFORMATION:
: APPLICANT: Sharma, Shubh
: TITLE OF INVENTION: Tuftsin Metallopeptides Analogs and Uses Thereof
: FILE REFERENCE: 1173/107940S1
: CURRENT APPLICATION NUMBER: US/09/387.715
: CURRENT FILING DATE: 1999-08-30
: PRIOR APPLICATION NUMBER: PCT/US99/05693
: PRIOR FILING DATE: 1999-03-18
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: PatentIn Ver.: 2.1
: SEQ ID NO 10
: LENGTH: 9
: TYPE: PPT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: synthetic
: OTHER INFORMATION: peptide

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: NAME/KEY: modified residue
: LOCATION: 3,6,8
: OTHER INFORMATION: D-amino acid
US-09-787-715-10

Query Match
Best Local Similarity 36.4%; Score 4; DB 11; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 3 AKPK 6

RESULT 2
US-10-364-842-10
: Sequence 10, Application US/10364842
: Publication No. US20030165427A1
: GENERAL INFORMATION:
: APPLICANT: Sharma, Shubb
: TITLE OF INVENTION: Tufsin Metallopeptides Analogs and Uses Thereof
: FILE REFERENCE: 1173/1D7940S1
: CURRENT APPLICATION NUMBER: US/0/364,842
: CURRENT FILING DATE: 2003-02-11
: PRIOR APPLICATION NUMBER: PCT/US99/05694
: PRIOR FILING DATE: 1999-03-18
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 10
: LENGTH: 9
: TYPE: PPT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: synthetic
: OTHER INFORMATION: peptide
: FEATURE:
: NAME/KEY: modified residue
: LOCATION: 3,6,8
: OTHER INFORMATION: D-amino acid
US-10-364-842-10

Query Match
Best Local Similarity 36.4%; Score 4; DB 12; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 3 AKPK 6

RESULT 3
US-08-344-824-179
: Sequence 179, Application US/08344824
: Publication No. US20030152580A1
: GENERAL INFORMATION:
: APPLICANT: SEITE, Alessandro
: APPLICANT: SIDNEY, John
: TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
: NUMBER OF SEQUENCES: 399
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kleinfelder & New
: STREET: One Market Plaza, Steuart Street Tower, 20th
: STREET: Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:

: NAME/KEY: modified residue
: LOCATION: 3,6,8
: OTHER INFORMATION: D-amino acid
US-09-787-715-10

Query Match
Best Local Similarity 36.4%; Score 4; DB 11; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 3 AKPK 6

RESULT 4
US-09-572-404B-1880
: Sequence 1880, Application US/09572404B
: Publication No. US20030078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide ligands from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572,404B
: CURRENT FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProtPatent version 1.0
: SEQ ID NO 1880
: LENGTH: 10
: TYPE: PPT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: sequence located in PCD17 at 230-239 and may interact with S
US-09-572-404B-1880

Query Match
Best Local Similarity 36.4%; Score 4; DB 11; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 7 ARAL 10

RESULT 5
US-09-572-404B-1882
: Sequence 1882, Application US/09572404B
: Publication No. US20030078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide ligands from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572,404B
: CURRENT FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProtPatent version 1.0
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SEQ ID NO 1882
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in p0117 at 229-248 and may interact with Sequen
OTHER INFORMATION: in this patent.
US-09-572-404B-1882

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 6 ARAL 9

RESULT 6
US-09-572-404B-3136
Sequence 3136, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide variants from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 3136
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in TP11 at 84-93 and may interact with Sequence
US-09-572-404B-3136

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AKPK 11
DB 6 AKPK 5

RESULT 7
US-09-572-270A-891
Sequence 891, Application US/09572270A
Publication No. US20030148366A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Inter-complementary peptide listing
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/572,270A
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 1144
SOFTWARE: ProPatent version 1.0
SEQ ID NO 891
LENGTH: 10
TYPE: PRT
ORGANISM: Arabidopsis Thaliana
OTHER INFORMATION: Sequence located in LFW1 at 79-88 and may interact with
US-09-572-270A-891

Query Match 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 1111

us-09-787-443-3.oli.rapb

SEQ ID NO 1882
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in p0117 at 229-248 and may interact with Sequen
OTHER INFORMATION: in this patent.
US-09-572-404B-1882

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 6 ARAL 9

RESULT 6
US-09-572-404B-3136
Sequence 3136, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide variants from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 3136
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in TP11 at 84-93 and may interact with Sequence
US-09-572-404B-3136

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AKPK 11
DB 6 AKPK 5

RESULT 7
US-09-572-270A-891
Sequence 891, Application US/09572270A
Publication No. US20030148366A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Inter-complementary peptide listing
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/572,270A
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 1144
SOFTWARE: ProPatent version 1.0
SEQ ID NO 891
LENGTH: 10
TYPE: PRT
ORGANISM: Arabidopsis Thaliana
OTHER INFORMATION: Sequence located in LFW1 at 79-88 and may interact with
US-09-572-270A-891

Query Match 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 1111

Db 3 ARAL 6

RESULT 8
US-09-572-270A-893
Sequence 893, Application US/09572270A
Publication No. US20030148366A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Inter-complementary peptide listing
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/572,270A
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 1144
SOFTWARE: ProPatent version 1.0
SEQ ID NO 893
LENGTH: 10
TYPE: PRT
ORGANISM: Arabidopsis Thaliana
OTHER INFORMATION: Sequence located in LFW1 at 78-87 and may interact with
US-09-572-270A-893

Query Match 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 4 ARAL 7

RESULT 9
US-10-239-313A-480
Sequence 480, Application US/10239313A
Publication No. US20030175285A1
GENERAL INFORMATION:
APPLICANT: KLINGUER - HAMOUR, Christine
APPLICANT: CORVAIA, Nathalie
APPLICANT: BECK, Alain
APPLICANT: GOETSCH, Liliane
TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
FILE REFERENCE: 343 727 - US
CURRENT APPLICATION NUMBER: US/10/239,313A
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: FR 00/03711
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT 01/70772
PRIOR FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 697
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 480
LENGTH: 10
TYPE: PRT
ORGANISM: Mus musculus
US-10-239-313A-480

Query Match 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 3 ARAL 6

RESULT 10
US-09-810-385-26
Sequence 26, Application US/09810385
Patent No. US20020137662A1
GENERAL INFORMATION:
APPLICANT: Laughon, Allen

```

? TITLE OF INVENTION: COMPOSITIONS AND MEHS FOR NEGATIVE REGULATION OF TGF-BETA PATH
? FILE REFERENCE: WARF-0002
? CURRENT APPLICATION NUMBER: US/09/810.385
? PRIOR FILING DATE: 2001-03-16
? NUMBER OF SEQ ID NOS: 40
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 26
? LENGTH: 12
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Shc peptide.
US-09-810 385-26

Query Match          36.4%  Score 4: 10 10 Length 12;
Best Local Similarity 100.0%  Prod. No. 4.4e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 9 AKPK 12

RESULT 11:
US-10-050-200-59
? Sequence 59, Application US/10050200
? Publication No. US20030166037A1
? GENERAL INFORMATION:
? APPLICANT: Colles, Fawn
? APPLICANT: Karlsson, Lars
? TITLE OF INVENTION: Aggrecaasone-1 and 2 Peptide Substrates and Methods
? FILE REFERENCE: ORT-1417
? CURRENT APPLICATION NUMBER: US/10/950.200
? CURRENT FILING DATE: 2002-01-16
? NUMBER OF SEQ ID NOS: 60
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 59
? LENGTH: 12
? TYPE: PRT
? ORGANISM: artificial sequence
? FEATURE:
? OTHER INFORMATION: peptide substrate.
US-10-050 200-59

Query Match          36.4%  Score 4: 05 02 Length 12;
Best Local Similarity 100.0%  Prod. No. 4.4e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
DB 8 RALN 11

RESULT 12:
US-09-753-126-85
? Sequence 85, Application US/09753126
? Patent No. US20020127219A1
? GENERAL INFORMATION:
? APPLICANT: OKRELS, JENS SIGURD
? APPLICANT: JENSEN, ANNE DAM
? APPLICANT: BAKKIER, TORBEN
? APPLICANT: JENSEN, RIKKE BOLDING
? TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMS AND LYSOSOMAL ENZYME
? TITLE OF INVENTION: ACTIVATORS
? FILE REFERENCE: 31-00060005
? CURRENT APPLICATION NUMBER: US/09/753.126
? CURRENT FILING DATE: 2001-06-11
? PRIOR FILING DATE: 1999-12-10
? PRIOR APPLICATION NUMBER: PA 1999 0189
? PRIOR FILING DATE: 1999-12-10
? PRIOR APPLICATION NUMBER: 60/174,512
? PRIOR FILING DATE: 2000-01-06
? PRIOR APPLICATION NUMBER: PA 200 03905

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? PRIOR FILING DATE: 2000-06-02
? PRIOR APPLICATION NUMBER: 60/210.984
? PRIOR FILING DATE: 2000-06-12
? PRIOR APPLICATION NUMBER: 60/211.124
? PRIOR FILING DATE: 2000-06-12
? PRIOR APPLICATION NUMBER: PA 2000 01027
? PRIOR FILING DATE: 2000-06-30
? PRIOR APPLICATION NUMBER: 60/217.497
? PRIOR FILING DATE: 2000-07-11
? NUMBER OF SEQ ID NOS: 147
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 85
? LENGTH: 13
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
? OTHER INFORMATION: peptide
US-09-753-126-85

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Query Match          36.4%  Score 4: DB 10 Length 13;
Best Local Similarity 100.0%  Prod. No. 4.6e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 ALNW 6
DB 1 ALNW 4

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RESULT 13:
US-09-896-896A-49
? Sequence 49, Application US/09896896A
? Publication No. US20030016181A1
? GENERAL INFORMATION:
? APPLICANT: MAXIGEN APS
? TITLE OF INVENTION: PEPTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES
? FILE REFERENCE: 0217us210
? CURRENT APPLICATION NUMBER: US/09/896.896A
? CURRENT FILING DATE: 2001-06-29
? PRIOR APPLICATION NUMBER: US 60/217.497
? PRIOR FILING DATE: 2000-07-11
? PRIOR APPLICATION NUMBER: US 60/225.558
? PRIOR FILING DATE: 2000-08-16
? PRIOR APPLICATION NUMBER: PK PA 2000 01027
? PRIOR FILING DATE: 2000-06-10
? PRIOR APPLICATION NUMBER: PK PA 2000 01092
? PRIOR FILING DATE: 2000-07-14
? PRIOR APPLICATION NUMBER: PCT/DK00/00743
? PRIOR FILING DATE: 2000-12-29
? PRIOR APPLICATION NUMBER: PCT/DK01/00090
? PRIOR FILING DATE: 2001-02-09
? NUMBER OF SEQ ID NOS: 123
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 49
? LENGTH: 13
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
? OTHER INFORMATION: peptide
US-09-896-896A-49

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```

Query Match          36.4%  Score 4: DB 11 Length 13;
Best Local Similarity 100.0%  Prod. No. 4.6e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 ALNW 6
DB 1 ALNW 4

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RESULT 14:
US-10-020-661A-2

```



```

1 Sequence 20, Application US/10d27961A
2 Publication No. US2003032796A1
3 GENERAL INFORMATION:
4 APPLICANT: MCNEILL, GARY P.
5 APPLICANT: MCNEILL, JOSEPH A.
6 TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
7 CYCLOOXYGENASE 2
8 FILE REFERENCE: 19029PCADA
9 CURRENT APPLICATION NUMBER: US/10/027,061A
10 CURRENT FILING DATE: 2001-10-25
11 PRIOR APPLICATION NUMBER: 09/599,781
12 PRIOR FILING DATE: 2000-06-21
13 PRIOR APPLICATION NUMBER: 08/930,559
14 PRIOR FILING DATE: 1996-02-22
15 PRIOR APPLICATION NUMBER: PCT/CA94/00501
16 PRIOR FILING DATE: 1999-09-13
17 PRIOR APPLICATION NUMBER: 08/084,039
18 PRIOR FILING DATE: 1993-05-27
19 PRIOR APPLICATION NUMBER: 08/064,271
20 PRIOR FILING DATE: 1993-05-06
21 PRIOR APPLICATION NUMBER: 07/994,750
22 PRIOR FILING DATE: 1992-12-22
23 NUMBER OF SEQ ID NOS: 23
24 SOFTWARE: FASTSEQ for Windows Version 4.0
25 SEQ ID NO 20
26 LENGTH: 13
27 TYPE: PRI
28 ORGANISM: Human
29 US-10-027 961A-20

```

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Query Match: 36.4%, Score 4, DB 13, Length 13
Best Local Similarity: 100.0%, Pred. No. 4, 6e+02
Matches 4: Conservative 0; Mismatches 0; Gaps 0;

CY 1 AKPK 4
DB 3 AKPK 6

RESULT 15
US-10-229 967 47
1 Sequence 37, Application US/10d27967
2 Publication No. US20030092080A1
3 GENERAL INFORMATION:
4 APPLICANT: Braden, Jonathan
5 APPLICANT: Cahavy, Ofir
6 TITLE OF INVENTION: Diagonosis, Prevention and Treatment of
7 Infectious Diseases and Fungal Subtypes Thereof, Using
8 Microbial Lipid Analysis
9 NUMBER OF SEQUENCES: 47
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Campbell, N. Nathan
12 STREET: 4370 La Jolla Village Drive, Suite 200
13 CITY: San Diego
14 STATE: California
15 COUNTRY: USA
16 ZIP: 92122
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: FLOPPY DISK
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC DOS/MS DOS
21 SOFTWARE: Patent Release #10, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/10/229,967
24 FILING DATE: 27-Aug-2002
25 CLASSIFICATION: <Unknown>
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US/09/417,294
28 FILING DATE: <Unknown>
29 APPLICATION NUMBER: US 09/841,859
30 FILING DATE: <Unknown>
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Campbell, Cathryn A.

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1 REGISTRATION NUMBER: 41,815
2 REFERENCE/DOCKET NUMBER: P-PM 3006
3 TELECOMMUNICATION INFORMATION:
4 TELEPHONE: (619) 535-9001
5 TELEFAX: (619) 535-8949
6 INFORMATION FOR SEQ ID NO: 37:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 13 amino acids
9 TOPOLOGY: linear
10 MOLECULE TYPE: Peptide
11 SEQUENCE DESCRIPTION: SEQ ID NO: 37:
12 US-10 229-567-37

```

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Query Match: 36.4%, Score 4, DB 15, Length 13
Best Local Similarity: 100.0%, Pred. No. 4, 6e+02
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 8 AKPK 11
DB 10 AKPK 13

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RESULT 16
US-10-024-123-13
1 Sequence 13, Application US/10d24123
2 Publication No. US2003022263A1
3 GENERAL INFORMATION:
4 APPLICANT: Kastan, Michael
5 APPLICANT: Canman, Christine
6 APPLICANT: Kim, Seong-fae
7 APPLICANT: Lim, Dao-Suk
8 APPLICANT: St. Jude Children's Research Hospital
9 TITLE OF INVENTION: ATM Kinase Modulation for Screening and
10 TITLE OF INVENTION: Therapies
11 FILE REFERENCE: 2427/1F142
12 CURRENT APPLICATION NUMBER: US/10/024,123
13 CURRENT FILING DATE: 2001-12-17
14 PRIOR APPLICATION NUMBER: 09/400,653
15 PRIOR FILING DATE: 1999-09-21
16 PRIOR APPLICATION NUMBER: 09/448,061
17 PRIOR FILING DATE: 1999-02-10
18 NUMBER OF SEQ ID NOS: 49
19 SOFTWARE: FASTSEQ for Windows Version 3.0
20 SEQ ID NO 13
21 LENGTH: 14
22 TYPE: PRI
23 ORGANISM: Homo Sapiens
24 US 10-024-123 13

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Query Match: 36.4%, Score 4, DB 15, Length 14
Best Local Similarity: 100.0%, Pred. No. 4, 9e+02
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CY 1 AKAL 4
DB 2 AKAL 5

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RESULT 17
US 09-873-409-17
1 Sequence 17, Application US/09873409
2 Patent No. US20020037522A1
3 GENERAL INFORMATION:
4 APPLICANT: Frank, Markus
5 APPLICANT: Sayegh, Mohamed
6 TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
7 TITLE OF INVENTION: Homologue on Chromosome 7p13-21 and Uses Thereof
8 FILE REFERENCE: 81934/268611
9 CURRENT APPLICATION NUMBER: US/09/873,409
10 CURRENT FILING DATE: 2001-06-05
11 NUMBER OF SEQ ID NOS: 19
12 SOFTWARE: Patentin version 3.0

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: SEQ ID NO 17
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-873-439-17

Query Match          36.4%   Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 5,2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
   1111
Lb 12 ARAL 15

RESULT 18
US-10-268-561-16
: Sequence 16, Application US/10268561
: Publication No. US20030148333A1
: GENERAL INFORMATION:
: APPLICANT: Ortho-Clinical Diagnostics, Inc.
: TITLE OF INVENTION: HCV Anti-Core Monoclonal Antibodies
: FILE REFERENCE: CDS0286
: CURRENT APPLICATION NUMBER: US/10/268,561
: CURRENT FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: US 60/337453
: PRIOR FILING DATE: 2001-11-05
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 16
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Hepatitis C virus
US-10-268-561-16

Query Match          36.4%   Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 5,2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
   1111
Lb 3 ARAL 5

RESULT 19
US-10-268-569-16
: Sequence 16, Application US/10268569
: Publication No. US20030152965A1
: GENERAL INFORMATION:
: APPLICANT: Ortho-Clinical Diagnostics, Inc.
: TITLE OF INVENTION: HCV Core Protein Sequences
: FILE REFERENCE: CDS-0288
: CURRENT APPLICATION NUMBER: US/10/268,569
: CURRENT FILING DATE: 2002-10-10
: PRIOR APPLICATION NUMBER: 60/347,303
: PRIOR FILING DATE: 2001-11-11
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 16
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Hepatitis C virus
US-10-268-569-16

Query Match          36.4%   Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 5,2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
   1111
Lb 3 ARAL 5

RESULT 20
US-10-014-322A-11
: Sequence 11, Application US/10014322A
: Publication No. US20030167129A1
: GENERAL INFORMATION:
: APPLICANT: Nestor, Jr., John
: APPLICANT: Wilson, Carol
: APPLICANT: Tan Behr, Christina
: APPLICANT: Kates, Steven
: APPLICANT: Krstenansky, John
: TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compou
: FILE REFERENCE: CNS-008
: CURRENT APPLICATION NUMBER: US/10/014,322A
: CURRENT FILING DATE: 2002-07-08
: PRIOR APPLICATION NUMBER: US 60/243,587
: PRIOR FILING DATE: 2000-10-27
: PRIOR APPLICATION NUMBER: US 09/813,651
: PRIOR FILING DATE: 2001-03-20
: PRIOR APPLICATION NUMBER: US 09/813,653
: PRIOR FILING DATE: 2001-03-20
: PRIOR APPLICATION NUMBER: US 09/813,448
: PRIOR FILING DATE: 2001-03-20
: NUMBER OF SEQ ID NOS: 126
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 11
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: CXCK4 binding peptide
US-10-014-322A-11

Query Match          36.4%   Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 5,2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
   1111
Lb 2 ARAL 5

RESULT 21
US-10-174-105A-94
: Sequence 94, Application US/10174105A
: Publication No. US2003008652A1
: GENERAL INFORMATION:
: APPLICANT: Cell Signaling Technology, Inc.
: APPLICANT: ZHANG, Hui
: APPLICANT: COMB, Michael, Jr.
: APPLICANT: TAN, Yi
: TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPBC
: FILE REFERENCE: CSI-138 CIP3
: CURRENT APPLICATION NUMBER: US/10/174,105A
: CURRENT FILING DATE: 2002-06-18
: PRIOR APPLICATION NUMBER: US 04/148,712
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: US 09/535,364
: PRIOR FILING DATE: 2000-03-24
: NUMBER OF SEQ ID NOS: 193
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 94
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Peptide
: NAME/KEY: MOD-RES
: LOCATION: (8)...(8)
: OTHER INFORMATION: PHOSPHORYLATION; threonine at position 8 is phosphorylated
US-10-174-105A-94

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Query Match          36.4% Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WQAK 9
      1111
Db      10 WQAK 13

RESULT 24
US-10-174-105A-95
: Sequence 95, Application US/10174.105A
: Publication No. US2003006852A1
: GENERAL INFORMATION:
: APPLICANT: Cell Signaling Technology, Inc.
: APPLICANT: ZHANG, Hui
: APPLICANT: COMB, Michael J.
: APPLICANT: TAN, Yi
: TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC
: TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
: FILE REFERENCE: CST-138 CIP3
: CURRENT APPLICATION NUMBER: US/10/174.105A
: CURRENT FILING DATE: 2002-06-18
: PRIOR APPLICATION NUMBER: US 09/148.712
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: US 09/535.564
: PRIOR FILING DATE: 2000-03-24
: NUMBER OF SEQ ID NOS: 193
: SOFTWARE: Patent in version 3.1
: SEQ ID NO 95
: LENGTH: 15
: TYPE: PRI
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Replid.
US-10-174-105A-95

Query Match          36.4% Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WQAK 9
      1111
Db      10 WQAK 13

RESULT 24
US-10-229-567-16
: Sequence 15, Application US/10229.567
: Publication No. US2003009298A1
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Cohavy, Ofer
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: TITLE OF INVENTION: Microbial UC PANCA antigens
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/229.567
: FILING DATE: 27-Aug-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/417.264
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US 09/041.889
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31.815
: REFERENCE/DOCKET NUMBER: P-PM 3006
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear

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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/417.264
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US 09/041.889
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31.815
: REFERENCE/DOCKET NUMBER: P-PM 3006
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-229-567-15

Query Match          36.4% Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 AKPK 11
      1111
Db      12 AKPK 15

RESULT 24
US-10-229-567-16
: Sequence 16, Application US/10229.567
: Publication No. US2003009298A1
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Cohavy, Ofer
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: TITLE OF INVENTION: Microbial UC PANCA antigens
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/229.567
: FILING DATE: 27-Aug-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/417.264
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US 09/041.889
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31.815
: REFERENCE/DOCKET NUMBER: P-PM 3006
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear

```

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; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-229-567-16
Query Match 36.4%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 2 AKPK 5

RESULT 25
US-10-229-567-22
; Sequence 22, Application US/10229567
; Publication No. US20030092080A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; Cohavy, Offer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/229,567
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,264
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 09/041,889
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-229-567-24
Query Match 36.4%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 4 AKPK 7

RESULT 27
US-10-229-567-35
; Sequence 35, Application US/10229567
; Publication No. US20030092080A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; Cohavy, Offer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; Microbial UC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/229,567
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/417,264
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 09/041,889
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PM 3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-229-567-22
Query Match 36.4%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 6 AKPK 9

RESULT 26
US-10-229-567-24
; Sequence 24, Application US/10229567
; Publication No. US20030092080A1
; GENERAL INFORMATION:

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,567
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/417,264
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-28 4006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US 10-229-567-35

Query Match 36.4%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AKPK 11
DB 12 AKPK 15

RESULT 24
US 10-229-567-35
Sequence 16, Application US/10/229,567
Publication No. US2003009280A1
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
Colavy, Olier
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
Glucagon Receptor and Clinical Subtypes Incretin Using
Microbial or PAN-7 antibody
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Edwards LLP
STREET: 4470 La Jolla Village Drive Suite 200
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,567
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/417,264
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-28 4006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US 10-229-567-36

Query Match 36.4%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 2 AKPK 5

RESULT 29
US 10-103-327-2
Sequence 2, Application US/10103327
Publication No. US20030106095A1
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPS06
CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 15
TYPE: PKT
ORGANISM: Homo sapiens
US 10-103-327-2

Query Match 36.4%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 5 ARAL 8

RESULT 30
US 09-756-283A 51
Sequence 51, Application US/09756283A
Patent No. US20020151478A1
GENERAL INFORMATION:
APPLICANT: Chernajovsky, Yuri
APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
TITLE OF INVENTION: Latent Fusion Protein
FILE REFERENCE: 0623.100000
CURRENT APPLICATION NUMBER: US/09/756,283A
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 51
LENGTH: 8
TYPE: PKT
ORGANISM: Rattus sp.
US 09-756-283A-51

Query Match 27.4%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;

```
Matches 3: Conservative 27 Mismatches 0 Indels 0 Gaps 0
QY 7 GAK 9
   III
DB 1 GAK 3

RESULT 31
US-09-778-200-3
Sequence 3, Application US/09/778200
Patent No. US20020160471A1
GENERAL INFORMATION:
APPLICANT: Kisdav, John
APPLICANT: Grodzinsky, Alan
APPLICANT: Zhang, Shuquan
TITLE OF INVENTION: Peptide Scaffold Encapsulation of Tissue
FILE REFERENCE: 01997/537001
CURRENT APPLICATION NUMBER: US/09/778,200
CURRENT FILING DATE: 2000-02-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Designed Peptide
US-09-778-200-3

Query Match 27.3% Score 3: DB 10: Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 1 ARA 3
   III
DB 4 ARA 6

RESULT 34
US-09-910-552-43
Sequence 43, Application US/09/910552
Publication No. US20020197260A1
GENERAL INFORMATION:
APPLICANT: Grubisic, Dan M.
APPLICANT: Mac, Gregory R.
TITLE OF INVENTION: USE OF FUNCTIONAL ANTIBODIES THAT DEFINE UNIQUE
FILE REFERENCE: 1249.002
CURRENT APPLICATION NUMBER: US/09/910,552
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/494,822
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 68
SOFTWARE: Patentic Ver. 2.0
SEQ ID NO 43
LENGTH: 8
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sequence from
US-09-910-552-43

Query Match 27.3% Score 3: DB 10: Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 3 ALN 5
   III
DB 5 ALN 7

RESULT 35
US-09-726-470A-68
Sequence 68, Application US/09/726470A
Publication No. US20030046628A1
GENERAL INFORMATION:
APPLICANT: Zheleva, Daniela I
APPLICANT: Fischer, Peter M
APPLICANT: McInnes, Campbell
```

APPLICANT: Andrews, Martin JI
APPLICANT: Chan, Weng C
APPLICANT: Atkinson, Gail E
TITLE OF INVENTION: p21 Peptides
FILE REFERENCE: CCI-014
CURRENT APPLICATION NUMBER: US/09/726.470A
CURRENT FILING DATE: 2000-11-24
PRIORITY APPLICATION NUMBER: GB 992812A.1
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 275
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 68
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: p21 derived
OTHER INFORMATION: peptide
FEATURE:
OTHER INFORMATION: Synthesised with free amino terminus and as the
OTHER INFORMATION: C-terminal carboxamide
US-09-726-470A-68

Query Match 27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPK 4
DB 4 KPK 6

RESULT 36
US-09-726-470A-125
Sequence 125, Application US/09/726.470A
Publication No. US20030036628A1
GENERAL INFORMATION:
APPLICANT: Zheleva, Daniela
APPLICANT: Fischer, Peter M
APPLICANT: McInnes, Campbell
APPLICANT: Andrews, Martin JI
APPLICANT: Chan, Weng C
APPLICANT: Atkinson, Gail E
TITLE OF INVENTION: p21 Peptides
FILE REFERENCE: CCI-014
CURRENT APPLICATION NUMBER: US/09/726.470A
CURRENT FILING DATE: 2000-11-24
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 275
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 125
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: p21 derived
OTHER INFORMATION: peptide
FEATURE:
OTHER INFORMATION: Synthesised with free amino ter. as and as the
OTHER INFORMATION: C-terminal carboxamide
FEATURE:
NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: p-Fluorophenylalanine
US-09-726-470A-125

Query Match 27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 11

DB 1 GAK 3

RESULT 37

US-09-876-904A-57
Sequence 57, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: IB-2002-00
CURRENT APPLICATION NUMBER: US/09/876.904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/216,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 624
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Chicken ELs1
OTHER INFORMATION: Core NLS peptide
US-09-876-904A-57

Query Match 27.4%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 6 KPK 8

RESULT 38

US-09-876-904A-537
Sequence 537, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: IB-2002-00
CURRENT APPLICATION NUMBER: US/09/876.904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/216,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 537
LENGTH: 8
TYPE: PRT
ORGANISM: Xenopus laevis
FEATURE:
OTHER INFORMATION: Xenopus laevis t1 ribosomal protein (homologous to
OTHER INFORMATION: yeast L2).

Query Match 27.4%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 2 KPK 4

RESULT 39

US-10-079-167-4

```
: Sequence 4, Application US/10079167
: Publication No. US20030138454A1
: GENERAL INFORMATION:
: APPLICANT: Hill, Adrian V.S.
: APPLICANT: McShane, Helen
: APPLICANT: Gilbert, Sarah C.
: APPLICANT: Reece, William
: APPLICANT: Schneider, Joerg
: TITLE OF INVENTION: Vaccination Method
: CURRENT APPLICATION NUMBER: US/10/079,167
: PRIOR FILING DATE: 2002-02-19
: PRIOR FILING DATE: 2002-02-19
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: US 09/454,204
: PRIOR FILING DATE: 1999-12-09
: PRIOR APPLICATION NUMBER: PCT/GB98/0,681
: PRIOR FILING DATE: 1998-06-09
: PRIOR APPLICATION NUMBER: GB 97 11957.2
: PRIOR FILING DATE: 1997-06-09
: PRIOR APPLICATION NUMBER: PCT/GB01/04116
: PRIOR FILING DATE: 2001-09-13
: PRIOR APPLICATION NUMBER: GB 00 24203.3
: PRIOR FILING DATE: 2001-09-21
: NUMBER OF SEQ ID NOS: 99
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: CTL Epitope of the Malaria String
US 10-079-167-4

Query Match      27.3%   Score 3:   DB 12:   Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches      3:   Conservative      0:   Mismatches      0:   Indels      0:   Gaps      0:

QY      9 KPK 11
DB      1 KPK 3

RESULT 40
US-10-350-258-2
: Sequence 2, Application US/10350258
: Publication No. US20030139345A1
: GENERAL INFORMATION:
: APPLICANT: MATTHIAS RATH
: TITLE OF INVENTION: SYNTHETIC PEPTIDES AND METHODS FOR TREATING CANCER INVASION AND METASTASIS
: FILE REFERENCE: 11957/23
: CURRENT APPLICATION NUMBER: US/10/350,258
: PRIOR FILING DATE: 2003-01-22
: PRIOR APPLICATION NUMBER: 60/351,317
: PRIOR FILING DATE: January 23, 2002
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-350-258-2

Query Match      27.3%   Score 4:   DB 12:   Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches      3:   Conservative      0:   Mismatches      0:   Indels      0:   Gaps      0:

QY      9 KPK 11
DB      3 KPK 5

RESULT 41
US-10-209-167A-4
: Sequence 4, Application US/10209187A
: Publication No. US20030148383A1
: GENERAL INFORMATION:
: APPLICANT: Maurer-Stroh, Sebastian
: APPLICANT: Eisenhaber, Birgit
: APPLICANT: Eisenhaber, Frank
: TITLE OF INVENTION: Methods for Identifying Proteins with N-Terminal N-Myristoyle
: FILE REFERENCE: 0652.2560000
: CURRENT APPLICATION NUMBER: US/10/209,187A
: CURRENT FILING DATE: 2002-08-01
: PRIOR APPLICATION NUMBER: EP 01 118 627.7
: PRIOR FILING DATE: 2001-08-02
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Synthetic octapeptide
US-10-209-187A-5

Query Match      27.3%   Score 3:   DB 12:   Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches      3:   Conservative      0:   Mismatches      0:   Indels      0:   Gaps      0:

QY      9 KPK 11
DB      6 KPK 8

RESULT 42
US-10-209-187A-5
: Sequence 5, Application US/10209187A
: Publication No. US20030148383A1
: GENERAL INFORMATION:
: APPLICANT: Maurer-Stroh, Sebastian
: APPLICANT: Eisenhaber, Birgit
: APPLICANT: Eisenhaber, Frank
: TITLE OF INVENTION: Methods for Identifying Proteins with N-Terminal N-Myristoyle
: FILE REFERENCE: 0652.2560000
: CURRENT APPLICATION NUMBER: US/10/209,187A
: CURRENT FILING DATE: 2002-08-01
: PRIOR APPLICATION NUMBER: EP 01 118 627.7
: PRIOR FILING DATE: 2001-08-02
: NUMBER OF SEQ ID NOS: 22
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 5
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Synthetic octapeptide
US-10-209-187A-5

Query Match      27.3%   Score 3:   DB 12:   Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches      3:   Conservative      0:   Mismatches      0:   Indels      0:   Gaps      0:

QY      1 ARA 3
DB      2 ARA 4

RESULT 43
US-10-283-423-51
: Sequence 51, Application US/10283423
: Publication No. US20030162223A1
: GENERAL INFORMATION:
: APPLICANT: Lowery, David F.
: APPLICANT: Smith, Vaidin G.
: APPLICANT: Kubiak, Teresa M.
: APPLICANT: Larsen, Martha J.
: TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Me
```



```

: TITLE OF INVENTION: Related To The Same
: FILE REFERENCE: PHRM0002-102
: Application Project
:
: CURRENT APPLICATION NUMBER: US/10/283,423
: CURRENT FILING DATE: 2002-10-30
: Earlier Applications
:
: PRIOR APPLICATION NUMBER: PriorAppNumber: 10/099,746
: PRIOR FILING DATE: PriorFilingDate: 2000-10-20
: PRIOR APPLICATION NUMBER: PriorAppNumber: 10/142,675
: PRIOR FILING DATE: PriorFilingDate: 1999-10-22
: NUMBER OF SEQ ID NOS: 187
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 51
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: No. US20030162223A1; Sequence
US 10-283-423 5;

Query Match          27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 2 GAK 4

RESULT 44
US-10-283-423-80
: Sequence 80, Application US/10/283423
: Publication No. US20030162223A1
: GENERAL INFORMATION:
: APPLICANT: Lowery, David E.
: APPLICANT: Smith, Valdin G.
: APPLICANT: Kubiak, Teresa M.
: APPLICANT: Larsen, Martha J.
: TITLE OF INVENTION: Drosophila G Protein-Coupled Receptors, Nucleic Acids, And Method
: TITLE OF INVENTION: Related To The Same
: FILE REFERENCE: PHRM0002-102
: Application Project
:
: CURRENT APPLICATION NUMBER: US/10/283,423
: CURRENT FILING DATE: 2002-10-30
: Earlier Applications
:
: PRIOR APPLICATION NUMBER: PriorAppNumber: 10/099,746
: PRIOR FILING DATE: PriorFilingDate: 2000-10-20
: PRIOR APPLICATION NUMBER: PriorAppNumber: 10/142,675
: PRIOR FILING DATE: PriorFilingDate: 1999-10-22
: NUMBER OF SEQ ID NOS: 187
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 80
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: No. US20030162223A1; Sequence
US 10-283-423-80

Query Match          27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 2 GAK 4

RESULT 45
US-10-283-423-80
: Sequence 80, Application US/10/283423
: Publication No. US20030162223A1
: GENERAL INFORMATION:
: APPLICANT: Lowery, David E.
: APPLICANT: Smith, Valdin G.
: APPLICANT: Kubiak, Teresa M.
: APPLICANT: Larsen, Martha J.
: TITLE OF INVENTION: Drosophila G Protein-Coupled Receptors, Nucleic Acids, And Method
: TITLE OF INVENTION: Related To The Same
: FILE REFERENCE: PHRM0002-102
: Application Project
:
: CURRENT APPLICATION NUMBER: US/10/283,423
: CURRENT FILING DATE: 2002-10-30
: Earlier Applications
:
: PRIOR APPLICATION NUMBER: PriorAppNumber: 10/099,746
: PRIOR FILING DATE: PriorFilingDate: 2000-10-20
: PRIOR APPLICATION NUMBER: PriorAppNumber: 10/142,675
: PRIOR FILING DATE: PriorFilingDate: 1999-10-22
: NUMBER OF SEQ ID NOS: 187
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 80
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: No. US20030162223A1; Sequence
US 10-283-423-80

Query Match          27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 2 GAK 4

RESULT 46
US-10-224-999A-1325
: Sequence 1325, Application US/10224999A
: Publication No. US20030171318A1
: GENERAL INFORMATION:
: APPLICANT: Myriad Genetics, Inc.
: APPLICANT: Morham, Scott
: APPLICANT: Zavitz, Kenton
: APPLICANT: Hobden, Adrian
: TITLE OF INVENTION: Composition and Method for Treating Viral Infection
: FILE REFERENCE: 5004.01
: CURRENT APPLICATION NUMBER: US/10/224,999A
: CURRENT FILING DATE: 2003-03-03
: PRIOR APPLICATION NUMBER: US 60/313,695
: PRIOR FILING DATE: 2001-08-20
: NUMBER OF SEQ ID NOS: 3484
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1325
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Human papillomaviruses
US-10-224-999A 1325

Query Match          27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 6 KPK 6

RESULT 47
US-10-224-999A-1326
: Sequence 1326, Application US/10224999A
: Publication No. US20030171318A1
: GENERAL INFORMATION:
: APPLICANT: Myriad Genetics, Inc.
: APPLICANT: Morham, Scott
: APPLICANT: Zavitz, Kenton
: APPLICANT: Hobden, Adrian
: TITLE OF INVENTION: Composition and Method for Treating Viral Infection
: FILE REFERENCE: 5004.01
```

; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1326
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-224-999A-1326

Query Match 27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 5 KPK 7

RESULT 48
US-10-293-580-41
; Sequence 41, Application US/10/293580
; Publication No. US20030170767A1
; GENERAL INFORMATION:
; APPLICANT: Aurora Biosciences Corporation
; TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
; FILE REFERENCE: AU01270 (08366/G31001)
; CURRENT APPLICATION NUMBER: US/10/293,580
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/129,192
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Adenovirus endoproteidase
US-10-293-580-41

Query Match 27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 4 GAK 5

RESULT 49
US-10-192-832-3
; Sequence 3, Application US/10192832
; Publication No. US20030176335A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, SHUGUANG
; APPLICANT: VAUTHEY, SYLVAIN
; TITLE OF INVENTION: SURFACTANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF
; FILE REFERENCE: MTV-043.01
; CURRENT APPLICATION NUMBER: US/10/192,832
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,256
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-192-832-3

Query Match 27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
DB 4 ARA 6

RESULT 50
US-10-192-832-5
; Sequence 5, Application US/10192832
; Publication No. US20030176335A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, SHUGUANG
; APPLICANT: VAUTHEY, SYLVAIN
; TITLE OF INVENTION: SURFACTANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF
; FILE REFERENCE: MTV-043.01
; CURRENT APPLICATION NUMBER: US/10/192,832
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,256
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-192-832-5

Query Match 27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
DB 2 ARA 4

Search completed: September 30, 2003, 10:32:54
Job time : 24.5 secs

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OR protein - protein search, using sw model

Run on: September 30, 2003, 13:07:04 : Search time 11.333 Seconds
(without alignment)
50.440 Million cell updates/sec

Title: US-09-787-443-4

Perfect score: 11

Sequence: 1 AGSAVKLKKA 11

Scoring table:

OLIGO Gapop 60.0, Gapext 65.0

Searched: 283308 seqs, 9616082 residues

Word size: 6

Total number of hits satisfying chosen parameters: 2064

Minimum OR seq length: 8

Maximum OR seq length: 15

Post-processing: listing first 500 summaries

Database:

PIR-76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB	IL	Description
1	4	36.4	9	2	A11576	xylose isomerase (
2	4	36.4	13	2	B64124	hypothetical prote
3	4	36.4	13	2	S61904	glucanase
4	4	36.4	14	2	S14864	methyl xanthine M
5	3	27.3	8	2	S14934	apolipoprotein A-I
6	3	27.3	9	2	S15439	gene NF2 protein -
7	3	27.3	9	2	PT0225	14 heavy chain CLK
8	3	27.3	9	2	PT0225	spectrin alpha cha
9	3	27.3	11	2	A44255	26kDa-hydroxyste
10	3	27.3	11	2	S33519	probable secreted
11	3	27.3	11	2	S33519	gallbladder stone
12	3	27.3	11	2	PH0941	T-cell receptor be
13	3	27.3	11	2	PH0941	dextranase (EC
14	3	27.3	12	2	S58502	58K bile acid sulb
15	3	27.3	13	2	S78519	ribosomal protein
16	3	27.3	13	2	S48210	collagen alpha 1(V
17	3	27.3	13	2	S32478	lysozyme
18	3	27.3	14	2	PA0109	porin por 1B - Aa
19	3	27.3	14	2	B34135	DNA binding protei
20	3	27.3	14	2	S14335	mastoparan B - hor
21	3	27.3	14	2	A47421	leukotriene B-4 12
22	3	27.3	14	2	PH0800	T-cell receptor al
23	3	27.3	14	2	PH0800	T-cell receptor al
24	3	27.3	14	4	S00843	hypothetical prote
25	3	27.3	15	2	S21240	alpha-glucosidase
26	3	27.3	15	2	PH0116	hemoglobin beta ch
27	3	27.3	15	2	PH0117	hemoglobin alpha c
28	3	27.3	15	2	S36896	ribosomal protein
29	3	27.3	15	2	S14749	1-nucleotidylase

T-cell receptor al	27.3	3	27.3	15	2	G41299
T-cell receptor al	27.3	3	27.3	15	2	PH0775
T-cell receptor al	27.3	3	27.3	15	2	PH0779
T-cell receptor al	27.3	3	27.3	15	2	PH1455
transcription fact	27.3	3	27.3	15	2	A49887
cytochrome P450-3b	27.3	3	27.3	15	2	S09073
complement factor	27.3	3	27.3	15	2	PL0110
probable msrA lead	27.3	3	27.3	15	2	LFAME
hypothetical prote	27.3	3	27.3	15	2	S37141
unidentified 4.5/4	27.3	3	27.3	15	2	S16324
leucokinin V - Mad	27.3	3	27.3	15	2	J50315
penicillin - Adell	27.3	3	27.3	15	2	A61467
Ig heavy chain CRD	27.3	3	27.3	15	2	PT0311
Ig heavy chain CRD	27.3	3	27.3	15	2	PT0323
T-cell receptor al	27.3	3	27.3	15	2	PH0803
T-cell receptor al	27.3	3	27.3	15	2	A35768
T-cell receptor be	27.3	3	27.3	15	2	PT0627
T-cell receptor be	27.3	3	27.3	15	2	PT0530
T-cell receptor be	27.3	3	27.3	15	2	PT0527
T-cell receptor be	27.3	3	27.3	15	2	PT0509
T-cell receptor be	27.3	3	27.3	15	2	PT0631
prealbumin - veste	27.3	3	27.3	15	2	I49404
cytochrome P450 AL	27.3	3	27.3	15	2	A61597
major postsynaptic	27.3	3	27.3	15	2	A42689
aspartate kinase (27.3	3	27.3	15	2	B47594
ubiquitin - celery	27.3	3	27.3	15	2	A61496
MHC class I histoc	27.3	3	27.3	15	2	A59028
citrate synthase -	27.3	3	27.3	15	2	S53008
thymic factor - pi	27.3	3	27.3	15	2	YFPG
locustamininhibiti	27.3	3	27.3	15	2	AKLQIM
thymocyte growth p	27.3	3	27.3	15	2	A60957
litorin 2-Glu - Au	27.3	3	27.3	15	2	S07205
litorin I - Austr	27.3	3	27.3	15	2	S07204
caldesmon - rabbit	27.3	3	27.3	15	2	A4873
vitamin D3 26-mono	27.3	3	27.3	15	2	S15850
cat gene leader pe	27.3	3	27.3	15	2	S30494
chloramphenicol O-	27.3	3	27.3	15	2	B24362
sperm-activating p	27.3	3	27.3	15	2	A60522
sperm-activating p	27.3	3	27.3	15	2	A60522
delta sleep-induci	27.3	3	27.3	15	2	QDRB
kidney and bladder	27.3	3	27.3	15	2	S58502
orf AB protein - S	27.3	3	27.3	15	2	S19523
dextranase (EC	27.3	3	27.3	15	2	B39841
sucrose 3-glucosyl	27.3	3	27.3	15	2	A49841
photosystem II pro	27.3	3	27.3	15	2	C41170
glycine cleavage s	27.3	3	27.3	15	2	S0253
endosperm protein,	27.3	3	27.3	15	2	S70332
hypothetical prote	27.3	3	27.3	15	2	T31612
neuropeptide Grb-A	27.3	3	27.3	15	2	D57444
caliifMRAamide 13	27.3	3	27.3	15	2	D44787
venom protein HR-3	27.3	3	27.3	15	2	S10920
[Phe-6]-mosact - s	27.3	3	27.3	15	2	JN0027
C-rel protein - ch	27.3	3	27.3	15	2	S10633
MHC class I histoc	27.3	3	27.3	15	2	JQ0914
118K stomach cance	27.3	3	27.3	15	2	A60356
Ig heavy chain CRD	27.3	3	27.3	15	2	PT0247
Ig heavy chain CRD	27.3	3	27.3	15	2	PT0326
macrophage chemota	27.3	3	27.3	15	2	A37027
macrophage cytotox	27.3	3	27.3	15	2	A60427
gastin - domestic	27.3	3	27.3	15	2	PC2197
alpha-2-macroglobu	27.3	3	27.3	15	2	C60070
alpha-adaptin - bo	27.3	3	27.3	15	2	S66636
collagen alpha 2(V	27.3	3	27.3	15	2	B46250
cytokeratin 4 - bo	27.3	3	27.3	15	2	S58865
enamelin i - bovin	27.3	3	27.3	15	2	I46016
Ig H chain V-D-J r	27.3	3	27.3	15	2	S10784
Ig heavy chain V r	27.3	3	27.3	15	2	PH1591
Ig kappa chain C r	27.3	3	27.3	15	2	S36850
T-cell receptor ga	27.3	3	27.3	15	2	B36740
translation elonga	27.3	3	27.3	15	2	G41946
unidentified 48.7K	27.3	3	27.3	15	2	PC7074
	27.3	3	27.3	15	2	PC7078

103	2	18.2	9	2	A33527	fructose-2,6 bisph	176	2	18.2	11	2	YHXAE	morphogenetic neur
104	2	18.2	9	2	I52974	seminal vesicle pr	177	2	18.2	11	2	YHJFYH	morphogenetic neur
105	2	18.2	9	2	B30572	T-cell receptor be	178	2	18.2	11	2	B26744	megascoliakinin -
106	2	18.2	9	2	S78426	5L 5K protein - sp	179	2	18.2	11	2	S42449	anti protein - pha
107	2	18.2	9	2	PC7073	uniquinol cytochro	180	2	18.2	11	2	A58502	38K kidney stone p
108	2	18.2	9	4	I73804	hypothetical E2 pr	181	2	18.2	11	2	F58501	43.5K bile stone p
109	2	18.2	10	1	EC125M	tachykinin 111 - m	182	2	18.2	11	2	JQ0395	hypothetical prote
110	2	18.2	10	2	S28055	cytochrome b559 co	183	2	18.2	11	2	S66606	quinoline 2-oxidor
111	2	18.2	10	2	C24947	unspecific monooxy	184	2	18.2	11	2	S58244	pyroloquinoline q
112	2	18.2	10	2	A43405	6-phosphofructo 2-	185	2	18.2	11	2	B43669	hypothetical prote
113	2	18.2	10	2	S24190	tryptase (EC 3.4.2	186	2	18.2	11	2	E41476	probable antigen 5
114	2	18.2	10	2	S33834	alpha-2-macroglobu	187	2	18.2	11	2	S70338	napin small chain
115	2	18.2	10	2	PC0177	neurexin C - bou	188	2	18.2	11	2	S19775	wound-induced prot
116	2	18.2	10	2	A60547	neurexin C - bov	189	2	18.2	11	2	A38590	transforming protei
117	2	18.2	10	2	I36893	apolipoprotein A-I	190	2	18.2	11	2	A34135	DNA-binding protei
118	2	18.2	10	2	C45474	thrombospondin 2 -	191	2	18.2	11	2	A61512	variant surface gl
119	2	18.2	10	2	C60787	sperm-activating p	192	2	18.2	11	2	S43626	cytochrome-C oxida
120	2	18.2	10	2	E60787	sperm-activating p	193	2	18.2	11	2	D42965	talin - chicken (f
121	2	18.2	10	2	E60584	sperm-activating p	194	2	18.2	11	2	S21727	gamma-interferon-1
122	2	18.2	10	2	H60586	gastric juice pept	195	2	18.2	11	2	PT0287	Ig heavy chain CRD
123	2	18.2	10	2	GKHU1	neurokinin A-relat	196	2	18.2	11	2	S57575	T-cell receptor V-
124	2	18.2	10	2	S27178	neurokinin A-relat	197	2	18.2	11	2	S51732	T-cell receptor al
125	2	18.2	10	2	B33143	pneumadin - human	198	2	18.2	11	2	A32428	amine oxidase (cop
126	2	18.2	10	2	A33143	pneumadin - rat	199	2	18.2	11	2	A61483	pyridoxal kinase (
127	2	18.2	10	2	A61617	ecdysteroid upfqlu	200	2	18.2	11	2	PD0442	NIPSNAP2 protein -
128	2	18.2	10	2	G58521	48K bile/gallbladg	201	2	18.2	11	2	PT0044	protein kinase C 1
129	2	18.2	10	2	A24457	amylin - Paraco	202	2	18.2	11	2	PT0209	T-cell receptor al
130	2	18.2	10	2	S06954	hypothetical prote	203	2	18.2	11	2	PD2118	T-cell receptor be
131	2	18.2	10	2	JF0072	ribosomal protein	204	2	18.2	11	2	D41946	T-cell receptor ga
132	2	18.2	10	2	C39745	sphingomyelinase -	205	2	18.2	11	2	B41946	T-cell receptor ga
133	2	18.2	10	2	S69159	cystathionine gamm	206	2	18.2	11	2	C38887	T-cell receptor ga
134	2	18.2	10	2	C38955	seed storage prote	207	2	18.2	11	2	I41946	T-cell receptor ga
135	2	18.2	10	2	S70336	napin small chain	208	2	18.2	11	2	A49037	T-cell receptor ga
136	2	18.2	10	2	S66248	processing enzyme,	209	2	18.2	11	2	B49037	TCR gamma V-J regi
137	2	18.2	10	2	I28027	protein p7 - curle	210	2	18.2	11	2	C49037	TCR gamma V-J regi
138	2	18.2	10	2	PT0038	glutathione transt	211	2	18.2	11	2	PD0441	translation elonga
139	2	18.2	10	2	C61440	polylacturonase	212	2	18.2	11	2	S65377	cytochrome-c oxida
140	2	18.2	10	2	E61512	variant surface gl	213	2	18.2	11	2	S09349	microtubule-associ
141	2	18.2	10	2	S19617	glutin - polychaet	214	2	18.2	11	2	S18385	NADP-cytochrome P4
142	2	18.2	10	2	S65728	hemoglobin, extrac	215	2	18.2	11	2	S78422	ribosomal protein
143	2	18.2	10	2	A58335	neuropeptide FRFA	216	2	18.2	11	2	PH0939	T-cell receptor be
144	2	18.2	10	2	B61708	hemocyanin subunit	217	2	18.2	11	2	PH0940	T-cell receptor be
145	2	18.2	10	2	A42085	transcription fact	218	2	18.2	11	2	PC2254	T-cell receptor be
146	2	18.2	10	2	C44787	calliferramide 12	219	2	18.2	11	2	A34243	cytochrome P450 3A
147	2	18.2	10	2	JNC025	mesact - sea urchi	220	2	18.2	11	2	H-phosphorin - Ja	
148	2	18.2	10	2	A24196	acetylcholinestera	221	2	18.2	11	2	H40082	hypothetical prote
149	2	18.2	10	2	S41946	cytochrome-c oxida	222	2	18.2	11	4	I52708	ELAV-like neuronal
150	2	18.2	10	2	PH1344	Ig heavy chain CRD	223	2	18.2	11	4	U06M2	retinoic acid rece
151	2	18.2	10	2	S24371	T-cell receptor al	224	2	18.2	12	1	A43975	urotensin II - lon
152	2	18.2	10	2	C10212	T-cell receptor ga	225	2	18.2	12	1	JTJG0	locustamyotrophin -
153	2	18.2	10	2	PH1344	glutathione, 22K - bo	226	2	18.2	12	2	A23169	tremorgen A-10 -
154	2	18.2	10	2	PH1344	T-cell receptor al	227	2	18.2	12	2	S11286	phospholipase A2 (
155	2	18.2	10	2	PH1344	T-cell receptor ga	228	2	18.2	12	2	S09082	exo-alpha-sialidas
156	2	18.2	10	2	A41946	T-cell receptor ga	229	2	18.2	12	2	C49215	protease chain 1
157	2	18.2	10	2	A41946	T-cell receptor ga	230	2	18.2	12	2	S25485	urease (EC 3.5.1.5
158	2	18.2	10	2	A41946	placental lactogen	231	2	18.2	12	2	S24765	transcription fact
159	2	18.2	10	2	A47364	cytochrome-c oxida	232	2	18.2	12	2	J50423	urotensin II - tel
160	2	18.2	10	2	S65387	lysosome-associate	233	2	18.2	12	2	S26541	urotensin II-A pep
161	2	18.2	10	2	PK0060	T-cell receptor be	234	2	18.2	12	2	S25056	T-cell receptor be
162	2	18.2	10	2	C30572	T-cell receptor be	235	2	18.2	12	2	S65409	Ig heavy chain - m
163	2	18.2	10	2	PH0927	T-cell receptor be	236	2	18.2	12	2	A19233	histone H2B - huma
164	2	18.2	10	2	C54226	light-harvesting p	237	2	18.2	12	2	S15815	myosin heavy chain
165	2	18.2	10	2	A32196	Na/K+-exchanging	238	2	18.2	12	2	E45691	translation elonga
166	2	18.2	10	2	PA0116	ferredoxin-NADP re	239	2	18.2	12	2	E58502	probable minor cap
167	2	18.2	10	2	PS0220	glyceraldehyde 3-p	240	2	18.2	12	2	G49215	43.2K bile stone p
168	2	18.2	10	2	S74147	probable trypsin lea	241	2	18.2	12	2	E64573	urease (EC 3.5.1.5
169	2	18.2	11	1	IFTWME	alcohol dehydrogen	242	2	18.2	12	2	S71022	hypothetical prote
170	2	18.2	11	2	S66596	dihydroorotase (EC	243	2	18.2	12	2	S71034	type I DNA methyl
171	2	18.2	11	2	A33917	rhodopsin homo-log	244	2	18.2	12	2	A26093	potB protein - Sal
172	2	18.2	11	2	A38841	morphogenetic neur	245	2	18.2	12	2	S34447	microbial collagen
173	2	18.2	11	2	YHRT	morphogenetic neur	246	2	18.2	12	2	A60757	binr protein - Sta
174	2	18.2	11	2	YHRT	morphogenetic neur	247	2	18.2	12	2	D28551	enterotoxin C-1 -
175	2	18.2	11	2	YHRT	morphogenetic neur	248	2	18.2	12	2		hypothetical prote

249	2	18.2	12	2	140663	hma protein - Cios	322	2	18.2	13	2	A38929	glutathione peroxl
250	2	18.2	12	2	PA0019	acidic ribosomal p	323	2	18.2	13	2	PQ0445	utrotensin II - lau
251	2	18.2	12	2	PA0047	protein QAI00045 -	324	2	18.2	13	2	A28505	neutrotensin [valid
252	2	18.2	12	2	S67528	napin - rape (frag	325	2	18.2	13	2	A61067	neutrotensin - comm
253	2	18.2	12	2	S70337	napin small chain	326	2	18.2	13	2	B35245	histone H1.c - mou
254	2	18.2	12	2	JU0356	cycloleucunin -	327	2	18.2	13	2	A35245	histone H1.c - mou
255	2	18.2	12	2	P00696	1,4-alpha-glucac: b	328	2	18.2	13	2	A23695	myosin heavy chain
256	2	18.2	12	2	PS0213	28K protein: 4412 -	329	2	18.2	13	2	A60336	outer membrane pro
257	2	18.2	12	2	PQ0730	unidentified 5.4/3	330	2	18.2	13	2	S01119	photosystem II pro
258	2	18.2	12	2	PN0170	alcohol dehydrogen	331	2	18.2	14	2	E37390	trAA protein - Esc
259	2	18.2	12	2	PN0162	ma-ate dehydrogena	332	2	18.2	13	2	E37390	lactose phosphotra
260	2	18.2	12	2	T46656	hypothetical protei	333	2	18.2	13	2	E37390	alpha-2 collagen -
261	2	18.2	12	2	C34135	RNA-binding protei	334	2	18.2	13	2	PN0122	alpha-2 collagen -
262	2	18.2	12	2	S65730	hemocobin, extrac	335	2	18.2	13	2	A60409	bombesin-like pept
263	2	18.2	12	2	J50424	utrotensin II-B pep	336	2	18.2	13	2	A59487	VCAM-1 5'UTR bindi
264	2	18.2	12	2	S10626	lipovitellin - Afr	337	2	18.2	13	2	P00038	alpha-peptide/alg
265	2	18.2	12	2	A49261	coagulation factor	338	2	18.2	13	2	T08533	hypothetical prote
266	2	18.2	12	2	A55637	5-aminimidazole r	339	2	18.2	13	2	S22995	hypothetical prote
267	2	18.2	12	2	S29830	dimethylamine mo	340	2	18.2	13	2	B36042	oxfx protein - Esc
268	2	18.2	12	2	I77529	estrogen receptor	341	2	18.2	13	2	B26093	microbial collagen
269	2	18.2	12	2	PT0274	Ig heavy chain CRD	342	2	18.2	13	2	A46463	preabsorbing anti g
270	2	18.2	12	2	PT0319	Ig heavy chain CRD	343	2	18.2	13	2	A61288	spore proteinase g
271	2	18.2	12	2	S43957	Ig mu chain V regi	344	2	18.2	13	2	A01825	botulinum toxins -
272	2	18.2	12	2	S43170	kinesin light chai	345	2	18.2	13	2	S36887	ribosomal protein
273	2	18.2	12	2	S47391	T-cell antigen: rec	346	2	18.2	13	2	S23103	erythronolide synt
274	2	18.2	12	2	S47395	T-cell antigen: rec	347	2	18.2	13	2	S20578	ribosomal protein
275	2	18.2	12	2	PH1190	T-cell receptor al	348	2	18.2	13	2	S14316	photosystem I 9K c
276	2	18.2	12	2	PH1187	T-cell: receptor al	349	2	18.2	13	2	S38736	lipid transfer pro
277	2	18.2	12	2	PH1184	T-cell: receptor al	350	2	18.2	13	2	PA0049	protein QAI00046 -
278	2	18.2	12	2	PH1182	T-cell receptor al	351	2	18.2	13	2	JN0310	insulin-binding pr
279	2	18.2	12	2	PH1185	T-cell receptor al	352	2	18.2	13	2	S00316	photosystem I 13K
280	2	18.2	12	2	PH1180	T-cell receptor al	353	2	18.2	13	2	S09733	photosystem I prot
281	2	18.2	12	2	PH1183	T-cell receptor al	354	2	18.2	13	2	S60046	early nodulin 40 -
282	2	18.2	12	2	PH1188	T-cell receptor al	355	2	18.2	13	2	JQ2309	hypothetical 1.6K
283	2	18.2	12	2	PH1172	T-cell receptor al	356	2	18.2	13	2	JQ2319	hypothetical 1.6K
284	2	18.2	12	2	PH1171	T-cell receptor al	357	2	18.2	13	2	PS0453	36K protein 3124 -
285	2	18.2	12	2	PH1175	T-cell: receptor al	358	2	18.2	13	2	PS0250	ribulose-bisphosph
286	2	18.2	12	2	PH1174	T-cell: receptor al	359	2	18.2	13	2	PS0325	tetrahydroberberin
287	2	18.2	12	2	PH1174	T-cell receptor al	360	2	18.2	13	2	PQ0700	unidentified 6.3/4
288	2	18.2	12	2	PH1181	T-cell receptor al	361	2	18.2	13	2	JQ1350	hypothetical prote
289	2	18.2	12	2	A49031	T-cell receptor de	362	2	18.2	13	2	PA0089	protein QF200053 -
290	2	18.2	12	2	B49033	T-cell receptor de	363	2	18.2	13	2	E60396	antigen 7H6/2 - ma
291	2	18.2	12	2	C49033	T-cell receptor de	364	2	18.2	13	2	S32471	lymnaDFamide 1 - g
292	2	18.2	12	2	A69528	insulin-like growt	365	2	18.2	13	2	S32472	lymnaDFamide 2 - g
293	2	18.2	12	2	S74196	3-hydroxy-3-methyl	366	2	18.2	13	2	S32474	lymnaDFamide 4 - g
294	2	18.2	12	2	A37933	Ig lambda chain J	367	2	18.2	13	2	S32475	lymnaDFamide 5 - g
295	2	18.2	12	2	PN0663	dyatrophin-associa	368	2	18.2	13	2	S29488	GTP-binding protei
296	2	18.2	12	2	A20937	Ig kappa chain J1	369	2	18.2	13	2	S09018	hemolytic protein
297	2	18.2	12	2	C20937	Ig kappa-1 chain J	370	2	18.2	13	2	A60379	factor X activator
298	2	18.2	12	2	D20937	Ig kappa-1 chain J	371	2	18.2	13	2	A57789	galbladder stone
299	2	18.2	12	2	P20937	Ig kappa-2 chain J	372	2	18.2	13	2	S52356	hypothetical prote
300	2	18.2	12	2	S65626	phosphorylase b -	373	2	18.2	13	2	PT0305	Ig heavy chain CRD
301	2	18.2	12	2	S60228	Ig H chain V-D-J r	374	2	18.2	13	2	PH1316	Ig heavy chain DJ
302	2	18.2	12	2	PH1635	Ig H chain V-D-J r	375	2	18.2	13	2	PH1316	Ig kappa chain V-I
303	2	18.2	12	2	PH1587	Ig H chain V-D-J r	376	2	18.2	13	2	B61458	Ig kappa chain V-I
304	2	18.2	12	2	PH1611	Ig H chain V-D-J r	377	2	18.2	13	2	D61458	Ig kappa chain V-I
305	2	18.2	12	2	A33520	inhibitory diffus	378	2	18.2	13	2	E61458	Ig lambda chain V-I
306	2	18.2	12	2	PH1454	T-cell receptor al	379	2	18.2	13	2	G61458	Ig lambda chain V-I
307	2	18.2	12	2	PH1458	T-cell receptor be	380	2	18.2	13	2	PH1772	T cell receptor al
308	2	18.2	12	2	PH1457	T-cell receptor be	381	2	18.2	13	2	S57571	T cell receptor al
309	2	18.2	12	2	PH1459	T-cell receptor be	382	2	18.2	13	2	S57567	T-cell antigen rec
310	2	18.2	12	2	S39762	cytochrome P450 Uf	383	2	18.2	13	2	S47361	T-cell antigen rec
311	2	18.2	12	2	A2324	cytochrome P450c27	384	2	18.2	13	2	S47372	T-cell antigen rec
312	2	18.2	12	2	PH0334	T-cell receptor be	385	2	18.2	13	2	S47373	T-cell antigen rec
313	2	18.2	12	2	PH0331	T-cell receptor be	386	2	18.2	13	2	S47383	T-cell antigen rec
314	2	18.2	12	2	PH0520	T-cell receptor be	387	2	18.2	13	2	S47384	T-cell antigen rec
315	2	18.2	12	2	PC4377	telomeric and tet	388	2	18.2	13	2	S47388	T-cell antigen rec
316	2	18.2	12	2	S71380	lebetin 1 isoform	389	2	18.2	13	2	S23372	T-cell receptor al
317	2	18.2	12	2	PD0021	muconate cycloisom	390	2	18.2	13	2	PH0138	T-cell receptor be
318	2	18.2	12	2	A55524	ubiquinol: cytochr	391	2	18.2	13	2	B61233	conceptus protein
319	2	18.2	12	4	PC2123	aminotransferase c	392	2	18.2	13	2	S66235	sperm motility inh
320	2	18.2	12	4	S49073	frame shifted cya	393	2	18.2	13	2	S78766	ribosomal protein
321	2	18.2	13	1	UNOPRT	neurotensin - brus	394	2	18.2	13	2	B20907	Ig kappa-1 chain J

A:Authors: Gehrm, G.L.; McDonald, L.A.; Smith, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.
 A:Title: Whole genome random sequencing and assembly of *Haemophilus influenzae* Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: H64124
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-13 <TIGR>
 A:Cross-references: GB:U32824; GB:U4203; NID:q1574299; PID:q1574306; TIGR:H11460

Query Match 36.4%, Score 4, DB 2, Length 13;
 Best Local Similarity 100.0%, Pred. No. 5, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KLKK 8
 DB 3 KLKK 6

RESULT 3
 S01904
 H:Transporting two-sector ATPase (EC 3.6.3.14) beta chain - Arabidopsis thaliana chloroplast
 C:Species: Chloroplast Arabidopsis thaliana (mouse-ear cress)
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 03-Jun-2002
 C:Accession: S01904
 R:Chen, H.C.; Wintz, H.; Weil, J.H.; Pillay, D.D.N.
 Nucleic Acids Res. 16, 10372, 1988
 A:Title: Nucleotide sequence of chloroplast CF1-ATPase epsilon subunit and elongator rRNA
 A:Reference number: S01903; MUID:89057486; PMID:290414
 A:Accession: S01904
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-15 <CHES>
 A:Cross-references: EMBL:X14889; NID:q11432; PID:q825297
 C:Genetics: atpB
 A:Gene: atpB
 A:Genome: chloroplast
 C:Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 36.4%, Score 4, DB 2, Length 13;
 Best Local Similarity 100.0%, Pred. No. 5, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
 DB 10 KLKK 13

RESULT 4
 S13864
 methyl coenzyme M reductase (EC 1.8.1.7) from *Methanobacterium thermoautotrophicum*
 C:Species: *Methanobacterium thermoautotrophicum*
 A:Variety: strain Matburg
 C:Date: 19-Mar-1997 #sequence_revision 19-Sep-1997 #text_change 30-Oct-1998
 C:Accession: S13864
 R:Rospert, S.; Binder, D.; Ellermann, J.; Hauner, K.K.
 Eur. J. Biochem. 194, 871-877, 1996
 A:Title: Two genetically distinct methyl coenzyme M reductases in *Methanobacterium thermoautotrophicum*
 A:Reference number: S13864; MUID:91093470; PMID:225450
 A:Accession: S13864
 A:Molecule type: protein
 A:Residues: 1-14 <ROS>
 A:Experimental source: strain Matburg
 C:Keywords: methanogenesis; oxidoreductase

Query Match 36.4%, Score 4, DB 2, Length 14;
 Best Local Similarity 100.0%, Pred. No. 3, 4e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKKK 10
 DB 11 LKKK 14

RESULT 5
 I48934
 apolipoprotein A-II - mouse (fragment)
 C:Species: *Mus musculus* (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I48934
 R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maesaki, Y.; Nadeau, J.M.
 Mamm. Genome 5, 349-355, 1994
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A:Reference number: I48934; MUID:94319082; PMID:8043949
 A:Accession: I48934
 A:Status: preliminary; translated from GR/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-8 <RES>
 A:Cross-references: EMBL:U05691; NID:q497010; PID: AAB60462.1; PID:q642826

Query Match 27.3%, Score 3, DB 2, Length 8;
 Best Local Similarity 100.0%, Pred. No. 2, 8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
 DB 4 GSA 6

RESULT 6
 I54379
 gene NF2 protein - human (fragment)
 C:Species: *Homo sapiens* (man)
 C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
 C:Accession: I54379
 R:Arai, E.; Ikeuchi, T.; Nakamura, Y.
 Hum. Mol. Genet. 3, 937-939, 1994
 A:Title: Characterization of the translocation breakpoint on chromosome 22q12.2 in a human with neurofibromatosis type 1
 A:Reference number: I54379; MUID:95038750; PMID:7951241
 A:Accession: I54379
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-9 <RES>
 A:Cross-references: GB:S7584; NID:q861532; PID: AAD14190.1; PID:q4261890
 C:Genetics: NF2
 A:Gene: GDN, NF2
 A:Cross-references: GDN:126242; OMIM:101000
 A:Map position: 22q12.2-22q12.2

Query Match 27.3%, Score 3, DB 2, Length 9;
 Best Local Similarity 100.0%, Pred. No. 2, 8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 8
 DB 4 KLKK 6

RESULT 7
 PT0225
 Ig heavy chain CDR3 region (clone 1-103) - human (fragment)
 C:Species: *Homo sapiens* (man)
 C:Date: 10-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0225
 R:Yamada, M.; Wasserman, K.; Reichard, H.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 355-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity 2
 A:Reference number: PT0225; MUID:91108337; PMID:1899102
 A:Accession: PT0225
 A:Molecule type: DNA
 A:Residues: 1-9 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 27.3%, Score 3, DB 2, Length 9;
 Best Local Similarity 100.0%, Pred. No. 2, 8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 8
 DB 4 KLKK 6

QY 1 AGS 4
 III
 DB 7 AGS 9

RESULT 8
 PC7076
 Spectrin alpha chain, non-erythroid - mouse (fragment)
 N:Alternate names: fodrin alpha chain
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Aug-2000 #sequence_revision 18 Aug 2000 #text_change 14 Aug 2000
 C:Accession: PC7076
 R:Tsukida, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kawa, M.; Matsui, I.; Watanabe, Y.
 Electrophoresis 21: 1853-1871, 2000
 A:Title: Proteome analysis of mouse brain: two distinct and distinct phosphoproteomes of
 A:Reference number: PC7072
 A:Accession: PC7076
 A:Molecule type: protein
 A:Residues: 1-9 <TSU>
 A:Experimental source: strain C57BL/6J Slc, male; brain, striatum
 C:Keywords: brain

Query Match 27.3% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0% Pred. No. 2 8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKK 10
 III
 DB 6 KKK 5

RESULT 9
 A44755
 20alpha hydroxysteroid dehydrogenase (EC 1.1.1.17) - clostridium scindens (fragment)
 C:Species: Clostridium scindens
 C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 17-Mar-1999
 C:Accession: A44755
 R:Kralic, A.E.; Hylemon, P.B.
 J. Bacteriol. 171: 2925-2932, 1989
 A:Title: Purification and characterization of a novel form of 20alpha hydroxysteroid de
 A:Reference number: A44755; MUID:6255043; PMID:2722796
 A:Accession: A44755
 A:Molecule type: protein
 A:Residues: 1-11 <KRA>
 C:Comment: This enzyme was purified to homogeneity and shown to have 20alpha hydroxyster
 20alpha dehydrogenase (GAPDH) activity and that the fragment shows great identity to known
 C:Keywords: hemotetrimer; NAD; NADP; oxidoreductase

Query Match 27.3% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0% Pred. No. 1 1e+01;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AVK 6
 III
 DB 1 AVK 3

RESULT 10
 S33519
 Probable secreted protein - Acholeplasma laidlawii (fragment)
 C:Species: Acholeplasma laidlawii
 C:Date: 06-Jan-1995 #sequence_revision 06 Jan 1995 #text_change 22-Oct 1995
 C:Accession: S33519
 R:Boyer, M.J.; Jarhede, T.K.; Teague, V.; Wieslander, A.
 Submitted to the EMBL Data Library, June 1993
 A:Description: Sequence regions from Acholeplasma laidlawii which restore export of beta
 A:Reference number: S33518
 A:Accession: S33519
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-11 <BOY>
 A:Cross-references: EMBL:222875; NID:0311760; PIDN CAA80427.1; FID:0311708

Query Match 27.3% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0% Pred. No. 4.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKK 8
 III
 DB 3 KKK 5

RESULT 11
 C57789
 Gallbladder stone matrix protein, 14.5K - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 23-Feb-1996 #sequence_revision 23-Feb 1996 #text_change 23-Feb-1996
 C:Accession: C57789
 R:Binette, J.P.; Binette, M.F.
 submitted to the Protein Sequence Database, February 1996
 A:Description: The proteins of gallbladder stones.
 A:Reference number: A57789
 A:Accession: C57789
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <BIN>

Query Match 27.3% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0% Pred. No. 4.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGS 3
 III
 DB 7 AGS 9

RESULT 12
 PH0941
 T cell receptor beta chain V-D-J region (clone 12) - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C:Accession: PH0941
 R:Goid, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174: 1467-1476, 1991
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental all
 A:Reference number: PH0891; MUID:92078857; PMID:1816012
 A:Accession: PH0941
 A:Molecule type: mRNA
 A:Residues: 1-11 <GOI>
 A:Experimental source: Complete Freund's adjuvant-immunized lymph node
 C:Keywords: T cell receptor

Query Match 27.3% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0% Pred. No. 4.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SAV 5
 III
 DB 4 SAV 6

RESULT 13
 PU0034
 Dextranucrase (EC 2.4.1.5) - Streptococcus bovis (fragment)
 C:Species: Streptococcus bovis
 C:Date: 04-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 18-Sep-1996
 C:Accession: PU0034
 R:Dezono, Y.; Tsumori, H.; Mukasa, H.
 submitted to JIPID, October 1993
 A:Description: Purification and properties of glucosyltransferase synthesizing 1,6-a
 A:Reference number: PU0034
 A:Accession: PU0034
 A:Molecule type: protein
 A:Residues: 1-11 <DEZ>
 A:Experimental source: ATCC 9809

C:Keywords: glycosyltransferase; hexosyltransferase

Query Match: 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SAV 5

DB 4 SAV 6

RESULT 14

C58502

58K bile and gallbladder stone protein - unidentified bacterium (fragment)

C:Species: unidentified bacterium

C>Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998

C:Accession: C58502

R:Binette, J.P.; Binette, M.B.

A:Submitted to the Protein Sequence Database, October 1998

A:Description: The proteins of kidney and gallbladder stones.

A:Reference number: A58501

A:Accession: C58502

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <BIN>

A:Experimental source: human bile and gallbladder stones

Query Match: 27.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4

DB 8 GSA 10

RESULT 15

S78519

Ribosomal protein S16, chloroplast - ginkgo (fragment)

C:Species: chloroplast Ginkgo biloba (ginkgo)

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998

C:Accession: S78519

R:Richard, M.; Tremblay, C.; Bellemare, G.

C:Gene: Genet. 26, 159-165, 1994

A:Title: Chloroplast genomes of Ginkgo biloba and Chlamydomonas monensis contain a chi

A:Reference number: S45486; MUID:950943.3; PMID:951171

A:Molecule type: DNA

A:Residues: 1-13 <R1C>

A:Cross-references: EMBL:U01531

C:Genes: rps16

A:Gene: rps16

A:Genome: chloroplast

C:Superfamily: Escherichia coli ribosomal protein S16

C:Keywords: chloroplast; protein biosynthesis; ribosomes

Query Match: 27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VKL 7

DB 2 VKL 4

RESULT 16

S48210

collagen alpha 1(V) chain - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 15-Jul-1995 #sequence_revision 25-Jul-1996 #text_change 16-Feb-1997

C:Accession: S48210

R:Niyibizi, C.; Eyre, D.R.

Eur. J. Biochem. 224, 943-950, 1994

A:Title: Structural characteristics of cross-linking sites in type V collagen of bo

A:Reference number: S48210; MUID:95010086; PMID:7925418

A:Accession: S48210

A:Molecule type: protein

A:Residues: 1-13 <NIY>

C:Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homo

Query Match: 27.3%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGS 3

DB 10 AGS 12

RESULT 17

S12473

LymnaeaFamide 3 - great pond snail

C:Species: Lymnaea stagnalis (great pond snail)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999

C:Accession: S12473

R:Johnsen, A.H.; Rehfeld, J.F.

Eur. J. Biochem. 213, 875-879, 1993

A:Title: LymnaeaFamides, a new family of neuropeptides from the pond snail, Lymnaea s

A:Reference number: S12471; MUID:9423877; PMID:8477756

A:Accession: S12473

A:Molecule type: protein

A:Residues: 1-13 <JOH>

A:Cross-references: PIDN:AAB26364.1; PID:q299831

A:Experimental source: ganglia

C:Keywords: amidated carboxyl end; neuropeptide

F.13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match: 27.3%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4

DB 7 GSA 9

RESULT 18

PA0109

porin por 1B - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 30-Jun-1995

C:Accession: PA0109

R:Kamo, M.; Kawakami, I.; Tsugita, A.

submitted to JIPID, March 1995

A:Reference number: PA0109

A:Accession: PA0109

A:Molecule type: protein

A:Residues: 1-14 <KAM>

A:Experimental source: root

Query Match: 27.3%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KKA 11

DB 12 KKA 14

RESULT 19

B34135

DNA-binding protein g - Crithidia fasciculata mitochondrion (fragment)

C:Species: mitochondrion Crithidia fasciculata

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999

C:Accession: B34135

R:Tittawella, I.

FERS Lett. 260, 57-61, 1990

A:Title: Kinoplast DNA-aggregating proteins from the parasitic protozoan *Critidia fasciculata*

A:Reference number: A34135

A:Accession: B34135

A:Molecule type: protein

A:Residues: 1-14 <TIT>

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC6

C:Keywords: mitochondrion

Query Match 27.3% Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKA 11

DB 7 KKA 9

RESULT 20

S14336

mastoparan B - hornet (*Vespa basalis*)

C:Species: *Vespa basalis*

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Apr-1999

C:Accession: S14336

R:Ho, C.L.; Hwang, L.C.

Biochem. J. 274, 453-456, 1991

A:Title: Structure and biological activities of a new mastoparan isolated from the venom of *Vespa basalis*

A:Reference number: S14336

A:Accession: S14336

A:Molecule type: protein

A:Residues: 1-14 <HOC>

A:Experimental source: venom

C:Function:

A:Description: possesses a potent hemolytic activity which acts in synergy with the lethal venom

C:Keywords: amidated carboxyl end; mast cell; venom

F:14/Modified site: amidated carboxyl end (see) #status experimental

Query Match 27.3% Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKK 8

DB 2 KKK 4

RESULT 21

A47421

leukotriene B 4 12-hydroxydehydrogenase (EC 1.1.1.134) (fragment)

C:Species: *Sus scrofa domestica* (domestic pig)

C:Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 17-Mar-1999

C:Accession: A47421

R:Yokoyama, T.; Izumi, T.; Takahashi, T.; Kasama, T.; Kawayashi, Y.; Sato, F.; Taketani, J. Biol. Chem. 268, 18128-18135, 1993

A:Title: Enzymatic inactivation of leukotriene B 4 by a novel enzyme found in the porcine

A:Reference number: A47421; MUID:93352633; EMBL:U08494.1

A:Accession: A47421

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <YOK>

C:Keywords: oxidoreductase

Query Match 27.3% Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKK 9

DB 8 LKK 10

RESULT 22

PH0800

T-cell receptor alpha chain (J3) - mouse (fragment)

C:Species: *Mus musculus* (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0800

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0800

A:Molecule type: mRNA

A:Residues: 1-14 <CAS>

A:Cross-references: EMBL:X60907

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4

DB 7 GSA 9

RESULT 23

PT0210

T-cell receptor alpha chain V-J region (4-1-K.1) - mouse (fragment)

C:Species: *Mus musculus* (house mouse)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C:Accession: PT0210

R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not res

A:Reference number: PT0209; MUID:91217621; PMID:1902501

A:Accession: PT0210

A:Molecule type: mRNA

A:Residues: 1-14 <NAK>

C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4

DB 11 GSA 13

RESULT 24

S00843

hypothetical protein ksqA 5'-region - *Escherichia coli*

C:Species: *Escherichia coli*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: S00843

R:van Gemen, B.; Koets, H.J.; Plooy, C.A.M.; Bodlaender, J.; van Knippenberg, P.H.

Biochimie 69, 841-848, 1987

A:Title: Characterization of the ksqA gene of *Escherichia coli* determining kasugamycin

A:Reference number: S00843; MUID:88107880; PMID:3122846

A:Accession: S00843

A:Molecule type: DNA

A:Residues: 1-14 <DNA>

A:Cross-references: EMBL:X06536; NID:q41884; PIDN:CAA29785.1; PID:q41885

C:Comment: This is the hypothetical translation of a sequence that was not reported

Query Match 27.3% Score 3; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SAV 5

DB 11

```

Db          2 SAV 4          Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 25
S21240
alpha-glucosidase (EC 3.2.1.20) I - Bacillus "thermoamyloliquefaciens" (fragment)
C:Species: Bacillus "thermoamyloliquefaciens"
C:Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 27-Aug-1998
C:Accession: S21240
R:Suzuki, Y.; Yonezawa, K.; Hattori, M.; Takii, Y.
E: J. Biochem. 205, 249-256, 1992
A:Title: Assignment of Bacillus thermoamyloliquefaciens KPI071 alpha-glucosidase I to an
ence and in structural parameters calculated from the amino acid composition.
A:Reference number: S21202; MUID:92209510; PMID:1555585
A:Accession: S21240
A:Molecule type: protein
A:Residues: 1-15 <SUZ>
A:Experimental source: strain KPI071
C:Superfamily: alpha-glucosidase; alpha-amylose core homology
C:Keywords: glycosidase; hydrolase

Query Match          27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 KKA 11
          III
Db          2 KKA 4

RESULT 26
PN0118
hemoglobin beta chain - red fox (fragment)
C:Species: Vulpes vulpes (red fox)
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 13-May-2000
C:Accession: PN0118
R:Sukhomlinov, B.F.; Konoshenko, S.V.
Mol. Biol. (Mosk.) 5, 415-418, 1971
A:Title: Study on N-terminal sequence of the haemoglobin of Vulpes vulpes fox.
A:Reference number: PN0117
A:Accession: PN0118
A:Molecule type: protein
A:Residues: 1-15 <SUK>
C:Superfamily: globin; globin homology
C:Keywords: blood; erythrocyte; heme; heterotetramer; oxygen carrier;

Query Match          27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 AVK 6
          III
Db          10 AVK 12

RESULT 27
PN0117
hemoglobin alpha chain - red fox (fragment)
C:Species: Vulpes vulpes (red fox)
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 13-May-2000
C:Accession: PN0117
R:Sukhomlinov, B.F.; Konoshenko, S.V.
Mol. Biol. (Mosk.) 5, 415-418, 1971
A:Title: Study on N-terminal sequence of the haemoglobin of Vulpes vulpes fox.
A:Reference number: PN0117
A:Accession: PN0117
A:Molecule type: protein
A:Residues: 1-15 <SUK>
C:Superfamily: globin; globin homology
C:Keywords: blood; erythrocyte; heme; heterotetramer; oxygen carrier;

Query Match          27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 AVK 6
          III
Db          10 AVK 12

us-09-787-443-4.oli.rpr
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 AVK 6
          III
Db          8 AVK 10

RESULT 28
S36896
ribosomal protein S16 - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S36896
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Myc
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36896
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OHA>
C:Keywords: protein biosynthesis; ribosome

Query Match          27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 AVK 6
          III
Db          1 AVK 3

RESULT 29
S14749
3-dehydroquinase - Neurospora crassa (fragment)
C:Species: Neurospora crassa
C:Date: 21-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 01-Sep-1995
C:Accession: S14749
R:Chaudhuri, S.; Duncan, K.; Graham, L.D.; Coggins, J.R.
Biochem. J. 275, 1-6, 1991
A:Title: Identification of the active-site lysine residues of two biosynthetic 3-de
A:Reference number: S14749; MUID:91207275; PMID:1826831
A:Accession: S14749
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <CHA>

Query Match          27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          5 VKL 7
          III
Db          8 VKL 10

RESULT 30
G41299
T-cell receptor alpha chain precursor J region (39) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 05-Nov-1999
C:Accession: G41299
R:Uematsu, Y.; Wege, H.; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayil,
Proc. Natl. Acad. Sci. U.S.A. 88, 8534-8538, 1991
A:Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheu
A:Reference number: A41299; MUID:92020887; PMID:1656449
A:Accession: G41299
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <DEM>
A:Cross-references: GB:S57457; MID:g236330; PIDN:AAB19962.1; PID:g236331
C:Keywords: T-cell receptor

```

Query Match 27.3%: Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGS 3
 III
 7 AGS 9

Db

RESULT 31
 PH0775
 T-cell receptor alpha chain (B2B) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PH0775
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.
 A:Reference number: PH0746; MUID:92078846; PMID:1836016
 A:Accession: PH0775
 A:Molecule type: mRNA
 A:Residues: 1-15 <CAS>
 A:Cross-references: EMBL:X60871
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 27.3%: Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
 III
 6 GSA 8

Db

RESULT 32
 PH0779
 T-cell receptor alpha chain (B83) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PH0779
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.
 A:Reference number: PH0746; MUID:92078846; PMID:1836016
 A:Accession: PH0779
 A:Molecule type: mRNA
 A:Residues: 1-15 <CAS>
 A:Cross-references: EMBL:X60871
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 27.3%: Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
 III
 6 GSA 8

Db

RESULT 33
 PH1455
 T-cell receptor alpha chain (clone A24/PEF4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 1; Apr-1995
 C:Accession: PH1455
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Pottier, C.; Pannetier, C.; Reynault, A.; Ko
 J. Exp. Med. 177, 811-820, 1993
 A:Title: T cell receptor selection: by and recognition of two class I major histocompatib
 A:Reference number: PH1430; MUID:93171421; PMID:845977

A:Accession: PH1455
 A:Molecule type: mRNA
 A:Residues: 1-15 <CAS>
 A:Experimental source: cytolytic T-lymphocyte
 C:Superfamily: immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 27.3%: Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
 III
 6 GSA 8

Db

RESULT 34
 A49887
 Transcription factor HNF-1 beta - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 07-May-1999
 C:Accession: A49887
 R:Sasaki, H.; Hogan, B.L.M.
 Cell 76, 103-115, 1994
 A:Title: HNF-3beta as a regulator of floor plate development.
 A:Reference number: A49887; MUID:94116056; PMID:8287471
 A:Accession: A49887
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-15 <SAS>
 C:Keywords: alternative initiators; alternative splicing; transcription factor

Query Match 27.1%: Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AVK 6
 III
 10 AVK 12

Db

RESULT 35
 S09073
 Cytochrome P450-3b - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1993
 C:Accession: S09073
 R:Imaoka, S.; Terano, Y.; Funae, Y.
 Arch. Biochem. Biophys. 278, 168-178, 1990
 A:Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes with st
 A:Reference number: S09072; MUID:90210577; PMID:2321956
 A:Accession: S09073
 A:Molecule type: protein
 A:Residues: 1-15 <IMA>

Query Match 27.3%: Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGS 3
 III
 5 AGS 7

Db

RESULT 36
 PL0110
 Complement factor B1-Hb and B2-Hb - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 15-Nov-1996
 C:Accession: PL0110
 R:Matsushita, M.; Okada, H.
 Mol. Immunol. 26, 669-676, 1989
 A:Title: Two forms of guinea pig factor B of the alternative complement pathway with

A:Reference number: A93136; MWID:89484669; PMID:2779589
 A:Accession: P10110
 A:Molecule type: protein
 A:Residues: 1-15 <MAT>
 C:Keywords: complement alternate pathway; glycoprotein

Query Match: 27.2%; Score 2; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGS 4
 ||
 Db 2 AGS 9

RESULT 47

LFSAME

Probable msra leader peptide - Staphylococcus epidermidis

C:Species: Staphylococcus epidermidis
 C:Date: 30-Sep-1991 #sequence_revision 10-Sep-1991 #text_change 16-Jul-1999
 C:Accession: S11157
 R:Ross, J.L.; Eady, E.A.; Cove, J.H.; Cunliffe, W.J.; Baumbard, S.; Wootton, J.C.
 Mol. Microbiol. 4, 1207-1214, 1990
 A:Title: Inducible erythromycin resistance in staphylococci is encoded by a member of the

A:Reference number: S11157; MWID:91041740; PMID:2243255
 A:Accession: S11157
 A:Molecule type: DNA
 A:Residues: 1-8 <ROS>
 A:Cross-references: EMBL:X52085; NID:q47406; PIDN:CAA6403.1; PID:q5b1653
 C:Superfamily: probable msra leader peptide

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IK 8
 ||
 Db 7 IK 8

RESULT 38

S3741

tpsa protein - Erwinia chrysanthemi

C:Species: Erwinia chrysanthemi
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Nov-1999
 C:Accession: S3741
 R:Deuillie, A.; Toussaint, A.; Faes, M.
 Submitted to the EMBL Data Library, August 1994
 A:Description: Identification of the integration host factor genes of E. chrysanthemi.

A:Reference number: S37139

A:Accession: S37141

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <DOU>

A:Cross-references: EMBL:X74750; NID:q394669; PIDN:CAA2769.1; PID:q581108

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SA 4
 ||
 Db 4 SA 5

RESULT 39

S16324

hypothetical protein 2 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 21-Nov-1993 #sequence_revision 12-May-1994 #text_change 21-Jan-2000
 C:Accession: S16324
 R:Ruberti, L.; Sessa, G.; Lucchetti, S.; Morel, L. G.
 EMBO J. 10, 1787-1791, 1991

A:Title: A novel class of plant proteins containing a homeodomain with a closely lin

A:Reference number: S16323; MWID:91266907; PMID:1675603

A:Accession: S16324

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <RUH>

A:Cross-references: EMBL:X58821; NID:q16327; PIDN:CAA1624.1; PID:q579259

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KL 7
 ||
 Db 4 KL 5

RESULT 43

P00726

unidentified 4.5/45K [imported] - rice (fragment)

C:Species: Oryza sativa (rice)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: P00726

R:Komatsu, S.; Kakiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A:Title: A rice protein library: a data-file of rice proteins separated by two-dime

A:Reference number: P00696

A:Accession: P00726

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <KOM>

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AV 5
 ||
 Db 1 AV 2

RESULT 41

JS0315

leucokinin V - Madella cockroach

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C:Accession: JS0315

R:Holman, G.M.; Cook, R.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 27-30, 1987

A:Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotr

A:Reference number: JS0315

A:Accession: JS0315

A:Molecule type: protein

A:Residues: 1-8 <HOL>

C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile

C:Keywords: amidated carboxyl end; cephalomyotropic peptide

F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
 ||
 Db 1 GS 2

RESULT 42

A61467

penalbumin - Adelie penguin (fragment)

C:Species: Pygoscelis adeliae (Adelie penguin)

C:Date: 07-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 04-Nov-1994

C:Accession: A61467

R:Osega, D.T.; Aninlari, M.; Ho, C.Y.K.; Allison, R.G.; Feeney, R.F.
 J. Protein Chem. 2, 43-62, 1983
 A:Title: Sulfhydryl proteins of penguin egg white: ovalbumin and penalbumin. Comparisons
 A:Reference number: A61467
 A:Accession: A61467
 A:Molecule type: protein
 A:Residues: 1-8 <OSU>
 C:Comment: Penalbumin is a major protein component of egg whites from penguins but not of
 C:Keywords: egg white; glycoprotein

Query Match 18.2% Score 2: DB 2: Length 8:
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 GS 3
 II
 Db 1 GS 2

RESULT 44
 PT0411
 T:heavy chain CDR3 region (clone 6-106) - mouse (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0411
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shuter, S.; Gatten, A.; Rivera, G.
 J. Exp. Med. 273, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337, PMID:1899102
 A:Accession: PT0411
 A:Molecule type: DNA
 A:Residues: 1-8 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 18.2% Score 2: DB 2: Length 8:
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 SA 4
 II
 Db 2 SA 3

RESULT 45
 PT0423
 T:heavy chain CDR3 region (clone 62 1066) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0423
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shuter, S.; Gatten, A.; Rivera, G.
 J. Exp. Med. 273, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337, PMID:1899102
 A:Accession: PT0423
 A:Molecule type: DNA
 A:Residues: 1-8 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 18.2% Score 2: DB 2: Length 8:
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 GS 3
 II
 Db 1 GS 2

RESULT 45
 PT0423
 T:cell receptor alpha chain (J2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PH0803
 R:Casanova, J.L.; Romero, P.; Wildmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A:Title: T cell receptor genes in a series of class I major histocompatibility comp;
 allelic exclusion and antigen-specific repertoire
 A:Reference number: PH0746; MUID:92078846; PMID:1836010
 A:Accession: PH0803
 A:Molecule type: mRNA
 A:Residues: 1-8 <CAS>
 A:Cross-references: EMBL:X63412
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 18.2% Score 2: DB 2: Length 8:
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AG 2
 II
 Db 3 AG 4

RESULT 46
 A35769
 T:cell receptor alpha chain V-J region (34S-281) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 30-May-1997
 C:Accession: A35769
 R:Kosaki, H.; Imai, K.; Nakayama, F.; Sado, T.; Moriwaki, K.; Taniguchi, M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5248-5252, 1990
 A:Title: Homogenous junctional sequence of the VJ4+ T-cell antigen receptor alpha c
 A:Reference number: A35768; MUID:90319089; PMID:2371269
 A:Accession: A35768
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-8 <KOS>
 A>Note: the sequence shown follows the authors' translation at position 1 of IGT
 C:Keywords: T-cell receptor

Query Match 18.2% Score 2: DB 2: Length 8:
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 GS 3
 II
 Db 7 GS 8

RESULT 47
 PT0627
 T:cell receptor beta chain V-D-J region (100-2H) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0627
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal i cell receptor beta chains have few N region
 A:Reference number: PT5509; MUID:91277601; PMID:1711558
 A:Accession: PT0627
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-8 <FE>
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 18.2% Score 2: DB 2: Length 8:
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AG 2
 II
 Db 5 AG 6

A:Title: A novel class of plant proteins containing a homeodomain with a closely li:
 A:Reference number: A93136; MUID:89384686; PMID:2779589
 A:Accession: P10110
 A:Molecule type: protein
 A:Residues: 1-15 <MA>
 C:Keywords: complement alternate pathway; glycoprotein.

Query Match 27.3%; Score 2; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGS 3
 DB 7 AGS 9

RESULT 37

LFSAME

probable msra leader peptide - Staphylococcus epidermidis
 C:Species: Staphylococcus epidermidis
 C:Date: 30-Sep-1993; #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
 C:Accession: S11157
 R:Ross, J. L.; Eady, E. A.; Cove, J. H.; Cunliffe, W. J.; Baumberg, S.; Wootton, J. C.
 Mol. Microbiol. 4, 1207-1214, 1990

A:Title: Inducible erythromycin resistance in Staphylococci is encoded by a member of the
 A:Reference number: S11157; MUID:91041740; PMID:2233255
 A:Accession: S11157
 A:Molecule type: DNA
 A:Residues: 1-8 <ROS>
 A:Cross-references: EMBL:X52085; NID:947000; PID:CAA46403.1; PID:9581653
 C:Superfamily: probable msra leader peptide

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LR 8
 DB 7 LR 8

RESULT 38

S17141

tpsa protein - Erwinia chrysanthemi

C:Species: Erwinia chrysanthemi

C:Date: 06-Jan-1995; #sequence_revision 06-Jan-1995 #text_change 08-Oct-1995

C:Accession: S37141

R:Doillie, A.; Toussaint, A.; Faelen, M.

Submitted to the EMBL Data Library August 1994

A:Description: Identification of the secreted host factor protease of E. chrysanthemi.

A:Reference number: S37139

A:Accession: S37141

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-8 <DSO>

A:Cross-references: EMBL:X74750; NID:959666; PID:CAA42769.1; PID:9581105

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SA 4
 DB 4 SA 5

RESULT 39

S16324

hypothetical protein 2 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 21-Nov-1993; #sequence_revision 12-May 1995 #text_change 21-Jul-2000

C:Accession: S16324

R:Robert, I.; Sessa, G.; Lucchetti, S.; Morelli, G.

EMBO J. 10, 1787-1791, 1991

A:Title: A novel class of plant proteins containing a homeodomain with a closely li:
 A:Reference number: S16323; MUID:91266907; PMID:1675603

A:Accession: S16324

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <RUB>

A:Cross-references: EMBL:X58821; NID:916327; PID:CAA41624.1; PID:9579259

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KL 7
 DB 4 KL 5

RESULT 40

PQ0726

unidentified 4.5/45k [imported] - rice (fragment)

C:Species: Oryza sativa (rice)

C:Date: 20-Apr-2000; #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: PQ0726

R:Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A:Title: A rice protein library: a data-file of rice proteins separated by two-dimer

A:Reference number: PQ0696

A:Accession: PQ0726

A>Status: Preliminary

A:Molecule type: protein

A:Residues: 1-8 <KOM>

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AV 5
 DB 1 AV 2

RESULT 41

JS0315

leucokinin V - Maduira cockroach

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 07-Sep-1990; #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C:Accession: JS0315

R:Holman, G. M.; Cook, B. J.; Nachman, R. J.

Comp. Biochem. Physiol. C 88, 27-30, 1987

A:Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotr

A:Reference number: JS0315

A:Accession: JS0315

A:Molecule type: protein

A:Residues: 1-8 <HOL>

C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile

C:Keywords: amidated carboxyl end; cephalomyotropic peptide

F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
 DB 1 GS 2

RESULT 42

A61467

penalubum - Adelle penguin (fragment)

C:Species: Pygoscelis adelle (Adelle penguin)

C:Date: 07-Oct-1994; #sequence_revision 04-Nov-1994 #text_change 04-Nov-1994

C:Accession: A61467

R:Casada, D.T.; Aminlari, M.; Ho, C.Y.K.; Allison, R.G.; Feeney, A.E.
 J. Protein Chem. 2: 43-62, 1983
 A:Title: Sulfhydryl proteins of penquin egg white: ovalbumin and penaltbumin. Comparisons
 A:Reference number: A61467
 A:Accession: A61467
 A:Molecule type: protein
 A:Residues: 1-8 <GS>
 C:Comment: Penaltbumin is a major protein component of egg whites from penquins but not B
 C:Keywords: egg white; glycoprotein

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
 II
 DB 1 GS 2

RESULT 43

PT0311

Ig heavy chain CRD3 region (clone 6-103) human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0311

R:Yamada, M.; Wasserman, K.; Reichard, B.A.; Shauer, S.; Caton, A.J.; Rivera, G.

J. Exp. Med. 173: 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0311

A:Molecule type: DNA

A:Residues: 1-8 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 18.2% Score 2: DB 2: Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SA 4
 II
 DB 2 SA 3

RESULT 44

PT0323

Ig heavy chain CRD3 region (clone J2-106B) human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0323

R:Yamada, M.; Wasserman, K.; Reichard, B.A.; Shauer, S.; Caton, A.J.; Rivera, G.

J. Exp. Med. 173: 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0323

A:Molecule type: DNA

A:Residues: 1-8 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 18.2% Score 2: DB 2: Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
 II
 DB 1 GS 2

RESULT 45

PT0803

T-cell receptor alpha chain (J2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PH0803
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174: 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility compl
 allelic exclusion and antigen-specific repertoire

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0803

A:Molecule type: mRNA

A:Residues: 1-8 <CAS>

A:Cross-references: SMH: X60912

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 18.2% Score 2: DB 2: Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
 II
 DB 3 AG 4

RESULT 46

A35768

T-cell receptor alpha chain V-J region (34S-281) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 30-May-1997

C:Accession: A35768

R:Koseki, H.; Imai, K.; Nakayama, F.; Sado, T.; Moriwaki, K.; Taniguchi, M.

Proc. Natl. Acad. Sci. U.S.A. 87: 5248-5252, 1990

A:Title: Homogenous junctional sequence of the V14+ T-cell antigen receptor alpha ch
 A:Reference number: A35768; MUID:90319089; PMID:2371269

A:Accession: A35768

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-8 <KOS>

A:Note: the sequence shown follows the authors' translation at position 1 of TGT

C:Keywords: T-cell receptor

Query Match 18.2% Score 2: DB 2: Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
 II
 DB 7 GS 8

RESULT 47

PT0627

T-cell receptor beta chain V D J region (100-2H) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0627

R:Feeney, A.J.

J. Exp. Med. 174: 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region
 A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0627

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2: DB 2: Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
 II
 DB 5 AG 6

RESULT 48

PT0549
T-cell receptor beta chain V-D-J region (100-48K) - Mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 40 May-1997
C:Accession: PT0530
R:Feeney, A.J.
J:Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of total T-cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711554
A:Accession: PT0530
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <FE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match: 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2 de-95;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SA 4
DB 3 SA 4

RESULT 49

PT0527
T-cell receptor beta chain V-D-J region (100-43) - Mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 40 May-1997
C:Accession: PT0527
R:Feeney, A.J.
J:Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T-cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0527
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <FE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match: 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2 de-95;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
DB 5 AG 6

RESULT 50

PT0509
T-cell receptor beta chain V-D-J region (100-48K) - Mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 40 May-1997
C:Accession: PT0509
R:Feeney, A.J.
J:Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of total T-cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711554
A:Accession: PT0509
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <FE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match: 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2 de-95;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AG 2
DB 5 AG 6
Search completed: September 30, 2003, 10:09:44
Job time : 12.4167 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2003, 10:57:04 / Search time 5.25 Seconds

{without alignment}

82,767 Million 0.1 updates/sec

Title: US-09-787-443-4

Perfect score: 11

Sequence: 1 ACSAVKXKKKA 11

Scoring table: CL130

Gapop 50.0 / Gapext 60.0

Sequences: 127863 seqs, 47026705 residues

Word size: 9

Total number of hits satisfying chosen parameters: 707

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database: SwissProt_41.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	9	1	XVIA_SIRSA
2	4	36.4	14	1	MKX_METIM
3	4	27.3	12	1	RM16_GINRI
4	3	27.3	13	1	TT55_BOVIN
5	4	27.3	13	1	NPL_LYMSI
6	4	27.3	13	1	UR71_LILHW
7	3	27.3	14	1	MAST_VESBA
8	3	27.3	14	1	MY14_PHEV
9	3	27.3	14	1	IKN1_SCHUR
10	3	27.3	15	1	DIDH_PSEB
11	3	27.3	15	1	MA17_PANF
12	3	27.3	15	1	ONC1_LYMSI
13	4	27.3	15	1	SD06_PENNS
14	3	27.3	15	1	THE_CUGRA
15	3	27.3	15	1	SP02_METAN
16	2	18.2	8	1	AL16_CARMA
17	2	18.2	8	1	ALL8_CARMA
18	2	18.2	8	1	CAD1_ENCEA
19	2	18.2	8	1	PAT7_ASNSU
20	2	18.2	8	1	LCK5_DEINA
21	2	18.2	8	1	RLMS_STAPH
22	2	18.2	8	1	RS15_ERWH
23	2	18.2	8	1	VGI6_HSVJB
24	2	18.2	8	1	WPL_PERAL
25	2	18.2	9	1	ALC_CHLRE
26	2	18.2	9	1	BUR_CUGRA
27	2	18.2	9	1	DSIP_PARIT
28	2	18.2	9	1	FAR6_PANPE
29	2	18.2	9	1	FAR6_CALVO
30	2	18.2	9	1	LT01_LILAN
31	2	18.2	9	1	LMP_LOCHI
32	2	18.2	9	1	LPKA_STAAJ
33	2	18.2	9	1	MOSF_CLYJA

34	2	18.2	9	1	MOSH_CLYJA
35	2	18.2	9	1	PPH1_LYCES
36	2	18.2	9	1	PPK1_PERAM
37	2	18.2	9	1	PTSP_BOMMO
38	2	18.2	9	1	RE42_LITRU
39	2	18.2	9	1	THYF_PIG
40	2	18.2	9	1	ULAD_HUMAN
41	2	18.2	10	1	AMPN_HILAM
42	2	18.2	10	1	COXK_ONCMY
43	2	18.2	10	1	COXM_RAT
44	2	18.2	10	1	FARC_CALVO
45	2	18.2	10	1	FARP_WYTED
46	2	18.2	10	1	FIBB_PERSI
47	2	18.2	10	1	GAJU_HUMAN
48	2	18.2	10	1	GRP_RANRI
49	2	18.2	10	1	LABA_JATMU
50	2	18.2	10	1	MALE_KLEPN
51	2	18.2	10	1	MOSU_CLYJA
52	2	18.2	10	1	NO40_TOBAC
53	2	18.2	10	1	ODP2_BOVIN
54	2	18.2	10	1	PNEU_HUMAN
55	2	18.2	10	1	PNEU_RAT
56	2	18.2	10	1	PPCK_FASHE
57	2	18.2	10	1	PSHF_CAPAN
58	2	18.2	10	1	PVK_LOCHI
59	2	18.2	10	1	RT02_BOVIN
60	2	18.2	10	1	SPI_HALRO
61	2	18.2	10	1	SYK_CAMUP
62	2	18.2	10	1	TEMK_RANTE
63	2	18.2	10	1	TKL3_LOCHI
64	2	18.2	10	1	TKNB_RANRI
65	2	18.2	10	1	TKU1_UREUN
66	2	18.2	10	1	TKU2_UREUN
67	2	18.2	10	1	TRP6_LEUMA
68	2	18.2	10	1	UPA8_HUMAN
69	2	18.2	10	1	UPA8_HUMAN
70	2	18.2	10	1	UXA6_HUMAN
71	2	18.2	10	1	UXA6_CHLTR
72	2	18.2	10	1	XYNB_DICB4
73	2	18.2	11	1	RRK_MEGFL
74	2	18.2	11	1	CA41_LITCI
75	2	18.2	11	1	CA42_LITCI
76	2	18.2	11	1	COXA_CANFA
77	2	18.2	11	1	CS15_BACSU
78	2	18.2	11	1	CX11_CONMR
79	2	18.2	11	1	LPW_THETH
80	2	18.2	11	1	MIB1_KLEPN
81	2	18.2	11	1	MORN_HUMAN
82	2	18.2	11	1	NUHM_CANFA
83	2	18.2	11	1	PGOC_PSEFL
84	2	18.2	11	1	Q29A_COMTE
85	2	18.2	11	1	RS30_ONCMY
86	2	18.2	12	1	FAR7_PENMO
87	2	18.2	12	1	H2AX_ONCMY
88	2	18.2	12	1	LMT1_LOCHI
89	2	18.2	12	1	NO40_LOTJA
90	2	18.2	12	1	NO40_SESRO
91	2	18.2	12	1	NO40_SOYBN
92	2	18.2	12	1	PORD_METIM
93	2	18.2	12	1	PSP1_PHYPA
94	2	18.2	12	1	PVK2_PERAM
95	2	18.2	12	1	RS19_CLYEP
96	2	18.2	12	1	RS19_ELYEP
97	2	18.2	12	1	RS19_TOBBP
98	2	18.2	12	1	SO15_BACSU
99	2	18.2	12	1	TA10_TREME
100	2	18.2	12	1	TM2A_METMA
101	2	18.2	12	1	UH03_RAT
102	2	18.2	12	1	UR2A_CATCO
103	2	18.2	12	1	UR2B_CATCO
104	2	18.2	12	1	UR2_GILMI
105	2	18.2	12	1	UR2_POLSP
106	2	18.2	13	1	AUF8_TENMO

P19852	clypeaster
P83380	lycopersico
P82691	periplaneta
P82003	bombux mori
P82075	litoria rub
P01255	sus scrofa
P31929	homo sapien
P81731	helicoverpa
P80332	oncorhynch
P80431	rattus norv
P41867	calliphora
P42560	mytilus edu
P14537	ceratotheri
P01358	homo sapien
P23260	rana ridibu
P13270	jatropha mu
Q05564	Klebsiella
P19962	clypeaster
P55962	nicotiana t
P11180	bos taurus
P22103	homo sapien
P21996	rattus norv
P80525	fasciola he
Q04367	capsicum an
P83382	locusta mig
P82923	bos taurus
Q10997	halocynthia
Q46464	campylobact
P56923	rana tempor
P30249	locusta mig
P29135	rana ridibu
P40751	urechis uni
P81738	leucophaea
P40930	homo sapien
P32080	homo sapien
P38007	chlamydia t
P80717	dictyoglomu
P12797	megascollia
P82091	litoria cit
P82092	litoria cit
P99501	canis fami
P81095	bacillus su
P58807	conus marmo
P05624	thermus the
P80580	Klebsiella
P01163	homo sapien
P49820	canis fami
P22395	locusta mig
O24246	lotus japon
O24369	seebania ro
P55960	glycine max
P80903	methanobact
P80662	physcomitre
P81555	periplaneta
Q46490	clover yell
Q47881	elm yellows
Q56251	tomato big
P80863	bacillus su
P01371	tremella me
P80652	methanosarc
P56572	rattus norv
P04558	catostomus
P04559	catostomus
P01427	gillichthys
P81022	polyodon sp
P83109	tenebrio mo

107	2	18.2	13	1	AU11_LITRA	P82385	litoria ran	180	2	18.2	15	1	AF11_MALPA	P83141	malva parvi
108	2	18.2	13	1	AU12_LITRA	P82387	litoria ran	181	2	18.2	15	1	ARCA_STRPS	P58827	streptococc
109	2	18.2	13	1	BML_PSGG	P42961	pseudophryn	182	2	18.2	15	1	ASPI_LACSN	P82648	lactobacilli
110	2	18.2	13	1	B317_LEUMA	P41754	leucophaea	183	2	18.2	15	1	ATP2_SPIOL	P80083	spinacia ol
111	2	18.2	13	1	CHEP_PARFC	P42718	parapolybia	184	2	18.2	15	1	CIQA_RAT	P31720	rattus norv
112	2	18.2	13	1	CP1_AKCA	Q10998	apiysia cal	185	2	18.2	15	1	CDN5_LITCE	P82077	litoria cae
113	2	18.2	13	1	CRH1_VESNA	P17215	vespa arali	186	2	18.2	15	1	CUN6_LITCE	P82078	litoria cae
114	2	18.2	13	1	CRH2_VESNA	P17216	vespa arali	187	2	18.2	15	1	CH11_PEA	P21225	pisum sativ
115	2	18.2	13	1	CRH3_VESNA	P17217	vespa arali	188	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
116	2	18.2	13	1	CRH4_VESNA	P17218	vespa arali	189	2	18.2	15	1	COX2_THUOB	P80979	thunus obe
117	2	18.2	13	1	CRH5_VESNA	P17219	vespa arali	190	2	18.2	15	1	ECDA_LYMDI	P80938	lymantria d
118	2	18.2	13	1	CRH6_VESNA	P17220	vespa arali	191	2	18.2	15	1	EGF1_CANFA	P18651	canis famli
119	2	18.2	13	1	CRH7_VESNA	P17221	vespa arali	192	2	18.2	15	1	EGF2_CANFA	P18652	canis famli
120	2	18.2	13	1	CRH8_VESNA	P17222	vespa arali	193	2	18.2	15	1	EGF3_CANFA	P18653	canis famli
121	2	18.2	13	1	CRH9_VESNA	P17223	vespa arali	194	2	18.2	15	1	EGF4_CANFA	P18654	canis famli
122	2	18.2	13	1	CRH10_VESNA	P17224	vespa arali	195	2	18.2	15	1	EGF5_CANFA	P18655	canis famli
123	2	18.2	13	1	CRH11_VESNA	P17225	vespa arali	196	2	18.2	15	1	EGF6_CANFA	P18656	canis famli
124	2	18.2	13	1	CRH12_VESNA	P17226	vespa arali	197	2	18.2	15	1	EGF7_CANFA	P18657	canis famli
125	2	18.2	13	1	CRH13_VESNA	P17227	vespa arali	198	2	18.2	15	1	EGF8_CANFA	P18658	canis famli
126	2	18.2	13	1	CRH14_VESNA	P17228	vespa arali	199	2	18.2	15	1	EGF9_CANFA	P18659	canis famli
127	2	18.2	13	1	CRH15_VESNA	P17229	vespa arali	200	2	18.2	15	1	EGF10_CANFA	P18660	canis famli
128	2	18.2	13	1	CRH16_VESNA	P17230	vespa arali	201	2	18.2	15	1	EGF11_CANFA	P18661	canis famli
129	2	18.2	13	1	CRH17_VESNA	P17231	vespa arali	202	2	18.2	15	1	EGF12_CANFA	P18662	canis famli
130	2	18.2	13	1	CRH18_VESNA	P17232	vespa arali	203	2	18.2	15	1	EGF13_CANFA	P18663	canis famli
131	2	18.2	13	1	CRH19_VESNA	P17233	vespa arali	204	2	18.2	15	1	EGF14_CANFA	P18664	canis famli
132	2	18.2	13	1	CRH20_VESNA	P17234	vespa arali	205	2	18.2	15	1	EGF15_CANFA	P18665	canis famli
133	2	18.2	13	1	CRH21_VESNA	P17235	vespa arali	206	2	18.2	15	1	EGF16_CANFA	P18666	canis famli
134	2	18.2	13	1	CRH22_VESNA	P17236	vespa arali	207	2	18.2	15	1	EGF17_CANFA	P18667	canis famli
135	2	18.2	13	1	CRH23_VESNA	P17237	vespa arali	208	2	18.2	15	1	EGF18_CANFA	P18668	canis famli
136	2	18.2	13	1	CRH24_VESNA	P17238	vespa arali	209	2	18.2	15	1	EGF19_CANFA	P18669	canis famli
137	2	18.2	13	1	CRH25_VESNA	P17239	vespa arali	210	2	18.2	15	1	EGF20_CANFA	P18670	canis famli
138	2	18.2	13	1	CRH26_VESNA	P17240	vespa arali	211	2	18.2	15	1	EGF21_CANFA	P18671	canis famli
139	2	18.2	13	1	CRH27_VESNA	P17241	vespa arali	212	2	18.2	15	1	EGF22_CANFA	P18672	canis famli
140	2	18.2	13	1	CRH28_VESNA	P17242	vespa arali	213	2	18.2	15	1	EGF23_CANFA	P18673	canis famli
141	2	18.2	13	1	CRH29_VESNA	P17243	vespa arali	214	2	18.2	15	1	EGF24_CANFA	P18674	canis famli
142	2	18.2	13	1	CRH30_VESNA	P17244	vespa arali	215	2	18.2	15	1	EGF25_CANFA	P18675	canis famli
143	2	18.2	13	1	CRH31_VESNA	P17245	vespa arali	216	2	18.2	15	1	EGF26_CANFA	P18676	canis famli
144	2	18.2	13	1	CRH32_VESNA	P17246	vespa arali	217	2	18.2	15	1	EGF27_CANFA	P18677	canis famli
145	2	18.2	13	1	CRH33_VESNA	P17247	vespa arali	218	2	18.2	15	1	EGF28_CANFA	P18678	canis famli
146	2	18.2	13	1	CRH34_VESNA	P17248	vespa arali	219	2	18.2	15	1	EGF29_CANFA	P18679	canis famli
147	2	18.2	13	1	CRH35_VESNA	P17249	vespa arali	220	2	18.2	15	1	EGF30_CANFA	P18680	canis famli
148	2	18.2	13	1	CRH36_VESNA	P17250	vespa arali	221	2	18.2	15	1	EGF31_CANFA	P18681	canis famli
149	2	18.2	13	1	CRH37_VESNA	P17251	vespa arali	222	2	18.2	15	1	EGF32_CANFA	P18682	canis famli
150	2	18.2	13	1	CRH38_VESNA	P17252	vespa arali	223	2	18.2	15	1	EGF33_CANFA	P18683	canis famli
151	2	18.2	13	1	CRH39_VESNA	P17253	vespa arali	224	2	18.2	15	1	EGF34_CANFA	P18684	canis famli
152	2	18.2	13	1	CRH40_VESNA	P17254	vespa arali	225	2	18.2	15	1	EGF35_CANFA	P18685	canis famli
153	2	18.2	13	1	CRH41_VESNA	P17255	vespa arali	226	2	18.2	15	1	EGF36_CANFA	P18686	canis famli
154	2	18.2	13	1	CRH42_VESNA	P17256	vespa arali	227	2	18.2	15	1	EGF37_CANFA	P18687	canis famli
155	2	18.2	13	1	CRH43_VESNA	P17257	vespa arali	228	2	18.2	15	1	EGF38_CANFA	P18688	canis famli
156	2	18.2	13	1	CRH44_VESNA	P17258	vespa arali	229	2	18.2	15	1	EGF39_CANFA	P18689	canis famli
157	2	18.2	13	1	CRH45_VESNA	P17259	vespa arali	230	2	18.2	15	1	EGF40_CANFA	P18690	canis famli
158	2	18.2	13	1	CRH46_VESNA	P17260	vespa arali	231	2	18.2	15	1	EGF41_CANFA	P18691	canis famli
159	2	18.2	13	1	CRH47_VESNA	P17261	vespa arali	232	2	18.2	15	1	EGF42_CANFA	P18692	canis famli
160	2	18.2	13	1	CRH48_VESNA	P17262	vespa arali	233	2	18.2	15	1	EGF43_CANFA	P18693	canis famli
161	2	18.2	13	1	CRH49_VESNA	P17263	vespa arali	234	2	18.2	15	1	EGF44_CANFA	P18694	canis famli
162	2	18.2	13	1	CRH50_VESNA	P17264	vespa arali	235	2	18.2	15	1	EGF45_CANFA	P18695	canis famli
163	2	18.2	13	1	CRH51_VESNA	P17265	vespa arali	236	2	18.2	15	1	EGF46_CANFA	P18696	canis famli
164	2	18.2	13	1	CRH52_VESNA	P17266	vespa arali	237	2	18.2	15	1	EGF47_CANFA	P18697	canis famli
165	2	18.2	13	1	CRH53_VESNA	P17267	vespa arali	238	2	18.2	15	1	EGF48_CANFA	P18698	canis famli
166	2	18.2	13	1	CRH54_VESNA	P17268	vespa arali	239	2	18.2	15	1	EGF49_CANFA	P18699	canis famli
167	2	18.2	13	1	CRH55_VESNA	P17269	vespa arali	240	2	18.2	15	1	EGF50_CANFA	P18700	canis famli
168	2	18.2	13	1	CRH56_VESNA	P17270	vespa arali	241	2	18.2	15	1	EGF51_CANFA	P18701	canis famli
169	2	18.2	13	1	CRH57_VESNA	P17271	vespa arali	242	2	18.2	15	1	EGF52_CANFA	P18702	canis famli
170	2	18.2	13	1	CRH58_VESNA	P17272	vespa arali	243	2	18.2	15	1	EGF53_CANFA	P18703	canis famli
171	2	18.2	13	1	CRH59_VESNA	P17273	vespa arali	244	2	18.2	15	1	EGF54_CANFA	P18704	canis famli
172	2	18.2	13	1	CRH60_VESNA	P17274	vespa arali	245	2	18.2	15	1	EGF55_CANFA	P18705	canis famli
173	2	18.2	13	1	CRH61_VESNA	P17275	vespa arali	246	2	18.2	15	1	EGF56_CANFA	P18706	canis famli
174	2	18.2	13	1	CRH62_VESNA	P17276	vespa arali	247	2	18.2	15	1	EGF57_CANFA	P18707	canis famli
175	2	18.2	13	1	CRH63_VESNA	P17277	vespa arali	248	2	18.2	15	1	EGF58_CANFA	P18708	canis famli
176	2	18.2	13	1	CRH64_VESNA	P17278	vespa arali	249	2	18.2	15	1	EGF59_CANFA	P18709	canis famli
177	2	18.2	13	1	CRH65_VESNA	P17279	vespa arali	250	2	18.2	15	1	EGF60_CANFA	P18710	canis famli
178	2	18.2	13	1	CRH66_VESNA	P17280	vespa arali	251	2	18.2	15	1	EGF61_CANFA	P18711	canis famli
179	2	18.2	13	1	CRH67_VESNA	P17281	vespa arali	252	2	18.2	15	1	EGF62_CANFA	P18712	canis famli

253	1	9.1	8	1	FUSS_FUSSO	P81010 fusarium so	326	1	9.1	9	1	OXYA_SQUAC	P42999 squalus aca
254	1	9.1	8	1	GLUR_HUMAN	PQ2729 homo sapien	327	1	9.1	9	1	OXYF_SCYCA	P42997 scyllorhinu
255	1	9.1	8	1	HTF1_PERAM	P04548 periplaneta	328	1	9.1	9	1	OXYT_BUFRE	P42995 bufo regula
256	1	9.1	8	1	HTF2_PERAM	P04549 periplaneta	329	1	9.1	9	1	OXYT_CYPCA	P23879 cyprinus ca
257	1	9.1	8	1	HTF_TENNO	P25419 tenebrio mo	330	1	9.1	9	1	OXYT_ELSFO	P42998 eisenia foe
258	1	9.1	8	1	LCK1_LEUMA	P21140 leucophaea	331	1	9.1	9	1	OXYT_OCTVO	P80027 octopus vul
259	1	9.1	8	1	LCK2_LEUMA	P21141 leucophaea	332	1	9.1	9	1	OXYT_RABIT	P32878 oryctolagus
260	1	9.1	8	1	LCK3_LEUMA	P21142 leucophaea	333	1	9.1	9	1	OXYT_RAJCL	P42994 raja clavat
261	1	9.1	8	1	LCK4_LEUMA	P21143 leucophaea	334	1	9.1	9	1	OXYV_SQUAC	P43000 squalus aca
262	1	9.1	8	1	LCK6_LEUMA	P19588 leucophaea	335	1	9.1	9	1	PGLK_DIAAB	P81179 diaprepes a
263	1	9.1	8	1	LCK7_LEUMA	P19589 leucophaea	336	1	9.1	9	1	RT33_BOVIN	P82926 bos taurus
264	1	9.1	8	1	LCK8_LEUMA	P19590 leucophaea	337	1	9.1	9	1	SAMP_MUSCA	P19095 mustelus ca
265	1	9.1	8	1	LMT2_LEUMI	P22396 locusta mig	338	1	9.1	9	1	SAP_STOVA	P24047 stomopneute
266	1	9.1	8	1	LPK_LEUMA	P10045 leucophaea	339	1	9.1	9	1	TAL1_PICJA	P17440 pichia jadi
267	1	9.1	8	1	NFB_BOVIN	P15507 bos taurus	340	1	9.1	9	1	TAL3_PICJA	P17441 pichia jadi
268	1	9.1	8	1	NS3_MYCTU	P41552 mycobacteri	341	1	9.1	9	1	TKC1_CALVO	P41517 calliphora
269	1	9.1	8	1	OMY_ORGLI	P42455 orconectes	342	1	9.1	9	1	TKL1_LOCMI	P16223 locusta mig
270	1	9.1	8	1	PJP_BRANA	P81707 brassica na	343	1	9.1	9	1	TRP4_LEUMA	P81736 leucophaea
271	1	9.1	8	1	PKR2_PERAM	P82692 periplaneta	344	1	9.1	9	1	UHA2_HUMAN	P40929 homo sapien
272	1	9.1	8	1	PKR3_PERAM	P82618 periplaneta	345	1	9.1	9	1	ULAE_HUMAN	P31931 homo sapien
273	1	9.1	8	1	RPH_PANRO	P08939 pandalus bo	346	1	9.1	9	1	ULAH_HUMAN	P31934 homo sapien
274	1	9.1	8	1	RS7_MYC17	P35564 mycobacteri	347	1	9.1	9	1	ULAK_MOUSE	P99031 mus musculu
275	1	9.1	8	1	RT34_BOVIN	P82929 bos taurus	348	1	9.1	9	1	UN19_CLOPA	P81355 clostridium
276	1	9.1	8	1	UC26_MAIZE	P80632 zea mays (m	349	1	9.1	9	1	UPA3_HUMAN	P30089 homo sapien
277	1	9.1	8	1	UFG6_MOUSE	P86844 mus musculu	350	1	9.1	9	1	UPA6_HUMAN	P30092 homo sapien
278	1	9.1	8	1	UH09_RAT	P56575 rattus norv	351	1	9.1	9	1	UPA7_HUMAN	P30093 homo sapien
279	1	9.1	8	1	UPA1_HUMAN	P30057 homo sapien	352	1	9.1	9	1	YBFR_AZOV1	P25825 azotobacter
280	1	9.1	8	1	UPAA_HUMAN	P30096 homo sapien	353	1	9.1	9	1	AEGL_AGRAE	P83465 agroclybe ae
281	1	9.1	9	1	ALI9_CARMA	P41813 carcinus ma	354	1	9.1	10	1	AH3_PRUSE	P29261 prunus sero
282	1	9.1	9	1	ALI1_CERUL	P81814 carcinus ma	355	1	9.1	10	1	AKYX_LOCMI	P81626 locusta mig
283	1	9.1	9	1	BS43_SERUL	P83375 serratia pl	356	1	9.1	10	1	ALI9_CARMA	P81822 carcinus ma
284	1	9.1	9	1	CCAP_CARMA	P38586 carcinus ma	357	1	9.1	10	1	ANG1_BOTJA	Q10581 bothrops ja
285	1	9.1	9	1	CONG_CONGE	P05486 conus geogr	358	1	9.1	10	1	ANGT_BOVIN	P01017 bos taurus
286	1	9.1	9	1	CONO_CONST	P05487 conus stria	359	1	9.1	10	1	ANGT_CHICK	P01018 gallus gall
287	1	9.1	9	1	COW_CONVE	P83047 conus ventr	360	1	9.1	10	1	APE_CAPGI	P80474 capocytoph
288	1	9.1	9	1	COW_THUOB	P83075 thunnus obe	361	1	9.1	10	1	BPP6_BOTIN	P80426 bothrops in
289	1	9.1	9	1	DL_NEPNO	P24816 nephrops no	362	1	9.1	10	1	BPP_VIPAS	P31351 vipera aspi
290	1	9.1	9	1	DNF1_LOCM1	P16349 locusta mig	363	1	9.1	10	1	BKK_ONCHY	Q9PRZ1 oncorhynch
291	1	9.1	9	1	FAE2_CALVO	P41857 calliphora	364	1	9.1	10	1	CA12_LITCI	P82086 litorea cit
292	1	9.1	9	1	FAE3_CALVO	P41858 calliphora	365	1	9.1	10	1	CAER_LITXA	P56264 litorea kan
293	1	9.1	9	1	FAE3_MARS	P83276 macrobrachi	366	1	9.1	10	1	CATB_SHEEP	P83205 ovis aries
294	1	9.1	9	1	FAE3_PENNO	P83319 penaeus mon	367	1	9.1	10	1	COXA_ONCHY	P80328 oncorhynch
295	1	9.1	9	1	FAE4_CALVO	P41859 calliphora	368	1	9.1	10	1	COXH_ONCHY	P80331 oncorhynch
296	1	9.1	9	1	FAE4_PENNO	P83329 penaeus mon	369	1	9.1	10	1	COXO_RAT	P80432 rattus norv
297	1	9.1	9	1	FAE5_ASYU	P43170 ascaris suu	370	1	9.1	10	1	COXO_THUOB	P80982 thunnus obe
298	1	9.1	9	1	FAE5_CALVO	P41860 calliphora	371	1	9.1	10	1	COXO_RABIT	P80336 oryctolagus
299	1	9.1	9	1	FAE5_PANKE	P42661 panagrellus	372	1	9.1	10	1	COXO_SHEEP	P80337 ovis aries
300	1	9.1	9	1	FAE5_PENNO	P83320 penaeus mon	373	1	9.1	10	1	CU30_LOCMI	P11735 locusta mig
301	1	9.1	9	1	FAE6_CALVO	P41861 calliphora	374	1	9.1	10	1	ESL_LACCA	P81758 lactobacilli
302	1	9.1	9	1	FAE6_MARS	P83279 macrobrachi	375	1	9.1	10	1	ESTA_SCHGA	P81012 schizaphis
303	1	9.1	9	1	FAE7_CALVO	P41862 calliphora	376	1	9.1	10	1	FAE2_PENMO	P83317 penaeus mon
304	1	9.1	9	1	FAE6_MARS	P83281 macrobrachi	377	1	9.1	10	1	FAE5_MACRS	P83278 macrobrachi
305	1	9.1	9	1	FAE9_ASYU	P43172 ascaris suu	378	1	9.1	10	1	FAE6_PANRE	P82660 panagrellus
306	1	9.1	9	1	FAE9_ASYU	P43172 ascaris suu	379	1	9.1	10	1	FAE7_MACRS	P83280 macrobrachi
307	1	9.1	9	1	FIBB_ASYU	P43145 erythrocebu	380	1	9.1	10	1	FARP_LOCMI	P38553 locusta mig
308	1	9.1	9	1	FIBB_MARCO	P19345 macaca tusc	381	1	9.1	10	1	FARP_MANSE	P18523 manduca sex
309	1	9.1	9	1	FIBB_PAPAN	P19344 papio anubi	382	1	9.1	10	1	GLEM_HUMAN	P02728 homo sapien
310	1	9.1	9	1	FIBB_PAPER	P19343 papio hamad	383	1	9.1	10	1	GONI_ALUMI	P37041 alligator m
311	1	9.1	9	1	FIBB_THERE	P19342 theropithec	384	1	9.1	10	1	GONI_CHEPR	P80677 chelysoma
312	1	9.1	9	1	FLA2_TREHY	P80159 trepionema h	385	1	9.1	10	1	GONI_CLUPA	P81749 clupea pall
313	1	9.1	9	1	FRF1_SARBO	P83350 sarcophaga	386	1	9.1	10	1	GONI_PETMA	P04378 petromyzon
314	1	9.1	9	1	HUTU_KLEAE	P12381 klebsiella	387	1	9.1	10	1	GON2_CHEPR	P80678 chelysoma
315	1	9.1	9	1	IPVR_RHCVI	P82992 rhodopseudo	388	1	9.1	10	1	GON2_CHICK	P37043 gallus gall
316	1	9.1	9	1	ISOT_CYPCA	P42991 cyprinus ca	389	1	9.1	10	1	GON3_ONCRE	P20367 oncorhynch
317	1	9.1	9	1	KNL3_HUMVA	P83058 bombina var	390	1	9.1	10	1	GON3_PETMA	P30948 petromyzon
318	1	9.1	9	1	LMTR_PHYKO	P08946 phyllomedusa	391	1	9.1	10	1	GONL_SQUAC	P27429 squalus aca
319	1	9.1	9	1	LMTR_LOCMI	P41489 locusta mig	392	1	9.1	10	1	GS09_BACSU	P80243 bacillus su
320	1	9.1	9	1	MGMT_BOVIN	P29177 bos taurus	393	1	9.1	10	1	HTF1_ROMMI	P18110 romalea mic
321	1	9.1	9	1	NEF_BIV25	P12483 human immun	394	1	9.1	10	1	HTF2_CARMO	P11385 carausius m
322	1	9.1	9	1	NEUO_CAVIO	P49666 cavia porce	395	1	9.1	10	1	HTF_HELZE	P16353 heliothis z
323	1	9.1	9	1	NEUX_HUMAN	P04277 homo sapien	396	1	9.1	10	1	HTF_NAUCI	P10939 nauphoeta c
324	1	9.1	9	1	NEUX_SARHC	P41492 sarcophaga	397	1	9.1	10	1	HTF_TABAT	P14596 tabanus atr
325	1	9.1	9	1	OXYA_SCYCA	P42996 scyllorhinu	398	1	9.1	10	1	LCMS_LEUMA	P21144 leucophaea

399	1	9.1	10	1	LPK2_LEJMA	P41488 locusta mig	472	1	9.1	11	1	TKN1_PSEGU	P42986 pseudophryn
400	1	9.1	10	1	LSK2_LEJMA	P05039 leucophaea	473	1	9.1	11	1	TKN1_OPERU	P8026 uperoleia r
401	1	9.1	10	1	MP2_MCOCC	P61533 microplitis	474	1	9.1	11	1	TKN1_OPERU	P08612 uperoleia r
402	1	9.1	10	1	NS1_MYCTE	P81135 mycobacteri	475	1	9.1	11	1	TKN2_PSEGU	P42987 pseudophryn
403	1	9.1	10	1	PAP1_PARMA	P81863 pardachurus	476	1	9.1	11	1	TKN2_PSEGU	P08616 uperoleia r
404	1	9.1	10	1	POR6_METIM	P80561 methanobact	477	1	9.1	11	1	TKN3_PSEGU	P42988 pseudophryn
405	1	9.1	10	1	QZ06_COMTE	P80465 romamonas t	478	1	9.1	11	1	TKN4_PSEGU	P42989 pseudophryn
406	1	9.1	10	1	QZ06_COMTE	P80465 romamonas t	479	1	9.1	11	1	TKN4_PSEGU	P42990 pseudophryn
407	1	9.1	10	1	RCA_PINES	P81084 pinus pinas	480	1	9.1	11	1	TKNA_CHICK	P19850 gallus gall
408	1	9.1	10	1	RL15_ACHIA	P25221 acholopasm	481	1	9.1	11	1	TKNA_GADMO	P28498 gadus morhu
409	1	9.1	10	1	RRPL_PIRAV	P45946 phorine dis	482	1	9.1	11	1	TKNA_HORSE	P01290 equus cabal
410	1	9.1	10	1	SLAP_BAVIG	P49325 bacillus th	483	1	9.1	11	1	TKNA_ONCMY	P28499 oncorhynch
411	1	9.1	10	1	SP34_DUMJO	P81545 dictyostell	484	1	9.1	11	1	TKNA_RANCA	P22688 rana catesb
412	1	9.1	10	1	TKL2_COMMI	P16224 locusta mig	485	1	9.1	11	1	TKNA_RANRI	P29207 rana ridibu
413	1	9.1	10	1	TKL2_COMMI	P16224 locusta mig	486	1	9.1	11	1	TKNA_SCYCA	P41333 scyllorhinu
414	1	9.1	10	1	TKN1_SCYCA	P06308 scyllorhinu	487	1	9.1	11	1	TKND_RANCA	P22691 rana catesb
415	1	9.1	10	1	TKNH_CHICK	P06657 gallus gall	488	1	9.1	11	1	TKND_ELEMO	P01293 eledone mos
416	1	9.1	10	1	TKNB_ONCMY	P26500 oncorhynch	489	1	9.1	11	1	TKN_PHYFU	P08615 physalaemus
417	1	9.1	10	1	TKNB_RANCA	P22689 rana catesb	490	1	9.1	11	1	UF05_MOUSE	P38643 mus musculu
418	1	9.1	10	1	TKNC_RANCA	P22590 rana catesb	491	1	9.1	11	1	ULAG_HUMAN	P31933 homo sapien
419	1	9.1	10	1	TKNK_FIG	P01292 sus scrofa	492	1	9.1	11	1	UXB2_YEAST	P99013 saccharomyc
420	1	9.1	10	1	TKNS_FHYBI	P05610 phyllomedus	493	1	9.1	11	1	CALM_FETTH	Q05055 tetrahymena
421	1	9.1	10	1	TKS1_AEAE	P42634 aedes aegypt	494	1	9.1	11	1	CD11_LITXA	P56245 litorea xan
422	1	9.1	10	1	TKS2_AEAE	P42634 aedes aegypt	495	1	9.1	11	1	CD14_LITXA	P56246 litorea xan
423	1	9.1	10	1	TKOF_AEAE	P19425 aedes aegypt	496	1	9.1	11	1	CXAL_CONIM	P50983 conus imper
424	1	9.1	10	1	TPIS_NICOB	P29114 nicotiana p	497	1	9.1	11	1	CXL3_CONMR	P58809 conus maro
425	1	9.1	10	1	TPPS_LEJMA	P81747 leucophaea	498	1	9.1	11	1	CXST_CONTE	P58846 conus texti
426	1	9.1	10	1	TRP5_LEJMA	P81749 leucophaea	499	1	9.1	11	1	FARI_CALVO	P41869 calliphora
427	1	9.1	10	1	TRP5_LEJMA	P81749 leucophaea	500	1	9.1	11	1	FIFI_SARBU	P83349 sarcophaga
428	1	9.1	10	1	TRP5_LEJMA	P81749 leucophaea							
429	1	9.1	10	1	UH05_FAI	P06573 rattus norv							
430	1	9.1	10	1	UPA2_HUMAN	P40288 homo sapien							
431	1	9.1	10	1	UPA4_HUMAN	P30590 homo sapien							
432	1	9.1	10	1	UPA5_HUMAN	P30591 homo sapien							
433	1	9.1	10	1	URAI_HUMAN	P22118 homo sapien							
434	1	9.1	10	1	URAI_HUMAN	P24590 homo sapien							
435	1	9.1	10	1	UXE3_MORNO	P17339 moroneilla							
436	1	9.1	10	1	UXA2_CHLIF	P38093 chlamydia l							
437	1	9.1	10	1	UXB1_YEAST	P09012 saccharomyc							
438	1	9.1	10	1	VEG6_BACSU	P00699 bacillus su							
439	1	9.1	11	1	ANG1_CRIGE	P09077 ericia geor							
440	1	9.1	11	1	ASL1_BAYSE	P81446 bacteroides							
441	1	9.1	11	1	ASL2_BAYSE	P81447 bacteroides							
442	1	9.1	11	1	BPP1_HOJIN	P44424 bothrops in							
443	1	9.1	11	1	BPP4_HOJIN	P44425 bothrops in							
444	1	9.1	11	1	BPP6_AKHA	P10221 agkistrodon							
445	1	9.1	11	1	BPP6_AKHA	P4562 agkistrodon							
446	1	9.1	11	1	CA21_LITXA	P82087 litorea cit							
447	1	9.1	11	1	CA22_LITXA	P82088 litorea cit							
448	1	9.1	11	1	CA31_LITXA	P82089 litorea cit							
449	1	9.1	11	1	CA42_LITXA	P82090 litorea cit							
450	1	9.1	11	1	CEP1_ACHIA	P23290 acholopasm							
451	1	9.1	11	1	CEB2_FESAP	P17446 periplaneta							
452	1	9.1	11	1	CEB6_O_NA	P88649 conus aulic							
453	1	9.1	11	1	CEG2_ACHIA	P81350 castridium							
454	1	9.1	11	1	ESI_FAI	P06571 rattus norv							
455	1	9.1	11	1	FAR6_PENMO	P41332 penaeus mon							
456	1	9.1	11	1	FAP9_CALVO	P41864 calliphora							
457	1	9.1	11	1	HS70_PINES	P81672 pinus pinas							
458	1	9.1	11	1	LAGG_POCMP	P81678 oncorhynch							
459	1	9.1	11	1	LSK1_LEJMA	P64428 leucophaea							
460	1	9.1	11	1	LSKP_PERAM	P64428 leucophaea							
461	1	9.1	11	1	MLC_THEIS	P41989 thecocyton							
462	1	9.1	11	1	NKSN_PSELE	P59072 psecudonaja							
463	1	9.1	11	1	PKCL_CARMU	P82684 carausius p							
464	1	9.1	11	1	PVK1_PERAM	P41837 periplaneta							
465	1	9.1	11	1	RANC_RANRI	P08951 rana pipen							
466	1	9.1	11	1	RE41_LITXA	P82074 litorea rub							
467	1	9.1	11	1	RR2_CONAM	P42341 conopliolis							
468	1	9.1	11	1	RRPL_CHAV	P11179 chandipura							
469	1	9.1	11	1	TIN4_PROVO	P31031 proteus vul							
470	1	9.1	11	1	TIN4_HOPTI	P82654 hoplocitrac							
471	1	9.1	11	1	TKG2_CALVO	P41518 calliphora							

ALIGNMENTS

RESULT 1
 XYLA_STRSQ ID XYLA_STRSQ STANDARD: PRI: 9 AA.
 AC P19149;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, last sequence update)
 DT 15-SEP-2003 (Rel. 42, last annotation update)
 DF Xylose isomerase (EC 5.3.1.5) (Fragment).
 GN XYLA.
 OS Streptomyces sp. (strain NCL 82-5-1).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCL_1axID-1911;
 RN [1]
 RP MEDLINE-88326345; PubMed 3415697;
 RX Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;
 RA *Purification and characterisation of glucose (xylose) isomerase from
 RI Chainia sp. (NCL 82-5-1).
 RL Biochem. Biophys. Res. Commun. 155:411-417(1988).
 CC -!- FUNCTION: Involved in D-xylose catabolism.
 CC -!- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
 CC -!- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
 CC -!- SUBUNIT: Homotetramer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
 DR PIR: A31576;
 DR HAMAP: MF_00455;
 DR PIR: A31576;
 DR InterPro: IPR001998; Xylose isom.
 DR PROSITE: PS00172; XYLOSE-ISOMERASE-1; PARTIAL.
 DR PROSITE: PS00173; XYLOSE-ISOMERASE-2; PARTIAL.
 KW Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA: 983 MW: F64BA1EDC5B87DD1 CRC64;

Query Match 16.4% Score 4: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AGSA 4
DB 6 AGSA 6

RESULT 2
MCRX_METM STANDARD; PRI: 14 AA;
AC P58815;
DT 28-FEB-2003 (Rel. 41, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DE Methyl-coenzyme M reductase II alpha subunit (partial) (MCP II
BE alpha) (Fragment).
GN MKIA
OS Methanobacterium thermoautotrophicum (Strain Marburg / DSM 2155).
OC Archaea: Euryarchaeota: Methanobacteria: Methanobacteriales.
CC Methanobacteriales; Methanobacteriales.
CX NCBI_TaxID:79929;
RN [1]
RP MEDLINE:9109470; PubMed:2269406;
RA Kospert S., Linder D., Ellermann J., Thauer R.K.
RT "Two genetically distinct methyl-coenzyme M reductases in
Methanobacterium thermoautotrophicum Strain Marburg and delta H.":
Eur. J. Biochem. 194:871-877(1990).
CC -1- FUNCTION: Reduction of methyl-coenzyme M (2-methylthio)
ethanesulfonic acid) with 7-methylthioheptanoyl:threonine phosphate
to methane and an heterodisulfide.
CC -1- CATALYTIC ACTIVITY: CH(3)-S-CoM + H-S-HEP. CH(4) + CoM S-S-HEP
CC -1- COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY)
TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW NICKEL
PORPHINOID.
CC -1- PATHWAY: Methanogenesis; Last step.
CC -1- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.
CC -1- DEVELOPMENTAL STAGE: THERE ARE TWO MR COMPLEXES IN THIS BACTERIA.
MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
CONTAINS MOSTLY MCR I.
CC Methanobacteriales; Oxidoreductases; Methyltransferase family.
KW Methanobacteriales; Oxidoreductases; Methyltransferase family.
FT NON_TER 14
SQ SEQUENCE 14 AA: 1718 MW; 5317.00562500E29 CRC64.

Query Match 36.4%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKKK 10
DB 11 LKKK 14

RESULT 4
RR16_GINB1 STANDARD; PRI: 12 AA;
AC P36207;
DT 01-JUN-1994 (Rel. 29, Created)
DI 01-JUN-1994 (Rel. 29, Last sequence update)
DE Integrin alpha v beta 5 (Fragment)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S16 (Fragment).
GN RPS16.
OS Ginkgo biloba (Ginkgo).
CC Chloroplast.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgoophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
CX NCBI_TaxID:3311;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE:95094313; PubMed:8001171;
RT "Chloroplastic genomes of Ginkgo biloba and Chlamydomonas moewusii
contain a chlB gene encoding one subunit of a light-independent
protochlorophyllide reductase.":
Kl. Curt. Genet. 26:159-165(1994).

Query Match 27.3%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
DB 7 GSA 9

RESULT 5
NP3_LYMST

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CC -1- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: J01531; AAA66977.1;
CC HAMAP: MF_00385; 1;
CC DR INTERPRO: IPR000407; RIBOSOMAL_S16.
CC DR PROSITE: PS00732; RIBOSOMAL_S16; 1;
CC KW Ribosomal protein; Chloroplast.
CC FT NON_TER 12
CC SQ SEQUENCE 12 AA: 1488 MW; 5700EDAF9D033734 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VKL 7
DB 2 VKL 4

RESULT 4
ITB5_BOVIN STANDARD; PRI: 13 AA;
AC P80747;
DT 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DE Integrin beta-5 (Fragment).
GN ITGB5.
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Rovidae; Bovinae; Bos.
CX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE
TISSUE:Mammary gland;
MEDLINE:97299777; PubMed:9154926;
RA Andersen M.H., Berlund L., Rasmussen J.T., Petersen T.E.;
RT "Bovine PAS-6/7 binds alpha v beta 5 integrins and anionic
phospholipids through two domains.":
Kl. Biochemistry 36:5441-5446(1997).
CC -1- FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.
IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
CC ASSOCIATES WITH ALPHA-V.
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
CC INTERPRO: IPR001169; Integrin_beta_C.
CC PROSITE: PS00243; INTEGRIN_BETA; PARTIAL
KW Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW Repeat.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1299 MW; 844197D005B9865 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
DB 7 GSA 9

RESULT 5
NP3_LYMST

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ID NP4_LYNS7 STANDARD: PRT: 13 AA.
AC P8080;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE Lymnaea DF-amide 3
DE Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora.
OC Lymnaeoidna; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN 11
RP SEQUENCE.
RC TISSUE:Gastric.
RX MEDLINE=9424877; PubMed=847775;
RA Johnson A.H., Reichle J.F.;
RT Lymnaeidae, a new family of neuro-peptides from the pond snail.
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?
RL Eur. J. Biochem. 213:875-879(1993).
CC -:- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR: S14273; S14273.
KW Neuropeptide; Amidation.
FT MOD_RES 13 13
FT UNSURE 12 12
SQ SEQUENCE 13 AA: 1462 MW: 9CA07BA3F505A855 CRC64.

Query Match 27.3%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSA 4
DB 7 GSA 9

RESULT 6
ID NP71_LITFW STANDARD: PRT: 13 AA.
AC P82050;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Spectin 7.1 [contains: Uperin 7.1.1].
DE Litoria ewingi (Brown tree frog) (Fowler's tree frog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104896;
RN 11
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE:Skin secretion;
RA Steinhorst S., Bowle J.H., Lyall M., Winkler C.;
RT "An unusual combination of peptides from the skin glands of Fowler's
RT tree frog, Litoria ewingi. Sequence determination and antimicrobial
RT activity."
RL Aust. J. Chem. 50:889-894(1997).
CC -:- FUNCTION: UPERIN 7.1 SHOWS AN BACTERIAL ACTIVITY AGAINST L. LACTIS
CC AND S. UBERIS. UPERIN 7.1.1 IS INACTIVE.
CC -:- SUBCELLULAR LOCATION: Secreted.
CC -:- TISSUE SPECIFICITY: Expressed by the skin gland glands.
CC -:- MASS SPECTROMETRY: MW=1427; METHIO-FAB; RANGE 1-13.
CC -:- MASS SPECTROMETRY: MW=1184; METHIO-FAB; RANGE 1-13.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT PEPTIDE 1 13 UPERIN 7.1
FT PEPTIDE 3 13 UPERIN 7.1.1
FT MOD_RES 13 13
FT UNSURE 13 13
SQ SEQUENCE 13 AA: 1429 MW: DE17C240CAE322 CRC64.

Query Match 27.3%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SAV 5

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DB 11 SAV 13

RESULT 7
ID MAST_VESBA STANDARD: PRT: 14 AA.
AC P21654;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastoparan B.
DE Vespa basalis (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7444;
RN 11
RP SEQUENCE.
RC TISSUE:Venom;
RX MEDLINE=91174755; PubMed=2006905;
RA Lo C.-L., Hwang L.-C.;
RT "Structure and biological activities of a new mastoparan isolated
RT from the venom of the hornet Vespa basalis."
RL Biochem. J. 274:453-456(1991).
CC -:- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR: S14336; S14336.
KW Mast cell degranulation; Amidation.
FT MOD_RES 14 14
FT UNSURE 14 14
SQ SEQUENCE 14 AA: 1613 MW: D35944CA193A19A2 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKK 8
DB 2 KKK 4

RESULT 8
ID MY14_PHEVI STANDARD: PRT: 14 AA.
AC P46980;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myoactive tetradecapeptide (PTP).
DE Pheretima vittata (Earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbirina; Megascolicidae; Pheretima.
OX NCBI_TaxID=46674;
RN 11
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE:Gut;
RX MEDLINE=96087879; PubMed=8512604;
RA Ukena K., Ouml T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "A novel gut tetradecapeptide isolated from the earthworm, Eisenia
RT foetida."
RL Peptides 16:995-999(1995).
CC -:- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
CC MUSCLES.
CC -:- SIMILARITY: TO INSECTS ALLATOTROPIN.
KW Neuropeptide; Amidation.
FT MOD_RES 14 14
FT UNSURE 14 14
SQ SEQUENCE 14 AA: 1522 MW: DA40BEE67CCD91AD CRC64;

Query Match 27.3%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=skin;
RA *Fernandes J.M.O., Smith V.J., Kemp J.L.
RT *Partial and N-terminal sequencing of a 4 kDa anti-bacterial
RL peptide from skin secretions of rainbow trout.
RL Submitted (MAY-2002) to the SWISS PROT data bank.
CC -1- FUNCTION: Has antibacterial activity against Gram positive
CC Lactococcus lactis.
CC -1- SUBCELLULAR LOCATION: Secreted
CC -1- TISSUE SPECIFICITY: Skin.
DR 334 334:Q05576; Cysticercoid; NAS
DR 334 334:Q05576; Cysticercoid; NAS
DR 334 334:Q05576; Cysticercoid; NAS
KW Antitumor
FT UNSURE 4 4 OR C.
FT UNSURE 5 9 OR T.
FT NON_TER 15 15
SQ SEQUENCE 15 AA: 1601 MW: 49225.28067200 (Fragm.)

Query Match: 27.3% Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KKA 11
DB 4 KKA 5

RESULT 13
SODP-PINIS
ID SODP-PINIS STANDARD: PRL 15 AA
AC P81082
DT 15-JUL-1998 (Rel. 36, Created)
DI 15-JUL-1998 (Rel. 36, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable superoxide dismutase [Cu,Zn], chloroplast (EC 1.15.1.1)
DE (Water stress responsive protein 15) (Fragment).
OS Pinus pinaster (Maritime pine).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
CX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE
RC TISSUE=Needle;
RX MEDLINE:98418576; PubMed-9747604;
RA Costa P., Rahman N., Frigerio J. M., Kramer A., Pionnon C.
RT *Water deficit-responsive proteins in maritime pine.
RL Plant Mol. Biol. 38:587-594(1992).
RN [2]
RP SEQUENCE
RC TISSUE=Needle;
RX MEDLINE:99274068; PubMed-10442913;
RA Costa P., Pionneau C., Bauw G., Bibus G., Rahman N., Kramer A.,
RA Frigerio J. M., Pionnon C.
RT *Separation and characterization of needle and xylenolime pine
RT proteins.
RC Electrophoresis 20:1098-1108(1999)
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) + 2 H(2)O -> (2)
CC -1- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (by
CC similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- INDUCTION: By water stress.
CC -1- SIMILARITY: BELONGS TO THE CU,ZN SUPEROXIDE DISMUTASE FAMILY.
DR InterPro: IPR001424; SOD_CU_ZN.
DR Pfam: PF00080; SODcu; 1.
DR PROSITE: PS00087; SOD_CU_ZN_1; PARTIAL.
DR PROSITE: PS00432; SOD_CU_ZN_2; PARTIAL.
KW Antioxidant; oxidoreductase; Metal-binding; Pin; Zinc; Chloroplast.
FT NON_TER 1 1
FT NON_TER 15 15

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SQ SEQUENCE 15 AA: 1381 MW: 0369BF9DBB69CA8 CRC64;

Query Match: 27.3% Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAS 3
DB 10 AAS 12

RESULT 14
THL-CO-FA
ID THL-CO-FA STANDARD: PRT 15 AA
AC P81347
DT 15-JUL-1998 (Rel. 36, Created)
DI 15-JUL-1998 (Rel. 36, Last sequence update)
DI 15-JUL-1998 (Rel. 36, Last annotation update)
DE Acetyl-CoA acetyltransferase (EC 2.3.1.9) (Acetoacetyl-CoA thiolase)
DE (CP 13) (Fragment).
OS Clostridium pasteurianum.
CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
CC Clostridium.
CX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE
RC STRAIN=W5;
RX MEDLINE:98291870; PubMed-9629918;
RA Fjendstad R., Skjeldal L.
RT *Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.
RC Electrophoresis 19:802-806(1998)
CC -1- CATALYTIC ACTIVITY: 2 acetyl-CoA -> CoA + acetoacetyl-CoA.
CC -1- PATHWAY: JUNCTION IN THE PATHWAY LEADING TO THE PRODUCTION OF
CC EITHER ACIDS (ACETATE OR BUTYRATE) OR SOLVENTS (ACETONE, BUTANOL
CC OR ETHANOL).
CC -1- SUBUNIT: Heterotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE THIOLASE FAMILY.
DR InterPro: IPR002155; Thiolase.
DR PROSITE: PS00098; THIOLASE_1; PARTIAL.
DR PROSITE: PS00737; THIOLASE_2; PARTIAL.
DR PROSITE: PS00049; THIOLASE_3; PARTIAL.
KW Transferase; Acyltransferase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA: 1496 MW: 9735820D61BB35FC CRC64;

Query Match: 27.3% Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SAV 5
DB 6 SAV 10

RESULT 15
UP02-METAN
ID UP02-METAN STANDARD: PRT 15 AA
AC P84339
DI 28-FEB-2003 (Rel. 41, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Unknown 70 kDa protein (Fragment).
OS Metarhizium anisopliae.
CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
CC Hypocreomycetidae; Hypocreales; Clavicipitaceae;
CC mitosporic Clavicipitaceae; Metarhizium.
CX NCBI_TaxID=5533;
RN [1]
RP SEQUENCE
RC STRAIN=54A-1b;

```

RX MEDLINE=22343006; PubMed=12455619;
 RA Kamp A.M., Bidochnka M.O.;
 RI "Protein analysis in a pleomorphically deteriorated strain of the
 insect-pathogenic fungus *Metarhizium anisopliae*."
 R2 Can. J. Microbiol. 48:787-792(2002).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined Mw of this unknown
 protein is: 70 kDa.
 CC NON_TER 15 15
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 15 AA: 1483 MW: 260A74F07C6B8153 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 3
 II
 DB 3 AGS 5

RESULT 16

AL15_CARMA STANDARD: PRT: 8 AA.
 AC P81618;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinus maenas.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 CC NCBI_TaxID=6759;
 RN [1]

RP SEQUENCE.
 RC TISSUE: Cerebral ganglion, and Thoracic ganglion.
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RI "Isolation and identification of multiple neuropeptides of the
 allatostatin superfamily in the shore crab *Carcinus maenas*."
 R2 Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptides; Amidation; Multigene family.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 811 MW: 922879D5A476E7D CRC64.

Query Match 18.2%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
 II
 DB 1 AG 2

RESULT 17

AL15_CARMA STANDARD: PRT: 8 AA.
 AC P81618;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinus maenas.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 CC NCBI_TaxID=6759;
 RN [1]

RP SEQUENCE.

RC TISSUE: Cerebral ganglion, and Thoracic ganglion;

RX MEDLINE=98121193; PubMed=9461295;

RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RI "Isolation and identification of multiple neuropeptides of the
 allatostatin superfamily in the shore crab *Carcinus maenas*."
 R2 Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptides; Amidation; Multigene family.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 795 MW: 922879D5A476E7D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
 II
 DB 1 AG 2

RESULT 18

CAD1_ENTFA STANDARD: PRT: 8 AA.
 AC P13268;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CAD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 CC NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85051889; PubMed=6437872;
 RA Mori M., Sakakami Y., Narita M., Itoai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B., Suzuki A.;
 RI "Isolation and structure of the bacterial sex pheromone, CAD1, that
 induces plasmid transfer in *Streptococcus faecalis*."
 R2 FEBS Lett. 178:97-100(1984).
 CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC HEMOLYSIN PLASMID PADI.
 KW Pheromone.
 SQ SEQUENCE 8 AA: 819 MW: 647DD732C735B9C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
 II
 DB 7 AG 6

RESULT 19

FAR7_ASCSU STANDARD: PRT: 8 AA.
 AC P43171;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 42, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRamide-like neuropeptide AF7.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 CC Ascarididae; Ascaris.
 CC NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95380362; PubMed=7651904;
 RA Cowden C., Sletten A.O.W.;
 RI "Eight novel FMRamide-like neuropeptides isolated from the nematode
 Ascaris suum."
 R2 Peptides 16:491-500(1995).
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)

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CC FAMILY
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 963 MW; 9CD40059D47687D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
DB 1 AG 2

RESULT 20
ID LK5_LFUMA STANDARD; PRT; 8 AA.
AC P19987;
DT 01-FEB-1991 (Rel. 17, Created)
DI 01-FEB-1991 (Rel. 17, Last sequence update)
DE Leucokinin V (L-V).
GS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
OC Blattellidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE Read.
RX MEDLINE: 87052651; PubMed-2877794.
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
KL myotropic peptides of Leucophaea maderae."
RL Comp. Biochem. Physiol. 88C:27-30(1987).
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC ACTIVITY OF COCKROACH PROTOPLASM (HINAGUTI).
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.
DR PIR: S0315; J06335.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 784 MW; 736365A89C665DE CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
DB 1 GS 2

RESULT 21
ID LIMS_STAEP STANDARD; PRT; 8 AA.
AC P43211;
DT 01-NOV-1991 (Rel. 20, Created)
DI 01-NOV-1991 (Rel. 20, Last sequence update)
DE Probable msA leader peptide.
GS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=948;
RX MEDLINE: 91041730; PubMed 2232255.
RA Ross J.L., Eady E.A., Cove J.H., Carlette-Wells, Baumbach S.;
RT "Inducible erythromycin resistance in Staphylococcus is encoded by a
member of the ATP-binding transport super gene family."
BC Mol. Microbiol. 4:1207-1214(1990).

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CC -!- FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE
CC PROTEIN.
CC -----
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CC -----
DR EMBL: X52085; CAA36433.1; -
DR PIR: S1157; LFSAME.
KW Leader peptide; Plasmid
SQ SEQUENCE 8 AA; 937 MW; FA173406858DC1A6 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LK 8
DB 7 LK 8

RESULT 22
ID RSL_ERWCH STANDARD; PRT; 8 AA.
AC P37985;
DT 01-OCT-1994 (Rel. 30, Created)
DI 01-OCT-1994 (Rel. 30, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE 30S ribosomal protein S1 (Fragment).
GN RPSA.
OS Brwinia chrysanthemi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3937;
RA Douillie A., Toussaint A., Faelen M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS MRNA: THUS FACILITATING RECOGNITION OF THE
CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT
CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X74750; CAA52769.1; -
DR PIR: S37141; S37141.
KW Ribosomal protein; Repeat; RNA-binding.
FT NON_TER 1
SQ SEQUENCE 8 AA; 837 MW; 9E18733DC5B339CD CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SA 4
DB 4 SA 5

RESULT 23
VGLG_HSV2H

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JD VGLG_HSV2B STANDARD: PRT: 8 AA.
 AC P81783;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Glycoprotein G (Fragment).
 OS Glycoprotein G (Fragment).
 OC Herpes simplex virus (type 2 / strain B422/BR).
 OC Viruses: JSNA viruses, no RNA stage; Herpesviridae;
 OX Alphaherpesvirinae; Simplexvirus.
 NCBI_TaxID=103921;
 RN 1;
 RP SEQUENCE.
 RA Liljeqvist J.-A., Svennerholm B., Bengtsson T.;
 RL Submitted (APR 1999) to the SWISS-prot data bank.
 CC -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
 CC 2: GH, GB, GC, GD, GI, AND GE.
 CC -!- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV 2 THAN IN
 CC HSV-1.
 KW Glycoprotein. 8
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 683 MW; 7B76786772C864B6 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 GS 3
 DB 1 GS 2

 RESULT 24
 WPI_PERAT STANDARD: PRT: 8 AA.
 AC P83195;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Wall protein-1 (PWP-1) (Fragment).
 OS Perkinsus atlanticus.
 OC Eukaryota; Alveolata; Perkinsea; Perkinidae; Perkinsida; Perkinsida; Perkinsus.
 OX Perkinsus atlanticus.
 NCBI_TaxID=106964;
 RN 1;
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RX MEDLINE=22044350; PubMed=12049410;
 RA Montes J.F., Durfort M., Llado A., Garcia-Valiente J.;
 RL *Characterization and immunolocalization of a wall proteinaceous
 RL component of the cell wall of the protozoan parasite Perkinsus
 RL atlanticus*;
 RL Parasitology 124:477-484(2002).
 CC -!- FUNCTION: Is a major protein component of the cell wall. May play
 CC a key role in the organization of the cell wall and in promoting
 CC the survival of this parasite.
 CC -!- SUBCELLULAR LOCATION: Cell wall. Discrete linked to other cell
 CC wall components.
 CC -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental
 CC stages.
 KW Cell wall.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 765 MW; F1767067B1AA1A CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 AG 2
 DB 6 AG 7

 RESULT 25
 ALC_CHLRE STANDARD: PRT: 9 AA.
 ID ALC_CHLRE

AC P92678;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Allantoicase (EC 3.5.3.4) (Allantoate amidohydrolase) (Fragment).
 OS Chlamydomonas reinhardtii.
 OC Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN 1;
 RP SEQUENCE.
 RC STRAIN=6145C;
 RX MEDLINE=20318328; PubMed=10860551;
 RA Piedras P., Muñoz A., Aguilar M., Pineda M.;
 RL *Allantoate amidohydrolase (Allantoicase) from Chlamydomonas
 RL reinhardtii: its purification and catalytic and molecular
 RL characterization*;
 RL Arch. Biochem. Biophys. 378:340-348(2000).
 CC -!- FUNCTION: Catalyzes the degradation of allantoate to (-)-
 CC ureidoglycolate and (-)-ureidoglycolate to glyoxylate.
 CC -!- CATALYTIC ACTIVITY: Allantoate + H(2)O - (-)-ureidoglycolate +
 CC urea.
 CC -!- PATHWAY: Degradation of allantoin (purine catabolism); second
 CC step.
 CC -!- SUBUNIT: Homohexamer.
 CC -!- MISCELLANEOUS: Optimum pH is 6.5 and 8 for the reactions with
 CC allantoate and ureidoglycolate, respectively.
 CC -!- SIMILARITY: BELONGS TO THE ALLANTOICASE FAMILY.
 KW Hydrolase; Purine metabolism.
 FT UNSURE 5 5 OR Y.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 943 MW; D934ADD9D6D871F2 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 AV 5
 DB 1 AV 2

 RESULT 26
 BUK_CLOPA STANDARD: PRT: 9 AA.
 ID BUK_CLOPA
 AC P81337;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).
 GN BUK.
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN 1;
 RP SEQUENCE.
 RC STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flengsrud R., Skjeldal L.;
 RL *Two-dimensional gel electrophoresis separation and N-terminal
 RL sequence analysis of proteins from Clostridium pasteurianum W5*;
 RL Electrophoresis 19:802-806(1998).
 CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl
 CC phosphate to butyrate (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate - ADP + butanoyl phosphate.
 CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the acetate kinase family.
 DR HAMAP: MF_00542; 1.
 DR InterPro: IPR000890; Acetate_kin.
 DR PROSITE: PS01075; ACETATE_KINASE_1; PARTIAL.
 DR PROSITE: PS01076; ACETATE_KINASE_2; PARTIAL.

KW Transferase: Kinase. 9
 FT NEN 1ER 9 9 1104 MW: 0550405057272428 CRC64:
 SQ SEQUENCE 9 AA: 1104 MW: 0550405057272428 CRC64:
 Query Match 18.2% Score 2: DB 1: Length 9:
 Best Local Similarity 100.0%: Pred. No. 1.3e-05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 6 AG 7
 DB 1
 3 AG 4
 RESULT 27
 USIP_RABIT
 ID USIP_RABIT STANDARD: PRT: 9 AA:
 AC P01158:
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Delta sleep inducing peptide (DSIP)
 DS oryctolagus cuniculus (Rabbit)
 EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 EC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
 CX NCBI_TaxID:9986;
 RN [1]
 RP SEQUENCE
 RX MEDLINE:77185-24; PubMed:862769;
 RA Mandier M., Dudier L., Gacster R., Maier P.F., Border B.A.,
 RA Schoenfelder G.A.:
 R "the delta sleep inducing peptide (DSIP): Comparative properties of
 R the original and synthetic nonapeptide";
 R Experimental Brain Res. 119:124(1978).
 RN [2]
 RP SEQUENCE AND SYNTHESIS.
 RX MEDLINE:73054421; PubMed:568769;
 RA Schoenfelder G.A., Maier P.F., Border B.A., Wilson K., Mandier M.:
 R "the delta EEG (sleep)-inducing peptide (DSIP): X: Amino acid
 R analysis, sequence, synthesis and activity of the nonapeptide";
 R Brain Res. Arch. 376:119-124(1978).
 RN [3]
 RP REVIEW.
 RX MEDLINE:87175129; PubMed:3550726;
 RA Graf M.V., Kastin A.J.:
 R "Delta-sleep-inducing peptide (DSIP): an update".
 R Peptides 7:1165-1187(1986).
 CC -1- FUNCTION: WHEN INFUSED INTO THE MESOCEPHALIC VENTRICLE OF
 CC RECENT RABBITS INDUCES SLEEP AND DECREASES ACTIVITY AND
 CC REDUCES MOTOR ACTIVITIES.
 CC -1- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM ANALYSES OF
 CC OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC
 CC STIMULATION OF THE THALAMUS.
 CC -1- DATABASE: NAME-Protein Spotting.
 CC Note: Issue 8 of March 2001.
 CC WWW: "http://www.expasy.org/spotting/sequences/spotting.html".
 DR PIR: A01422; GDRB.
 SQ SEQUENCE 9 AA: 849 MW: 100365804AA078703 CS764:
 Query Match 18.2% Score 2: DB 1: Length 9:
 Best Local Similarity 100.0%: Pred. No. 1.3e-05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 1 AG 2
 DB 2 AG 3
 RESULT 28
 FAR2_PANRE
 ID FAR2_PANRE STANDARD: PRT: 9 AA:
 AC P41873:
 DT 21-NOV-1995 (Rel. 32, Created)
 DT 21-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide PF2 (SADPNFLRF-amide).
 OS Panagrellus redivivus.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 CX NCBI_TaxID:6233;
 RN [1]
 RP SEQUENCE
 RX MEDLINE:93027659; PubMed:1408999;
 RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
 RA Garrison R.D., Williams J.F., Friedman A.R.:
 R "Two FMRFamide-like peptides from the free-living nematode
 R Panagrellus redivivus";
 R Peptides 13:209-214(1992).
 CC -1- FUNCTION: MYOACTIVE.
 CC -1- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
 CC CAUDALLY TO THE BASE OF THE PHARYNX.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide: Amidation.
 FT MOD_RES 9 AA: 1066 MW: DA00729C4576AAD CRC64:
 SQ SEQUENCE 9 AA: 1066 MW: DA00729C4576AAD CRC64:
 Query Match 18.2% Score 2: DB 1: Length 9:
 Best Local Similarity 100.0%: Pred. No. 1.3e-05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 3 SA 4
 DB 1 SA 2
 RESULT 29
 FAR2_CALVO
 ID FAR2_CALVO STANDARD: PRT: 9 AA:
 AC P41868:
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Calliphramide 13.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 CX NCBI_TaxID:27454;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE:92196111; PubMed:1549595;
 RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.:
 R "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 R neuropeptides (designated calliphramides) from the blowfly
 R Calliphora vomitoria";
 R Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC PIR: D44787; D44787.
 KW Neuropeptide: Amidation.
 FT MOD_RES 9 AA: 1028 MW: 22010695C87AB6D8 CRC64:
 SQ SEQUENCE 9 AA: 1028 MW: 22010695C87AB6D8 CRC64:
 Query Match 18.2% Score 2: DB 1: Length 9:
 Best Local Similarity 100.0%: Pred. No. 1.3e-05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 1 AG 2
 DB 1 AG 2
 RESULT 30
 FAR2_CITAC

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ID LITG_LITAU STANDARD; PRT: 9 AA.
AC 208945;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Litorin
OS Litoria aurea (Green and golden bell frog)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
CE Peleodyadinae; Litoria
CX NCBI_TaxID:8371;
KN [1]
KP SEQUENCE
KC TISSUE: Skin secretion;
RX MEDLINE:7518711; PubMed:1143241;
RA Anastasi A., Espamer V., Endean R.,
RF "Amino acid composition and sequence of litorin, a bombesin-like
RT nonapeptide from the skin of the Australian leopard-frog
Litoria aurea."
RC Experientia 31:510-511(1975).
RN [2]
RP SEQUENCE (METHYLATED VARIANT);
KC TISSUE: Skin secretion;
RX MEDLINE:78003546; PubMed:908397;
RA Anastasi A., Montecucchi R.C., Angeloni F., Espamer V., Endean R.,
RF "Guinea's litorin, the second bombesin-like peptide occurring in
RT methanol extracts of the skin of the Australian frog Litoria aurea."
RL Experientia 33:1289-1289(1977).
CC -1 SUBCELLULAR LOCATION: Secreted.
CC -1 TISSUE SPECIFICITY: Skin.
CC -1 SIMILARITY: BELONGS TO THE BOMBESIN/NEUR-PEPTIN B/RANATENSIN
FAMILY.
DR PIR: S07204; S07204.
DK InterPro: IPR000874; Bombesin.
LK Pfam: PF02044; Bombesin; 1.
LK PROSITE: PS00257; BOMBESIN; 2.
KW Amphibian defense peptide; bombesin family; Acetyl-L-homo-methyl-L-homo-
KW pyrrolidone carboxylic acid.
FT MISC_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MISC_RES 2 2 METHYLATION (PARILLA);
FT MISC_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA: 1103 MW; D70CC12M6JYQ306.1874;
Query Match 18.2% Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 4 AV 5
DB 4 AV 5
RESULT 3;
LIMP_LOCMI STANDARD; PRT: 9 AA.
AC P41799;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Locust amyloid-inhibiting peptide (LIM-MIP)
OS Locusta migratoria (Migratory locust)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Phryganea;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
CX Acridoidea; Acrididae; Oedipodinae; Locusta.
CX NCBI_TaxID:7004;
KN [1]
KP SEQUENCE
RX MEDLINE:92179466; PubMed:1746179;
RA Schoofs L., Holman G.M., Hayes T.K., Natchab W., de Zool A.;
RF "Isolation, identification and synthesis of locust amyloid-inhibiting
RT peptide (LIM-MIP), a novel biologically active non-peptide from
KI Locusta migratoria."
RL Regul. Pept. 36:111-119(1991).

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CC -1 FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINGOUT AND
CC CVIDUCT.
CC -1 TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS
CC IN THE SUBESOPHAGEAL GANGLION.
DR PIR: A60065; AKLQIM.
KW Amidation; Neuropeptide
FT MISC_RES 9 AA; 1050 MW; 48D7D004472AB6C3 CRC64;
SQ SEQUENCE 9 AA; 1050 MW; 48D7D004472AB6C3 CRC64;
Query Match 18.2% Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 AG 2
DB 7 AG 8
RESULT 32
LPCA_STAAU STANDARD; PRT: 9 AA.
ID LPCA_STAAU STANDARD; PRT: 9 AA.
AC P36884;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
OS Staphylococcus aureus, and
OS Streptococcus agalactiae.
OG Plasmid pSCS6, Plasmid pSCS7, and Plasmid pIP501.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID:1280, 1311;
KN [1]
RP SEQUENCE FROM N.A.
RC SPECIES: S. aureus; STRAIN: 436; PLASMID: pSCS7;
RX MEDLINE:92027652; PubMed:1925326;
RA Schwarz S., Cardoso M.;
RT "Nucleotide sequence and phylogeny of a chloramphenicol
RT acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
RT aureus."
RL Antimicrob. Agents Chemother. 35:1551-1556(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES: S. aureus; PLASMID: pSCS6;
RX MEDLINE:92388047; PubMed:1517170;
RA Cardoso M., Schwarz S.;
RT "Nucleotide sequence and structural relationships of a
RT chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
RT Staphylococcus aureus."
RL J. Appl. Bacteriol. 72:289-293(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES: S. aureus; PLASMID: pJB112;
RX MEDLINE:86081739; PubMed:3865770;
RA Brueckner R., Matzura H.;
RT "Regulation of the inducible chloramphenicol acetyltransferase gene
RT of the Staphylococcus aureus plasmid pJB112."
RL EMBO J. 4:2295-2300(1985).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES: S. agalactiae; PLASMID: pIP501;
RX MEDLINE:93096867; PubMed:1461942;
RA Trieu-Cuot P., de Cespedes G., Haurand T.;
RT "Nucleotide sequence of the chloramphenicol resistance determinant of
RT the streptococcal plasmid pIP501."
RL Plasmid 28:272-276(1992).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC -----
DR EMBL: M58515; AAA26612.1;
DR EMBL: M58516; AAA16528.1;
DR EMBL: X02872; CAA26630.1;
DR EMBL: X63827; CAA43217.1;
DR EMBL: X65462; CAA46454.1;
DR EMBL: X24362; R24362;
DR PIR: S30494; S30494;
KW Leader peptide; Antibiotic resistance; Plasmid
SQ SEQUENCE 9 AA: 1074 MW: 5394855AA56B133 CR614;

Query Match 18.2% Score 2: DB 1: Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KK 9
DB 11
2 KK 3

RESULT 34
MOSF_CLYJA STANDARD: PRT: 9 AA.
AC P19853;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE [Phe-6]-mosact.
OS Clypeaster japonicus (Sand dollar).
OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea; Echinoidea; Clypeasteroidea; Clypeasteridae; Clypeaster.
CX NCBI_TaxID=7544;
RN [1]
RP SEQUENCE.
RC TISSUE=Egg jelly;
RA Suzuki N., Kurita M., Yoshino K.I., Kajitani H., Nomura K.
RT "Purification and structure of mosact and its derivatives from the egg jelly of the sea urchin Clypeaster japonicus."
RL Zool. Sci. 4:649-656(1987).
CC -!- FUNCTION: Stimulates sperm respiration and motility.
DR PIR: JN0027; JN0027.
SQ SEQUENCE 9 AA: 924 MW: 93247293CBAB5 CRC64;

Query Match 18.2% Score 2: DB 1: Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SA 4
DB 11
4 SA 5

RESULT 35
PPH1_LYCES STANDARD: PRT: 9 AA.
AC P83380;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Purple acid phosphatase isozyme LeSAP1 (EC 3.1.3.2) (Fragment).
OS Lycopersicon esculentum (tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamids; Solanales; Solanaceae; Solanum.
CX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND GLYCOSYLATION.
RC STRAIN=cv. Moneymaker; TISSUE=Seed;
RA MEDLINE=22361242; PubMed=12474124;
RA Rozzo G.G., Raabothara K.G., Plaxton W.C.;
RT "Purification and characterization of two secreted purple acid phosphatase isozymes from phosphate-starved tomato (Lycopersicon esculentum) cell cultures."
RL Eur. J. Biochem. 269:6278-6286(2002).
CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O -> an alcohol + phosphate.
CX -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SURCELLULAR LOCATION: Secreted.
CC -!- PTM: Glycosylated.
CC -!- MISCELLANEOUS: In the esculentum there are at least two isozymes of purple acid phosphatase.
KW Hydrolase; Glycoprotein.
FT NON_TER 1 1
FT NON_TER 9 3
SQ SEQUENCE 9 AA: 1005 MW: 3F7C04B5042CAA8 CRC64;

Query Match 18.2% Score 2: DB 1: Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AC 2
DB 11
1 AC 2

RESULT 36
PPE1_PERAM STANDARD: PRT: 9 AA.
AC P82691;
DT 16-OCT-2001 (Rel. 40, Created)

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RT egg jelly of the sea urchin Clypeaster japonicus.*;
RL Zool. Sci. 4:649-656(1987).
RN [2]
RP BROMINATION OF HIS-6;
RA MEDLINE=91167743; PubMed=2076468;
RA Takao T., Yoshino K., Suzuki N., Shimomishi Y.;
RT "Analysis of post-translational modifications of proteins by accurate mass measurement in fast atom bombardment mass spectrometry.*;
RL Biomed. Environ. Mass Spectrom. 19:705-712(1990).
CC -!- FUNCTION: Stimulates sperm respiration and motility.
DR PIR: JN0026; JN0026.
KW Bromination.
FT MOD_RES 5 6 BROMINATION (PARTIAL).
SQ SEQUENCE 9 AA: 914 MW: 93245721EDC5BAB5 CRC64;

Query Match 18.2% Score 2: DB 1: Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SA 4
DB 11
4 SA 5

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DI 16-OCT-2001 (Rel. 40, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-1 (pea-PK-1) (FXPRL-amide)
 OS Eupikanina americana (American cockroach)
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattellidae;
 CC Blattella; Periplaneta.
 CX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE: Corpora cardiaca;
 RX MEDLINE=57151923; PubMed=9210164;
 RA Predel R., Reikert M.; Kaufmann K., Penzlin H., Juedo G.;
 RT "Isolation and structural elucidation of two pyrokinins from the
 RT retrocerebral complex of the American cockroach."
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -!- MASS SPECTROMETRY: MW=1010.4; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro: IPR001484; Pyrokinin.
 DR PROSITE: PS00539; PYROKININ; FALSE_NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 9 AA: 1011 MW: 88501760596987061 CRC64:
 SQ SEQUENCE 9 AA: 1011 MW: 88501760596987061 CRC64:
 Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AG 2
 DB 1 AG 4
 RESULT 47
 PTSP_HOMMO STANDARD; PRI: 9 AA.
 AC P82003;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Prothoracicostatic peptide (Bombyx).
 CC Prothoracicostatic peptide (Bombyx moth).
 CC Bombyx mori (Silk moth).
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Tortysia; Bombycoidea;
 CC Bombycidae; Bombyx.
 CX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=C145 X N140; TISSUE=Brain;
 RX MEDLINE=2002634; PubMed=10531308;
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Naito S.,
 RA Katoka H.;
 RT "Identification of a prothoracicostatic peptide in the larval brain of
 RT the silkworm, Bombyx mori."
 RL J. Biol. Chem. 274:31169-31173(1999).
 RN [2]
 RP ERATJM
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Naito S.,
 RA Katoka H.;
 RL J. Biol. Chem. 275:9892-9892(2000).
 CC -!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
 CC gland.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR.
 KW Hormone; Amidation.
 FT MOD_RES 9 AA: 1090 MW: 3878C5B4472AB6C3 CRC64:
 SQ SEQUENCE 9 AA: 1090 MW: 3878C5B4472AB6C3 CRC64:
 Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SA 4
 DB 7 SA 8
 RESULT 38
 RE42_LITRU STANDARD; PRI: 9 AA.
 ID RE42_LITRU STANDARD; PRI: 9 AA.
 AC P82075; P82093;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Rubellidin 4.2/4.3.
 CC Litoria rubella (Desert tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Pelodyadidae; Litoria.
 CX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion.
 RA Steinboerner S.I., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians."
 RL Aust. J. Chem. 49:955-963(1996).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Skin secretion.
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electra. Comparison with the skin peptides from Litoria
 RT rubella".
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
 CC activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- PTM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-
 CC terminal amidation.
 CC -!- MASS SPECTROMETRY: MW=883; METHOD=FAB.
 KW Amphibian defense peptide; Amidation.
 FT MOD_RES 9 AA: 884 MW: 2C2D77205AA72728 CRC64:
 SQ SEQUENCE 9 AA: 884 MW: 2C2D77205AA72728 CRC64:
 Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AG 2
 DB 1 AG 2
 RESULT 39
 THYF_PIG STANDARD; PRI: 9 AA.
 ID THYF_PIG STANDARD; PRI: 9 AA.
 AC P01255;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thymic factor.
 OS Sus scrofa (Pig).


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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE
RX MEDLINE 78026571; PubMed=914862;
RA Picau J.-M., Dardenne M., Blouquit Y., Buch J. P.
RT "Structural study of circulating thymic factor: a peptide isolated
from pig serum. II. Amino acid sequence."
RL J. Biol. Chem. 252:8045-8047(1977).
CC -!- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
CC PIR: A01523; YEPG.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
KW Pyruvate carboxylase.
FT MOD_RES 1 1 PYRUVATE CARBOXYLASE.
SQ SEQUENCE 9 AA; 876 MW; 250B878665B34D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
DB 7 GS 8

RESULT 40
ULAD_HUMAN STANDARD; PRT; 9 AA.
AC P1929;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spad 106) (Fragment).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE-9417969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
Tissot J.-D., Balloch A., Appci R.D., Hochstrasser D.F.
RT "Human liver protein map: update 1993."
RL Electrophoresis 14:1216-1222(1993).
CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6; ITS MW IS: 15 kDa.
CC SWISS-2UPAGE; P1929; HUMAN.
CC NON_TER 9 9
FT SEQUENCE 9 AA; 1129 MW; 202B878665B34D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VK 6
DB 2 VK 3

RESULT 41
AMPN_HELAM STANDARD; PRT; 10 AA
AC P81731;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Aminopeptidase N (EC 3.4.11.2) (CytA(N) receptor) (Fragment).
OS Helicoverpa armigera (Cotton bollworm).
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuidae;
CC Noctuidae; Heliothinae; Helicoverpa.

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OX NCBI_TaxID=29058;
RN [1]
RP SEQUENCE
RX TISSUE=Midgut;
RA Ingie S.S., Trivedi N., Prasad K., Rao K.K., Chatpar H.S.;
RT "Aminopeptidase-N as a receptor for Bacillus thuringiensis CryIAC
toxin from Helicoverpa armigera."
RL Submitted (MAR-1999) to the SWISS-PROT data bank.
CC -!- FUNCTION: ACTS AS A RECEPTOR FOR B.THURINGIENSIS TOXIN CRYIAC.
CC -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, xaa-1-
Xbb- from a peptide, amide or arylamide. xaa is preferably Ala, but
may be most amino acids including Pro (slow action). When a
terminal hydrophobic residue is followed by a prolyl residue, the
two may be released as an intact xaa-Pro dipeptide.
CC -!- COFACTOR: Binds 1 zinc ion (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family M1.
CC -!- INTERPRO: IPR006025; Zn_M1peptidse.
DR PROSITE: PS00142; ZINC_PROTEASE; PARTIAL.
KW Hydrolase; Metalloprotease; Aminopeptidase; Zinc.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1093 MW; 05042EB87B1F1BB CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
DB 7 GS 8

RESULT 42
COXK_ONCMY STANDARD; PRT; 10 AA.
AC P80332;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIa-heart (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
CC NCBI_TaxID=8022;
RN [1]
RP SEQUENCE
RX MEDLINE-94237150; PubMed=8181459;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
of cytochrome c oxidase isolated from rainbow trout."
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) -> 4 ferrocyclochrome
c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIA FAMILY.
DR PIR: S43631; S43631.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1174 MW; 4C8D81CAFAF772C3 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KL 7
DB 9 KL 10

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RESULT 43
COXM_RAT
ID COXM_RAT STANDARD PRT 10 AA.
AC P80431
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIb, Mitochondrial (P80431)
DE (Fragment)
GN COX7B
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC SPAIN-Mistar; TISSUE=Liver;
KA MEDLINE=95124529; PubMed=7601105;
RA Schaeffer H., Noack H., Halandik W., Prandt D., von Jagow G.;
RT "Cytochrome c oxidase in developing rat heart: Enzymic properties and
RT amino terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform."
RL Eur. J. Biochem. 230:235-241(1995)
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-ENCODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyanide + 2 e- + 2 H(2O) -> 4 ferri-
CC cytochrome c + 2 H(2O).
DR PIR: S65387; S65387
KW oxidoreductase; Mitochondrion.
FT NIN_TIR 10
SQ SEQUENCE 10 AA; 1210 MW; CFC7JER77IA332Z CRV64;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KK 9
DB 4 KK 5

RESULT 44
FARC_CALVO
ID FARC_CALVO STANDARD PRT 1 AA
AC P41867
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Calliphora vomitoria L2.
DE Calliphora vomitoria (Blue blowfly)
OS Calliphora vomitoria (Blue blowfly)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Protophyla;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscophora; Gastrophila;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
KA MEDLINE=92196111; PubMed=1549595;
RA Dwyer H., Johnson A.H., Sewell J.C., Scott A.G., Richard L.;
RA Reifel-Miller J.F., Thorpe A.;
RT "Isolation, structure, and activity of type III and type IV
RT neuropeptides (designated calliphrinamides) from the blowfly
RT Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2327-2330(1992)
CC -!- SIMILARITY: BELONGS TO THE FARP (FARFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: C44787; C44787
KW Neuropeptide; Amidation.
FT MOD_RFS 10
SQ SEQUENCE 10 AA; 1156 MW; 22810399C44A608 CRV64;

Query Match 18.2% Score 2; DB 1; Length 10;

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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
DB 2 AG 3

RESULT 45
FARP_MYTED
ID FARP_MYTED STANDARD PRT 10 AA.
AC P42560;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FMRFamide-like neuropeptide ALAGDHFFRF-amide.
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC MEDLINE=93047883; PubMed=1358534;
RA Walker R.J.;
RT "Neuroactive peptides with an N-terminus of Famide or Famide carboxyl terminal."
RL Comp. Biochem. Physiol. 102C:213-222(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FARFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: A58365; A58365
KW Neuropeptide; Amidation.
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1180 MW; C2F80CC9C1EAA87D CRV64;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
DB 3 AG 4

RESULT 46
FIBB_CERS1
ID FIBB_CERS1 STANDARD PRT 10 AA.
AC P14537;
DT 01-JAN-1996 (Rel. 33, Created)
DT 01-JAN-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX NCBI_TaxID=9807;
RN [1]
RP SEQUENCE.
RC O'Neill P.B., Poolittle R.F.;
RA "Mammalian phylogeny based on fibrinopeptide amino acid sequences."
RL Syst. Zool. 22:590-595(1973).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA). LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro: IPR002181; Fibrinogen_C.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 10 FIBRINOPEPTIDE B.

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CC -!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE
CC TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND
CC CHEMOAXIS TOWARD MALTOOLIGOSACCHARIDES
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SUGAR BINDING
CC PROTEIN FAMILY 1.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X68129; CAA48406.1;
DR InterPro: IPR006061; SBP_dom1.
DR PROSITE: PS01047; SBP_BACTERIAL_1; PARTIAL.
KW Transport; Sugar transport; Periplasmic.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1159 MW: 85086244.1566244A CR644:
Query Match 18.2% Score 27 DB 1 Length 107
Best Local Similarity 100.0% P-Val No. 2.5e-04
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 7 LK 8
DB 1 LK 2

Search completed: September 30, 2003, 10:26:02
Job Time : 8.25 secs

GenCore version: 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time: 31.9667 Seconds
(without alignment)
87.339 Million cell updates/sec

Title: US-09-787-443-4

Perfect score: 11

Sequence: 1 ACSAVKLKKA 1:

Scoring table:

Gapop 60.0 , Gapext 50.0

Searched: 830525 seqs, 258052604 residues

Word size : 3

Total number of hits satisfying chosen parameters: 3459

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database :

SPREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	9	2	Q46179 clostridium
2	4	36.4	14	2	Q9R782 bacillus li
3	4	36.4	14	2	Q52676 escherichia
4	4	36.4	15	2	Q52304 escherichia
5	3	27.3	8	2	Q9AGP4 arthrobacte
6	3	27.3	8	2	Q56429 thermus the
7	3	27.3	8	3	Q9HDS4 aspergillus
8	3	27.3	8	3	Q36808 nicotiana p
9	3	27.3	8	8	Q34909 locusta mig
10	3	27.3	8	11	Q50615 mus musculu
11	3	27.3	9	2	Q45852 clostridium
12	3	27.3	9	4	Q16276 homo sapien
13	3	27.3	9	4	Q4BX14 homo sapien
14	3	27.3	9	5	Q8W119 drosophila
15	3	27.3	9	11	Q9QMG3 mus musculu
16	3	27.3	9	11	Q9QWFO mus musculu

17	3	27.3	9	12	Q69100
18	3	27.3	10	2	Q60194
19	3	27.3	10	3	Q9HDS2
20	3	27.3	10	3	Q9HDS1
21	3	27.3	11	2	Q9S618
22	3	27.3	11	2	Q44090
23	3	27.3	11	3	Q9HDS9
24	3	27.3	11	3	Q43131
25	3	27.3	11	3	Q9HDS8
26	3	27.3	11	3	Q9HDS7
27	3	27.3	11	3	Q42762
28	3	27.3	11	3	Q43130
29	3	27.3	11	3	Q9HDS3
30	3	27.3	11	7	Q77908
31	3	27.3	11	11	Q9QXM6
32	3	27.3	12	4	Q9CE14
33	3	27.3	12	5	Q9TY79
34	3	27.3	12	5	Q61574
35	3	27.3	12	10	Q41744
36	3	27.3	12	10	Q94011
37	3	27.3	12	11	Q8CJ30
38	3	27.3	12	13	Q8JHC1
39	3	27.3	12	13	Q90XT2
40	3	27.3	12	13	Q90XT5
41	3	27.3	12	13	Q90XU4
42	3	27.3	12	13	Q90XT0
43	3	27.3	12	13	Q8JHC2
44	3	27.3	13	2	Q9R3R6
45	3	27.3	13	4	Q16141
46	3	27.3	13	4	Q9UJ73
47	3	27.3	13	6	Q9TQS2
48	3	27.3	13	6	Q9TQS1
49	3	27.3	13	8	Q9T569
50	3	27.3	13	8	Q33417
51	3	27.3	13	11	Q9QV14
52	3	27.3	13	11	Q9WT26
53	3	27.3	14	2	Q8KSE3
54	3	27.3	14	2	Q47335
55	3	27.3	14	3	Q8JLG5
56	3	27.3	14	4	Q96Q50
57	3	27.3	14	6	Q8HYM2
58	3	27.3	14	11	Q91Y24
59	3	27.3	14	11	Q99PB8
60	3	27.3	14	12	Q66201
61	3	27.3	14	15	Q98Y97
62	3	27.3	15	2	Q52586
63	3	27.3	15	2	Q46456
64	3	27.3	15	2	Q9R544
65	3	27.3	15	2	Q9R4F0
66	3	27.3	15	2	Q5S0V1
67	3	27.3	15	4	Q9UCCT
68	3	27.3	15	6	Q9TR45
69	3	27.3	15	8	Q37016
70	3	27.3	15	10	Q9SQ16
71	3	27.3	15	10	Q9S8D5
72	3	27.3	15	10	Q9S8L4
73	3	27.3	15	10	Q82431
74	3	27.3	15	10	P82439
75	3	27.3	15	11	P82446
76	3	27.3	15	11	Q9QVA9
77	3	27.3	15	11	Q9QVNO
78	2	18.2	8	2	Q9RQ49
79	2	18.2	8	2	Q9J5R0
80	2	18.2	8	2	Q56759
81	2	18.2	8	2	Q87471
82	2	18.2	8	2	Q9Z1E9
83	2	18.2	8	2	Q9R9E0
84	2	18.2	8	2	Q9R5R0
85	2	18.2	8	2	Q9R4M3
86	2	18.2	8	2	Q51594
87	2	18.2	8	2	P72221
88	2	18.2	8	2	P83158
89	2	18.2	8	2	P83152

Q69100	herpes simp
Q60194	spiroplasma
Q9HDS2	aspergillus
Q9HDS1	aspergillus
Q9S618	prochloroco
Q44090	acholeplasm
Q9HDS9	aspergillus
Q43131	aspergillus
Q9HDS8	aspergillus
Q9HDS7	aspergillus
Q42762	aspergillus
Q43130	aspergillus
Q9HDS3	aspergillus
Q77908	oreochromis
Q9QXM6	mus musculu
Q9CE14	homo sapien
Q9TY79	panulirus i
Q61574	ostertagia
Q41744	zea mays (m
P94011	arabidopsis
Q8CJ30	mus musculu
Q8JHC1	cyprinus ca
Q90XT2	larus glauc
Q90XT5	puffinus gr
Q90XU4	phalacrocor
Q90XT0	grus canad
Q8JHC2	carassius a
Q9R3R6	prochloroco
Q16141	homo sapien
Q9UJ73	homo sapien
Q9TQS2	equus cabal
Q9TQS1	equus cabal
Q9T569	zea mays (m
Q33417	digitalis p
Q9QV14	rattus sp.
Q9WT26	mus musculu
Q8KSE3	enterococcu
Q47335	escherichia
Q8JLG5	ashbya goss
Q96Q50	homo sapien
Q8HYM2	felis silve
Q91Y24	mus musculu
Q99PB8	mus musculu
Q66201	transmissib
Q98Y97	human immun
Q52586	agrobacteri
Q46456	clostridium
Q9R544	mycobacteri
Q9R4F0	desulfovibr
Q5S0V1	nitrogen fi
Q9UCCT	homo sapien
Q9TR45	bos taurus
Q37016	nicotiana a
Q9SQ16	oryza sativ
Q9S8D5	cynara card
Q9S8L4	zea mays (m
P82431	nicotiana t
P82439	nicotiana t
P82446	nicotiana t
Q9QVA9	rattus sp.
Q9QVNO	rattus sp.
Q9RQ49	buchnera ap
Q9J5R0	staphylococ
Q56759	xanthobacte
Q87471	haemophilus
Q9Z1E9	neisseria m
Q9R9E0	bacillus su
Q9R5R0	shigella dy
Q9R4M3	enterococcu
Q51594	escherichia
P72221	pseudomonas
P83158	anabaena sp
P83152	anabaena sp

90	2	18.2	8	2	Q94px7	Q94px7 felis silve
91	2	18.2	8	2	Q8mc34	Q8mc34 heimia myrt
92	2	18.2	8	2	Q8mc32	Q8mc32 rotaria indi
93	2	18.2	8	2	Q8mc42	Q8mc42 sonneratia
94	2	18.2	8	4	Q94px6	Q94px6 felis libyc
95	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
96	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
97	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
98	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
99	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
100	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
101	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
102	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
103	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
104	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
105	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
106	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
107	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
108	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
109	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
110	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
111	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
112	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
113	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
114	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
115	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
116	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
117	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
118	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
119	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
120	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
121	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
122	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
123	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
124	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
125	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
126	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
127	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
128	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
129	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
130	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
131	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
132	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
133	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
134	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
135	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
136	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
137	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
138	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
139	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
140	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
141	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
142	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
143	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
144	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
145	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
146	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
147	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
148	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
149	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
150	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
151	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
152	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
153	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
154	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
155	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
156	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
157	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
158	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
159	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
160	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
161	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued
162	2	18.2	8	4	Q8mc40	Q8mc40 nesata lued


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KW TRANSFERASE.
SQ SEQUENCE 4 AA: 1041 MW: 492402.24Z:Q52604.06.04.
Query Match 36.4% Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 8; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AVKX 7
III
DL 4 AVKX 7

RESULT 2
Q52604 PRELIMINARY: PRI: 4 AA.
AC Q9R782
BT 01-MAY-2006 (TRENBERG, 01, Created)
BT 01-MAY-2006 (TRENBERG, 13, Last sequence update)
BT 01-MAY-2006 (TRENBERG, 13, Last annotation update)
DE beta-lactamase (Fragment).
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1492;
RN 1;
RP SEQUENCE FROM N.A.
RX MESHLINE:0747668; PubMed 2499004;
SA Grossman M.J., Campen J.D.;
SC "Polypeptide and DNA binding proteins of the beta-lactamase repressor for the beta-lactamase gene, Bacillus."
RI Nucleic Acids Res. 15:6049-6052(1985).
RF EMBL: X05794; CAA29241.1;
FI N-TER 14
SQ SEQUENCE 14 AA: 1665 MW: 967442.41Z:Q9R782.06.04.

Query Match 36.4% Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKKK 9
III
DL 9 KKKK 12

RESULT 3
Q52604 PRELIMINARY: PRI: 4 AA.
AC Q52604
BT 01-MAY-1996 (TRENBERG, 01, Created)
BT 01-MAY-1996 (TRENBERG, 01, Last sequence update)
BT 01-MAY-2001 (TRENBERG, 19, Last annotation update)
DE beta-lactamase (Fragment).
OS Escherichia coli.
OX NCBI_TaxID=562;
RN 1;
RP SEQUENCE FROM N.A.
RX MESHLINE:86059219; PubMed 2499004;
SA Frost L.S., Finlay B.B., Oquendoth A., Patanchych W., Lee J.S.;
SC "Characterization and sequence analysis of pilin from E. coli."
RI Bacteriol. 164:1248-1247(1985).
RF EMBL: X05794; CAA29241.1;
FI N-TER 14
SQ SEQUENCE 14 AA: 1713 MW: 507591188B:Q52604.06.04.

Query Match 36.4% Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKKK 9
III
DL 9 KKKK 12

RESULT 4
Q52604 PRELIMINARY: PRI: 15 AA.
AC Q52604
BT 01-MAY-1996 (TRENBERG, 01, Created)
BT 01-MAY-1996 (TRENBERG, 01, Last sequence update)
BT 01-MAY-1999 (TRENBERG, 12, Last annotation update)
DE TRAL protein (Fragment).
OS Escherichia coli.
OX NCBI_TaxID=562;
RN 1;
RP SEQUENCE FROM N.A.
RX MESHLINE:86059219; PubMed 2499004;
SA Frost L.S., Finlay B.B., Oquendoth A., Patanchych W., Lee J.S.;
SC "Characterization and sequence analysis of pilin from E. coli."
RI Bacteriol. 164:1248-1247(1985).
RF EMBL: M19710; AAA32663.1;
FI N-TER 15
SQ SEQUENCE 15 AA: 1844 MW: 507591188B:Q52604.06.04.

Query Match 36.4% Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKKK 9
III
DL 8 KKKK 11

RESULT 5
Q52604 PRELIMINARY: PRI: 8 AA.
AC Q9A394
BT 01-JUN-2001 (TRENBERG, 19, Created)
BT 01-JUN-2001 (TRENBERG, 19, Last sequence update)
BT 01-MAR-2002 (TRENBERG, 20, Last annotation update)
DE Serine hydrolase (Fragment).
OS Actinobacter sp. 11N.
OX NCBI_TaxID=15602;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN 11N;
SA Meskys R., Harris R.J., Casati V., Hasran J., Scrutton N.S.;
SC "Genetic organization of the genes involved in dimethylglycine and sarcosine degradation in Actinobacter spp.: implications for glycine betaine catabolism."
RI Bacteriol. 164:1248-1247(1985).
RF EMBL: AF129478; AAK16481.1;
FI N-TER 1
SQ SEQUENCE 8 AA: 898 MW: 687053333:Q9A394.06.04.

Query Match 27.1% Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKKK 9
III

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KW TRANSFERASE.
SQ SEQUENCE 4 AA: 1041 MW: 492402.24Z:Q52604.06.04.
Query Match 36.4% Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 8; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AVKX 7
III
DL 4 AVKX 7

RESULT 2
Q52604 PRELIMINARY: PRI: 4 AA.
AC Q9R782
BT 01-MAY-2006 (TRENBERG, 13, Created)
BT 01-MAY-2006 (TRENBERG, 13, Last sequence update)
BT 01-MAY-2006 (TRENBERG, 13, Last annotation update)
DE beta-lactamase (Fragment).
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1492;
RN 1;
RP SEQUENCE FROM N.A.
RX MESHLINE:0747668; PubMed 2499004;
SA Grossman M.J., Campen J.D.;
SC "Polypeptide and DNA binding proteins of the beta-lactamase repressor for the beta-lactamase gene, Bacillus."
RI Nucleic Acids Res. 15:6049-6052(1985).
RF EMBL: X05794; CAA29241.1;
FI N-TER 14
SQ SEQUENCE 14 AA: 1665 MW: 967442.41Z:Q9R782.06.04.

Query Match 36.4% Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKKK 9
III
DL 9 KKKK 12

RESULT 3
Q52604 PRELIMINARY: PRI: 4 AA.
AC Q52604
BT 01-MAY-1996 (TRENBERG, 01, Created)
BT 01-MAY-1996 (TRENBERG, 01, Last sequence update)
BT 01-MAY-2001 (TRENBERG, 19, Last annotation update)
DE beta-lactamase (Fragment).
OS Escherichia coli.
OX NCBI_TaxID=562;
RN 1;
RP SEQUENCE FROM N.A.
RX MESHLINE:86059219; PubMed 2499004;
SA Frost L.S., Finlay B.B., Oquendoth A., Patanchych W., Lee J.S.;
SC "Characterization and sequence analysis of pilin from E. coli."
RI Bacteriol. 164:1248-1247(1985).
RF EMBL: X05794; CAA29241.1;
FI N-TER 14
SQ SEQUENCE 14 AA: 1713 MW: 507591188B:Q52604.06.04.

Query Match 36.4% Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKKK 9
III
DL 9 KKKK 12

RESULT 4
Q52604 PRELIMINARY: PRI: 15 AA.
AC Q52604
BT 01-MAY-1996 (TRENBERG, 01, Created)
BT 01-MAY-1996 (TRENBERG, 01, Last sequence update)
BT 01-MAY-1999 (TRENBERG, 12, Last annotation update)
DE TRAL protein (Fragment).
OS Escherichia coli.
OX NCBI_TaxID=562;
RN 1;
RP SEQUENCE FROM N.A.
RX MESHLINE:86059219; PubMed 2499004;
SA Frost L.S., Finlay B.B., Oquendoth A., Patanchych W., Lee J.S.;
SC "Characterization and sequence analysis of pilin from E. coli."
RI Bacteriol. 164:1248-1247(1985).
RF EMBL: M19710; AAA32663.1;
FI N-TER 15
SQ SEQUENCE 15 AA: 1844 MW: 507591188B:Q52604.06.04.

Query Match 36.4% Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKKK 9
III
DL 8 KKKK 11

RESULT 5
Q52604 PRELIMINARY: PRI: 8 AA.
AC Q9A394
BT 01-JUN-2001 (TRENBERG, 19, Created)
BT 01-JUN-2001 (TRENBERG, 19, Last sequence update)
BT 01-MAR-2002 (TRENBERG, 20, Last annotation update)
DE Serine hydrolase (Fragment).
OS Actinobacter sp. 11N.
OX NCBI_TaxID=15602;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN 11N;
SA Meskys R., Harris R.J., Casati V., Hasran J., Scrutton N.S.;
SC "Genetic organization of the genes involved in dimethylglycine and sarcosine degradation in Actinobacter spp.: implications for glycine betaine catabolism."
RI Bacteriol. 164:1248-1247(1985).
RF EMBL: AF129478; AAK16481.1;
FI N-TER 1
SQ SEQUENCE 8 AA: 898 MW: 687053333:Q9A394.06.04.

Query Match 27.1% Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8; Gaps 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKKK 9
III

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DB		4 LKK 5	
RESULT 6			
Q06429			
TD	Q76429	PRELIMINARY:	PRI: P AA
AC	Q76429:		
ET	01 NOV 1994 (JEMBLREL: 01; Created)		
ET	01 NOV 1994 (JEMBLREL: 01; Last sequence update)		
ET	01 DEC 2001 (JEMBLREL: 19; Last annotation update)		
DE	SADON (Fragment).		
DS	Thermus thermophilus.		
OS	Bacterium: Thermus thermophilus (Strain: ATCC 29640).		
PC	Thermus.		
OX	NHL TaxID=234;		
FN	SEQUENCE FROM N.A.		
RC	STRAIN BB 8;		
KX	MEDLINE 89025722; PubMed 3052447;		
KA	Rosen J., Littlechild J.A., Fetherall J.F., Watson H.C., Ball G.J.		
RT	*Nucleotide sequence of the phosphoenolpyruvate kinase gene from the		
KT	extreme thermophile, Thermus thermophilus *;		
NC	Biocompare J: 2543509-517(1989);		
DR	EMBL X12454; CAA31005.1[1];		
FT	NN TER		
SC	SEQUENCE 8 AA: 865 MW: 333874647-2372H (E94A)		
Quality Match:	27.8%; Score N: 30.24; Length B:		
Best Local Similarity:	100.0%; Prod. Num. Seqs:		
Matches:	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
QY	7 LKK 9		
LD	4 LKK 6		
RESULT 7			
Q06424			
TD	Q06424	PRELIMINARY:	PRI: P AA
AC	Q06424:		
ET	01 MAR 2001 (JEMBLREL: 16; Created)		
ET	01 MAR 2001 (JEMBLREL: 16; Last sequence update)		
ET	01 MAR 2001 (JEMBLREL: 16; Last annotation update)		
TE	TTP polypyrrolin (Fragment).		
GN	TTP*		
CS	Aspergillus nidulans.		
OS	Eukaryota, Eungi; Ascomycota; Pezizomycotina; Filicium; Aspergillaceae.		
FA	Fungalata; Trichosporales; Taphozoma; Taphozomaceae; Taphozomaceae; Aspergillaceae.		
OX	NHL TaxID=569;		
BN	C1;		
FC	SEQUENCE FROM N.A.		
RC	STRAIN AVE;		
PA	Gieseler D.W., Borner J.W., Kohn B.W., Taylor T.W.		
SA	"The phylogenetics of mycotoxin and secondary metabolite production in		
SI	Aspergillus nidulans and Aspergillus oryzae."		
SC	Submitted (AIR-2000) to the EMBL/GenBank/Land 1 databases.		
DR	EMBL AF241861; AAC15135.1;		
FW	Polypyrrolin.		
FT	NN TER		
SC	SEQUENCE 8 AA: 807 MW: 842872463-464 (E94B)		
Quality Match:	27.8%; Score N: 30.24; Length B:		
Best Local Similarity:	100.0%; Prod. Num. Seqs:		
Matches:	3; Conservative 0; Mismatches 0; Indels 0; Gaps 0		
QY	1 AIS 4		
LD	2 AIS 4		
RESULT 8			
Q06428			
TD	Q06428	PRELIMINARY:	PRI: P AA

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AC Q36604;
DI G1-NEW-1996 (ITEMBLERel_01, Created)
DT 01-MAY-1999 (ITEMBLERel_10, Last sequence update)
DI 01-JUN-2001 (ITEMBLERel_17, Last annotation update)
DE RPS19 protein (Fragment)
GN RPS19
OS Nicotiana glauca, and
OS Nicotiana glauca (Nicotianaceae).
GC Chloroplast
CC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta.
OC Spermatophytes; Malvales; Malvaceae; core eudicots;
DE Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
NCBI_TAXID 49453, 4948
CDS [1]
RP SEQUENCE FROM N.A.
RA Goulding S.F., Westhead K.G., Morgan C.W., Wolfe K.H.;
RI Mol. Gen. Genet. 019-0(1995);
DR EMBL: Z71234; CAA94933.f;
DR EMBL: Z71225; CAA94921.f;
KW Chloroplast.
FT NCNTER 6 8
SQ SEQUENCE 8 AA: 977 MW: FIV333735A41IA6 CRC64;
Query Match 27.1% Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred.No. 8.3e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 ILK 9
DB 5 ILK 7
RESULT 9
Q34905 PRELIMINARY: PRI: 8 AA.
AC Q34905;
DI G1-NOV-1996 (ITEMBLERel_01, Created)
DT 01-NOV-1996 (ITEMBLERel_01, Last sequence update)
DE 01-DES-2001 (ITEMBLERel_19, Last annotation update)
DE cytochrome b (fragment)
OS Locusta migratoria (Migratory locust).
GC Mitochondrion
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthoptera; Grylloperla; Caelifera; Acridoidea;
OC Acridoidae; Acridinae; Melipodinae; Locusta.
NCBI_TAXID 7604;
CDS [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 662347; ITEMED 284084;
DE McCracken A., Hilderson J., Gjullissen G.;
KT Structure of the coded locusta migratoria mitochondrial genome:
restriction mapping and sequence of ITS ND-1 (URF-1) gene.*;
Jurr. Genet. 11:625-630(1987)
DR EMBL: X65286; CAA28905.f;
KW Mitochondrion.
FT NON_TER 3 6
FI NON_TER 8 AA: 1019 MW: FBH337233G4B45B6 CRC64;
SQ SEQUENCE 8 AA: 1019 MW: FBH337233G4B45B6 CRC64;
Query Match 27.1% Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred.No. 8.3e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 ILK 8
DB 5 ILK 7
RESULT 10
Q3615 PRELIMINARY: PRI: 8 AA.
DI Q3615
AC Q3615;
DT 01-NOV-1996 (ITEMBLERel_01, Created)
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DT 01-NOV-1996 (TRENBLER). 01, Last sequence update)
DE Apolipoprotein A II (Fragment)
GN APOA2.
OS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sturniiformes; Muridae; Murinae; Mus.
OX NCBI_TaxID:10290.
RN 1.
RS SEQUENCE FROM N.A.
RT STRAIN C57BL/6J.
RX MEDLINE:9419082; PubMed:8469496.
KA Nakada S, et al.
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR."
RL Mamm. Genome 5:349-356(1994).
DR EMBL: 005511; AAB60462.1; .
DR MGI: M1148250; APOA2.
KW Apolipoprotein.
FT NON_TER.
SQ SEQUENCE 9 AA: 78 CDS:5861-5864 PROA2
Query Match 27.8% Score 3; Db 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 KKA 4
DB 1.
SQ 4 KKA 4
RESULT 11
Q4582 PRELIMINARY: PKT: 9 AA.
AC Q4582.
DT 01-NOV-1996 (TRENBLER). 01, Created)
DT 01-NOV-1996 (TRENBLER). 01, Last sequence update)
DE Chloramphenicol acetyltransferase (catB)
OS Clostridium Batyricum.
DR GenBank: F01800.
OX NCBI_TaxID:1492.
FN 11.
RS SEQUENCE FROM N.A.
RX MEDLINE:9414268; PubMed:1489200.
KA Douglas A S., Basam T L., Reed J L.
RT Comparative sequence analysis of the catB gene from Clostridium
RL Antimicrob. Agents Chemother. 36:216-220(1992).
DR EMBL: M01133; AAA74864.1; .
SQ SEQUENCE 9 AA: 1094 MW: 124133.621 AA: 9 AA.
Query Match 27.8% Score 3; Db 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 KKA 11
DB 6 KKA 8
SQ 9 KKA 11
RESULT 12
Q16276 PRELIMINARY: PKT: 9 AA.
AC Q16276.
DT 01-NOV-1996 (TRENBLER). 01, Created)
DT 01-NOV-2000 (TRENBLER). 15, Last sequence update)
DT 01-NOV-2000 (TRENBLER). 15, Last annotation update)
DE Neurofibromatosis type 2 (Fragment).
GN NF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606.
RN 1.
RS SEQUENCE FROM N.A.
RX MEDLINE:95038750; PubMed:751243.
KA Arai F., Ikeuchi T., Nakamura Y.
RT "Characterization of the translocation breakpoint on chromosome
RL Hum. Mol. Genet. 3:947-949(1994).
DR EMBL: S75843; AA014390.2; .
FT NON_TER.
SQ SEQUENCE 9 AA: 1044 MW: 154300.337212404 CRC64.
Query Match 27.8% Score 3; Db 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 KKA 8
DB 4 KKA 6
SQ 6 KKA 8
RESULT 13
Q9BX14 PRELIMINARY: PKT: 9 AA.
AC Q9BX14.
DT 01-JUN-2001 (TRENBLER). 17, Created)
DT 01-JUN-2001 (TRENBLER). 17, Last sequence update)
DT 01-JUN-2001 (TRENBLER). 17, Last annotation update)
DS BA254M13.1 (Novel protein); (Fragment).
GN C11C99015.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID:9606.
FN 11.
RS SEQUENCE FROM N.A.
KA Kline S.
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL353599; CAC34533.1; .
FT NON_TER.
SQ SEQUENCE 9 AA: 1609 MW: 171600.0903332580 CRC64.
Query Match 27.8% Score 3; Db 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AVK 6
DB 7 AVK 7
SQ 4 AVK 7
RESULT 14
Q8W119 PRELIMINARY: PKT: 9 AA.
AC Q8W119.
DT 01-MAR-2002 (TRENBLER). 20, Created)
DT 01-MAR-2002 (TRENBLER). 20, Last sequence update)
DT 01-MAR-2003 (TRENBLER). 23, Last annotation update)
DE Mod(mda4) protein (Fragment).
GN MOD(mda4) OR CG7836 OR CG8076 OR CG15500 OR CG15802 OR
GN CG1815; OR CG12491.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID:7227.
RN 11.
RS SEQUENCE FROM N.A.
RC STRAIN:mod(mda4)31; TRANSPOSON Stalker;
RX MEDLINE:21490778; PubMed:11604507;
RA Wei W., Brennan M.D.;
RT "The gypsy Insulator Can Act as a Promoter-Specific Transcriptional

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R1 Submitted (1998)
R2 Mol. Cell. Biol. 21:7314-7320(2001)
R3 EMBL: AF214650; AAL33875.1;
R4 Flybase: FBQC002787; mcd(mcd4)
R5 Non TER
R6 SEQUENCE 9 AA: 946 MW: 955490 32222276 28564
Query Match: 27.3% Score 4; DB 12; Length 9;
Best Local Similarity: 100.0% Prod. No. 9 3005;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 VKK 7
QZ 1
LB 5 VKK 5
RESULT 15
Q69100 PRELIMINARY: 9 AA:
AC Q69100
DT 01-JUN-2001 (EMBL:rel. 13, created)
DI 01-JUN-2001 (EMBL:rel. 13, last sequence update)
ID 01-JUN-2001 (EMBL:rel. 13, last annotation update)
DE Nucleon protein (Fragment)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Murinae; Mus
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Moore M J, Kirsch P, Roth J, F...
RT "Identification of NRCAM and ankrdin B regions in disordered runs
RT "in the region of Cutaract fragment".
RL Submitted (Feb 2001) to the EMBL/GenBank/DBJ databases.
R1 EMBL: AF464721; AAK258.4.1;
R2 Non TER
R3 SEQUENCE 9 AA: 1039 MW: 1072155527 28564
Query Match: 27.3% Score 4; DB 12; Length 9;
Best Local Similarity: 100.0% Prod. No. 9 3005;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 KKK 10
QZ 1
LB 5 KKK 5
RESULT 16
Q69100 PRELIMINARY: 9 AA:
AC Q69100
DT 01-MAY-2001 (EMBL:rel. 13, created)
DI 01-MAY-2001 (EMBL:rel. 13, last sequence update)
ID 01-DEC-2001 (EMBL:rel. 19, last annotation update)
DE Proteinase 3 (Fragment)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Murinae; Mus
OX NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Moore M J, Kirsch P, Roth J, F...
RT "Identification of NRCAM and ankrdin B regions in disordered runs
RT "in the region of Cutaract fragment".
RL Submitted (Jun 1998) to the EMBL/GenBank/DBJ databases.
R1 EMBL: A007040; CAA07429.1;
R2 EMBL: M0149350; P1013;
R3 Non TER
R4 SEQUENCE 9 AA: 947 MW: 957267743962 28564
Query Match: 27.3% Score 4; DB 12; Length 9;
Best Local Similarity: 100.0% Prod. No. 9 3005;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 KKK 7
QZ 1
LB 5 KKK 4

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QY 1 ASS 3
QZ 1
LB 2 ASS 4
RESULT 17
Q69100 PRELIMINARY: 9 AA:
AC Q69100
DT 01-MAY-1996 (EMBL:rel. 1, created)
DI 01-MAY-1996 (EMBL:rel. 1, last sequence update)
ID 01-MAY-1996 (EMBL:rel. 8, last annotation update)
DE Protein 62 (Fragment)
OS Herpes simplex virus (type 2)
OC Viruses; dsDNA viruses; in RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus
OX NCBI_TaxID:10330;
RN [1]
RP SEQUENCE FROM N.A.
RA Yee S, Chowdhary S, Bhattacharya M, Conley A J, Wold W S,
RA Patterson W J
RT "Identification and characterization of the Herpes simplex virus type
RT "2 gene encoded in the essential capsid protein ICP32/VP19c".
RL Submitted (May 1996) to the EMBL/GenBank/DBJ databases.
R1 EMBL: M34495; AAA45647.1;
R2 Non TER
R3 SEQUENCE 9 AA: 993 MW: 1136105881 20370 CRC64;
Query Match: 27.3% Score 4; DB 12; Length 9;
Best Local Similarity: 100.0% Prod. No. 9 3005;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 SAV 5
QZ 1
LB 5 SAV 5
RESULT 18
Q69100 PRELIMINARY: 10 AA:
AC Q69100
DT 01-MAY-1996 (EMBL:rel. 9, created)
DI 01-MAY-1996 (EMBL:rel. 9, last sequence update)
ID 01-DEC-2001 (EMBL:rel. 19, last annotation update)
DE Phosphotransferase (Fragment)
OS Spiroplasma pheniceum
OC Spiroplasma; Spirochaetes; Entomoplasmatales;
OC Spiroplasmataceae; Spiroplasma
OX NCBI_TaxID:47846;
RN [1]
RP SEQUENCE FROM N.A.
RA Foissac X, Sallard C, Boze J M,
RA "Identification and sequence analysis of Spiroplasma pheniceum and
RA "Spiroplasma kakehi spiroplasmodes".
RL Submitted (May 1996) to the EMBL/GenBank/DBJ databases.
R1 EMBL: U87458; AAR05467.1;
R2 Non TER
R3 SEQUENCE 10 AA: 1113 MW: 5624205670533 CRC64;
Query Match: 27.3% Score 4; DB 2; Length 10;
Best Local Similarity: 100.0% Prod. No. 1 1e-04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 KKK 3
QZ 1
LB 2 KKK 4

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OX NCBI_LtaxID: 50624;
RN [1]
SC SEQUENCE FROM N.A.
SA Geisel D.M., Barber J.W., Horn B.W., Taylor J.W.,
P. "The phylogenetics of mycetozoa and sclerotium production in
Aspergillus flavus and Aspergillus oryzae."
RL Submitted (APR 2000) to the EMBL/GenBank/DBJ databases
DR EMBL: AF261875; AAC16143.1;
KW POLYPEPTIDE.
FT NON-TER.
SQ SEQUENCE 11 AA: 1129 MW: 250460 DALY 40% ID
Query Match: 27.0% Score 3: DB 3: Length 11:
Best Local Similarity: 100.0% Prod. No.: 128-04;
Matches 3: Conservative 0: Mismatches 0: Gaps 0:
QY 1 AAS 3
DB 2 AAS 4
[1]
RESULT 24
QHDR
ID Q5H08 PRELIMINARY: FR1: 11 AA.
AC Q5H08
DT 01-MAR-2001 (EMBLrel: 16, Created)
DI 01-MAR-2001 (EMBLrel: 16, Last sequence update)
DI 01-MAR-2001 (EMBLrel: 16, Last annotation update)
DE TrpC polypeptide (fragment).
GN TrpC
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitospic Trichocomaceae; Aspergillus.
OX NCBI_LtaxID: 5062;
RN [1]
SC SEQUENCE FROM N.A.
SA Geisel D.M., Barber J.W., Horn B.W., Taylor J.W.,
P. "The phylogenetics of mycetozoa and sclerotium production in
Aspergillus flavus and Aspergillus oryzae."
RL Submitted (APR 2000) to the EMBL/GenBank/DBJ databases
DR EMBL: AF261875; AAC16143.1;
KW POLYPEPTIDE.
FT NON-TER.
SQ SEQUENCE 11 AA: 1128 MW: 250460 DALY 40% ID
Query Match: 27.0% Score 3: DB 3: Length 11:
Best Local Similarity: 100.0% Prod. No.: 128-04;
Matches 3: Conservative 0: Mismatches 0: Gaps 0:
QY 1 AAS 3
DB 2 AAS 4
[1]
RESULT 25
QHDR
ID Q5H08 PRELIMINARY: FR1: 11 AA.
AC Q5H08
DT 01-MAR-2001 (EMBLrel: 16, Created)
DI 01-MAR-2001 (EMBLrel: 16, Last sequence update)
DI 01-MAR-2001 (EMBLrel: 16, Last annotation update)
DE TrpC polypeptide (fragment).
GN TrpC
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitospic Trichocomaceae; Aspergillus.
OX NCBI_LtaxID: 5062;
RN [1]
SC SEQUENCE FROM N.A.
SA Geisel D.M., Barber J.W., Horn B.W., Taylor J.W.,
P. "The phylogenetics of mycetozoa and sclerotium production in
Aspergillus flavus and Aspergillus oryzae."
RL Submitted (APR 2000) to the EMBL/GenBank/DBJ databases
DR EMBL: AF261875; AAC16143.1;
KW POLYPEPTIDE.
FT NON-TER.
SQ SEQUENCE 11 AA: 1128 MW: 250460 DALY 40% ID
Query Match: 27.0% Score 3: DB 3: Length 11:
Best Local Similarity: 100.0% Prod. No.: 128-04;
Matches 3: Conservative 0: Mismatches 0: Gaps 0:
QY 1 AAS 3
DB 2 AAS 4
[1]
RESULT 26
QHDR
ID Q5H08 PRELIMINARY: FR1: 11 AA.
AC Q5H08
DT 01-MAR-2001 (EMBLrel: 16, Created)
DI 01-MAR-2001 (EMBLrel: 16, Last sequence update)
DI 01-MAR-2001 (EMBLrel: 16, Last annotation update)
DE TrpC polypeptide (fragment).
GN TrpC
OS Aspergillus flavus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitospic Trichocomaceae; Aspergillus.
OX NCBI_LtaxID: 5062;
RN [1]
SC SEQUENCE FROM N.A.

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RA STRAIN:1X12_10_2S;
 RA Geiser D.M., Gerner J.W., Horn B.W., Taylor J.W.;
 "The phylogenetics of mycotoxin and sclerotium production in
 Aspergillus flavus and Aspergillus oryzae."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBS databases.
 KW EMBL: AF261877; AAG16361.1;
 KW Polypeptide.
 FT NON_TER
 ST 11
 SQ SEQUENCE 11 AA: 114 MW: 8F0FE03B2C72AB5 CRC64;
 Query Match 27.4% Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e-04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGS 4
 DB 2 AGS 4
 RESULT 27
 042762 PRELIMINARY; PRT; 11 AA
 AC 042762
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE TrpC polypeptide (Fragment).
 GN TrpC.
 OS Aspergillus flavus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Mitosporic Trichocomaceae; Aspergillales.
 OX NCBI_TaxID:5059;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN:5.1;
 RA Geiser D.M., Pitt J.L., Taylor J.W.;
 "Cryptic speciation and recombination in the aflatoxin producers
 Aspergillus flavus."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBS databases.
 KW EMBL: AF046857; AAC01692.1;
 KW Polypeptide.
 FT NON_TER
 ST 11
 SQ SEQUENCE 11 AA: 1142 MW: 8F0FE03B2C72AB5 CRC64;
 Query Match 27.4% Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e-04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGS 4
 DB 2 AGS 4
 RESULT 28
 043100 PRELIMINARY; PRT; 11 AA
 AC 043100
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE TrpC polypeptide (Fragment).
 GN TrpC.
 OS Aspergillus parasiticus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Mitosporic Trichocomaceae; Aspergillales.
 OX NCBI_TaxID:5067;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN:CA-31, and CA1-C5;
 RA Geiser D.M., Pitt J.L., Taylor J.W.;
 "Cryptic speciation and recombination in the aflatoxin producers

FI fungus Aspergillus flavus."
 RA Proc. Natl. Acad. Sci. U.S.A. 95:368-393(1998).
 DR EMBL: AF036970; AAC01705.1;
 DR EMBL: AF036869; AAC01704.1;
 KW Polypeptide.
 FT NON_TER
 ST 11
 SQ SEQUENCE 11 AA: 1128 MW: 8F0FE03B2C72AB5 CRC64;
 Query Match 27.4% Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e-04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGS 3
 DB 2 AGS 4
 RESULT 29
 09HDS3 PRELIMINARY; PRT; 11 AA
 AC 09HDS3
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE TrpC polypeptide (Fragment).
 GN TrpC.
 OS Aspergillus flavus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Mitosporic Trichocomaceae; Aspergillales.
 OX NCBI_TaxID:5059;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN:A12C;
 RA Geiser D.M., Gerner J.W., Horn B.W., Taylor J.W.;
 "The phylogenetics of mycotoxin and sclerotium production in
 Aspergillus flavus and Aspergillus oryzae."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBS databases.
 KW EMBL: AF261862; AAG16361.1;
 KW Polypeptide.
 FT NON_TER
 ST 11
 SQ SEQUENCE 11 AA: 1133 MW: 8F0FE03B2C72AB5 CRC64;
 Query Match 27.4% Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e-04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGS 4
 DB 2 AGS 4
 RESULT 30
 077908 PRELIMINARY; PRT; 11 AA
 AC 077908
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 2 (Fragment).
 GN Oryzomys niloticus (Nile tilapia).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis
 OX NCBI_TaxID:8128;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC MEDLINE:9835113; PubMed:7649549;
 RA Malaga Trillo E., Zaleska-Rozynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultman H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci."
 RL Genetics 149:1527-1547(1998).

OK EMBL: AF036007.9; AAC41358.1; 27.38; Score 3; DB 5; Length 12;
 FT NON_TER 1 1
 FI NON_TER 11 11
 SQ SEQUENCE 11 AA; 1261 MW; 4440CSA7EB9 (RP+ CR+64)
 Query Match 27.38; Score 3; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;
 QY 5 SAV 5
 QZ 9 SAV 11
 RESULT 11
 Q00XME PRELIMINARY; PRI: 11 AA;
 AC Q00XME;
 DT 01-MAY-2000 (1-EMBLrel, 13; Created)
 DT 01-MAY-2000 (1-EMBLrel, 13; Last sequence update)
 DT 01-DEC-2001 (1-EMBLrel, 19; Last annotation update)
 FE glutamate receptor A (fragment);
 OS Mus musculus (mouse);
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurophagina; Muridae; Mus;
 CC NCBI TaxID: 10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bass P.L., Arusavaga P.J.
 RT "A phylogenetic analysis reveals an unusual sequence conservation
 within regions involved in RNA editing."
 RL Submitted (Nov 1999) To the EMBL/GenBank/DDBJ databases
 DR EMBL: AF211547; AAC23954.1;
 KW receptor;
 FT NON_TER 1 1
 FI NON_TER 11 11
 SQ SEQUENCE 11 AA; 1077 MW; 2837105762771AL (RP+64)
 Query Match 27.38; Score 3; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;
 QY 2 GSA 4
 QZ 9 GSA 10
 RESULT 12
 Q00E14 PRELIMINARY;
 AC Q00E14;
 DT 01-MAY-2000 (1-EMBLrel, 13; Created)
 DT 01-MAY-2000 (1-EMBLrel, 13; Last sequence update)
 DT 01-MAY-2000 (1-EMBLrel, 13; Last annotation update)
 FE Intersection short form (fragment);
 GN ITSN;
 OS Homo sapiens (human);
 CC Eukaryota; Metazoa; Chordata; Mammalia; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo;
 CC NCBI TaxID: 9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Guipponi M., Scott H.S., Chen H., Sotoca A., Sossner J.,
 RA Antonarakis S.E.;
 RT "Two isoforms of a human interstellar (ITSN) protein are produced by
 brain specific alternative splicing in a step-adding way."
 RL Genomics 53:469-476(1998)
 DR EMBL: AF064245; AAC80446.1;
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1363 MW; 4296144234A (RP+64)
 Query Match 27.4%; Score 3; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 VKL 7
 QZ 1 VKL 3
 RESULT 34
 Q01V79 PRELIMINARY; PRI: 12 AA;
 AC Q01V79;
 DT 01-MAY-2000 (1-EMBLrel, 13; Created)
 DT 01-MAY-2000 (1-EMBLrel, 13; Last sequence update)
 DT 01-DEC-2001 (1-EMBLrel, 19; Last annotation update)
 CE Potassium channel (fragment)
 GN SHAKER;
 OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Decapoda; Decapoda; Pleocyemata; Palinura;
 CC Palinuroidea; Palinuridae; Palinurus;
 CC NCBI TaxID: 6735;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 48340950; PubMed: 9666521;
 RA Kim M., Bore B.J., Lanning G.G., Doshi M., Moskowitz H.S., Farnham J.,
 RA Harris Warrick R.M.;
 RT "Expression of *Panulirus shaker* potassium channel splice variants."
 RL Recept. Channels 5:291-304(1998);
 DR EMBL: AF017131; AAC5911.1;
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1227 MW; 047990CA44D4D34 CRC64;
 Query Match 27.4%; Score 3; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAS 4
 QZ 9 AAS 10
 RESULT 34
 Q01574 PRELIMINARY; PRI: 12 AA;
 AC Q01574;
 DT 01-AUG-1998 (1-EMBLrel, 07; Created)
 DT 01-AUG-1998 (1-EMBLrel, 07; Last sequence update)
 DT 01-DEC-2001 (1-EMBLrel, 19; Last annotation update)
 DE Hypothetical 1.4 kDa protein (fragment);
 OS Ostertagia ostertagi;
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditia; Strongylida;
 CC Trichostrongylidae; Haemonchidae; Ostertagiinae; Ostertagia;
 CC NCBI TaxID: 6317;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 20233682; PubMed 10769181;
 RA Moore G., Tettley L., Devaney E.;
 RT "Identification of abundant mRNAs from the third stage larvae of the
 parasitic nematode, *Ostertagia ostertagi*."
 RL Biochem. J. 347:763-770(2000).
 DR EMBL: AF052045; AAC06297.1;
 KW Hypothetical protein;
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1369 MW; C0FF667C1CA776C6 CRC64;
 Query Match 27.4%; Score 3; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 KKA 11
 QZ 9 KKA 11


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CC Cyprinidae: Carassius.
CX NBL_TaxID 7957;
RN
SEQUENCE FROM N.A.
SA Li, S., H. W., Wang Y., Zhu Z.,
K. "Cloning and functional analysis of different promoters "
R. Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases
DR EMBL: AF51602; AAM77902;
P NBL_TaxID 12
SQ SEQUENCE 12 AA; 1292 MW; 91AF79AEFAAAACA (90%)
Query Match
Best Local Similarity 100.0%; Score 3; DB 4; Length 12;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;
QY 4 AVK 6
PQ 13 AVK 12
RESULT 44
C99496 PRELIMINARY: PRI: 13 AA
AC C99496;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2001 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN P876
OS Prochlorococcus sp.
OC Bacteria: Cyanobacteria: Prochlorophytes: Prochlorococcus.
CX NBL_TaxID 1420;
RN 111
RP SEQUENCE FROM N.A.
SA Trach E., Christl S.W.
R "Genetic diversity in Prochlorococcus (cyanobacteria)
R sorted from the Sargasso Sea and Red Sea".
R Limnol. oceanogr. 43:1515-1530 (1998).
DR EMBL: AF156221; AAL21275.1;
DR EMBL: AF076221; AAL21273.1;
FT NBL_TaxID 14
SQ SEQUENCE 14 AA; 1522 MW; 4084F79D46A6A6A6 (90%)
Query Match
Best Local Similarity 100.0%; Score 3; DB 2; Length 14;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;
QY 7 LKK 9
PQ 4 LKK 6
RESULT 45
C99496 PRELIMINARY: PRI: 14 AA
AC C99496;
DT 01-MAY-2000 (TrEMBLrel. 14, Created)
DT 01-MAY-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 13, Last annotation update)
DE Mutant RNA polymerase beta (Fragment).
GN Homo sapiens (Human).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
CX Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
CX NBL_TaxID 9606;
RN 111
RP SEQUENCE FROM N.A.
SA Sadekane Y., Masda K., Kuroda Y., Hori T.K.
R "Identification of mutations in DNA polymerase beta (PNAS) from
R patients with Werner syndrome".
R Biochem. Biophys. Res. Commun. 276:111-120 (2001)
DR EMBL: S09673; AAL14051.1;

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FT NBL_TaxID 13
SQ SEQUENCE 13 AA; 1568 MW; D88C62798C9542CD CRC64;
Query Match
Best Local Similarity 100.0%; Score 3; DB 4; Length 13;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;
QY 5 SAV 4
PQ 5 SAV 3
RESULT 46
C99496 PRELIMINARY: PRI: 13 AA
AC C99496;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
GN FBP2
OS Homo sapiens (Human).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
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CX NBL_TaxID 9606;
RN 111
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SA MEDLINE: 2027576; PubMed: 10773454;
SA Tillmann H., Stein S., Flierl F., Eschrich K.J.
R "Structure and chromosomal localization of the human and mouse muscle
R fructose-1,6-bisphosphatase genes".
R Gene 247:241-253 (2000).
DR EMBL: AI248462; CAB58561.1;
KW Hexokinase.
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CX NBL_TaxID 9746;
RN 111
RP SEQUENCE FROM N.A.
SA Gillard M., Brandon R.B., Bell T.K.
R "Further identification of single nucleotide polymorphisms in the
R equine transferrin gene".
R submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF185752; AAF05464.1;
DR EMBL: AF185748; AAF05462.1;
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Post-processing: listing first 500 summaries

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SUMMARY

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2	5	45.5	10	4	US-09-115-321-129	Sequence 129, Appl
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5	5	45.5	14	5	53045-41-0	Patent No. 5304531
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7	4	36.4	8	1	US-08-434-120-138	Sequence 108, Appl
8	4	36.4	8	1	US-08-465-325-137	Sequence 107, Appl
9	4	36.4	8	2	US-08-621-807-237	Sequence 237, Appl
10	4	36.4	8	2	US-08-621-250A-239	Sequence 239, Appl
11	4	36.4	8	2	US-08-621-250A-241	Sequence 241, Appl
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509	1	27.3	1	US-08-443-051-5	Sequence 21, App	462	1	27.3	9	2	US-08-986-244-86	Sequence 341, App
510	1	27.3	1	US-08-443-051-5	Sequence 21, App	463	1	27.3	9	2	US-08-986-244-86	Sequence 423, App
511	1	27.3	1	US-08-443-051-5	Sequence 21, App	464	1	27.3	9	2	US-08-986-244-86	Sequence 491, App
512	1	27.3	1	US-08-443-051-5	Sequence 21, App	465	1	27.3	9	2	US-08-986-244-86	Sequence 653, App
513	1	27.3	1	US-08-443-051-5	Sequence 21, App	466	1	27.3	9	2	US-08-986-244-86	Sequence 703, App
514	1	27.3	1	US-08-443-051-5	Sequence 21, App	467	1	27.3	9	2	US-08-986-244-86	Sequence 770, App
515	1	27.3	1	US-08-443-051-5	Sequence 21, App	468	1	27.3	9	2	US-08-986-244-86	Sequence 314, App
516	1	27.3	1	US-08-443-051-5	Sequence 21, App	469	1	27.3	9	2	US-08-986-244-86	Sequence 1163, App
517	1	27.3	1	US-08-443-051-5	Sequence 21, App	470	1	27.3	9	2	US-08-986-244-86	Sequence 5, Appl
518	1	27.3	1	US-08-443-051-5	Sequence 21, App	471	1	27.3	9	2	US-08-986-244-86	Sequence 5, Appl
519	1	27.3	1	US-08-443-051-5	Sequence 21, App	472	1	27.3	9	2	US-08-986-244-86	Sequence 209, App
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522	1	27.3	1	US-08-443-051-5	Sequence 21, App	475	1	27.3	9	2	US-08-986-244-86	Sequence 491, App
523	1	27.3	1	US-08-443-051-5	Sequence 21, App	476	1	27.3	9	2	US-08-986-244-86	Sequence 653, App
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532	1	27.3	1	US-08-443-051-5	Sequence 21, App	485	1	27.3	9	2	US-08-986-244-86	Sequence 423, App
533	1	27.3	1	US-08-443-051-5	Sequence 21, App	486	1	27.3	9	2	US-08-986-244-86	Sequence 491, App
534	1	27.3	1	US-08-443-051-5	Sequence 21, App	487	1	27.3	9	2	US-08-986-244-86	Sequence 653, App
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536	1	27.3	1	US-08-443-051-5	Sequence 21, App	489	1	27.3	9	2	US-08-986-244-86	Sequence 770, App
537	1	27.3	1	US-08-443-051-5	Sequence 21, App	490	1	27.3	9	2	US-08-986-244-86	Sequence 314, App
538	1	27.3	1	US-08-443-051-5	Sequence 21, App	491	1	27.3	9	2	US-08-986-244-86	Sequence 1163, App
539	1	27.3	1	US-08-443-051-5	Sequence 21, App	492	1	27.3	9	2	US-08-986-244-86	Sequence 5, Appl
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542	1	27.3	1	US-08-443-051-5	Sequence 21, App	495	1	27.3	9	2	US-08-986-244-86	Sequence 26, Appl
543	1	27.3	1	US-08-443-051-5	Sequence 21, App	496	1	27.3	9	2	US-08-986-244-86	Sequence 52, Appl
544	1	27.3	1	US-08-443-051-5	Sequence 21, App	497	1	27.3	9	2	US-08-986-244-86	Sequence 18, Appl
545	1	27.3	1	US-08-443-051-5	Sequence 21, App	498	1	27.3	9	2	US-08-986-244-86	Sequence 3, Appl
546	1	27.3	1	US-08-443-051-5	Sequence 21, App	499	1	27.3	9	2	US-08-986-244-86	Sequence 70, Appl
547	1	27.3	1	US-08-443-051-5	Sequence 21, App	500	1	27.3	9	2	US-08-986-244-86	Sequence 26, Appl

ALIGNMENTS

RESULT 1
 US-08-443-051-5 129
 Sequence 129, Application US/08465-125
 Patent No. 5686564
 GENERAL INFORMATION
 APPLICANT: Magellan Pharmaceuticals Inc.
 APPLICANT: 5110 Campus Drive
 APPLICANT: Plymouth Meeting, PA 19462
 TITLE OF INVENTION: Biologically Active Peptides Having
 TITLE OF INVENTION: N-Terminal Substitutions
 NUMBER OF SEQUENCES: 129
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Erimed, Henderson, Henderson, Garrett &
 ADDRESSEE: Erimed
 STREET: 1450 11th Street, N.W. Suite 700
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: DOS/MS-DOS
 SOFTWARE: Patent In Review #125, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/465-125
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: G14
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/462
 FILING DATE: 14-JAN-94
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/462


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1 FILING DATE: 01-JUN-92
2 ATTORNEY/AGENT INFORMATION:
3 NAME: Fordis, Jean B
4 REGISTRATION NUMBER: 32,984
5 REFERENCE/DOCKET NUMBER: 05/08/1992 32,984
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: (202) 408-4009
8 TELEFAX: (202) 408-4460
9 INFORMATION FOR SEQ ID NO: 129:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 10 amino acids
12 TYPE: amino acid
13 STRANDEDNESS: single
14 TOPOLOGY: linear
15 MOLECULE TYPE: peptide
16 US-09-465-025-129
17
18 Query Match 45.5% Score 5; DB 1; Length 10;
19 Best local Similarity 100.0%; Pred. No. 0;
20 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
21
22 QY 6 KKKK 10
23 DB 1 KKKK 5
24
25 RESULT 2
26 US-09-115-737-129 Query Match 45.5% Score 5; DB 1; Length 10;
27 Sequence 129, Application US/0915347
28 Patent No. 6348445
29 GENERAL INFORMATION:
30 APPLICANT: U. Prasad Kari
31 Jeffrey J. Williams
32 Michael McNamee
33 TITLE OF INVENTION: Biologically Active Peptides With Reduced
34 Toxicity in Animals and a Method for Preparation Same
35 NUMBER OF SEQUENCES: 156
36 CORRESPONDENCE ADDRESS:
37 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
38 Dunner, L.L.P.
39 STREET: 1300 I Street, N.W. Suite 100
40 CITY: Washington
41 STATE: D.C.
42 COUNTRY: USA
43 ZIP: 20005-3315
44 COMPUTER READABLE FORM:
45 MEDIUM TYPE: Floppy disk
46 COMPUTER: IBM PC compatible
47 OPERATING SYSTEM: PC DOS/MS-DOS
48 SOFTWARE: Patent In Release #1.0, Version #1.0
49 CURRENT APPLICATION DATA:
50 APPLICATION NUMBER: US/09/115-737
51 FILING DATE: 15-Jul-1998
52 CLASSIFICATION: Unknown
53 PRIOR APPLICATION DATA:
54 APPLICATION NUMBER: 08/465,030
55 FILING DATE: 05-JUN-1996
56 APPLICATION NUMBER: 08/184,462
57 FILING DATE: 18-JAN-94
58 APPLICATION NUMBER: 07/671,201
59 FILING DATE: 01-JUN-92
60 ATTORNEY/AGENT INFORMATION:
61 NAME: Fordis, Jean B
62 REGISTRATION NUMBER: 32,984
63 REFERENCE/DOCKET NUMBER: 05/08/1992 32,984
64 TELECOMMUNICATION INFORMATION:
65 TELEPHONE: (202) 408-4009
66 TELEFAX: (202) 408-4460
67 INFORMATION FOR SEQ ID NO: 129:
68 SEQUENCE CHARACTERISTICS:
69 LENGTH: 10 amino acids
70 TYPE: amino acid
71 STRANDEDNESS: single

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1 TOPOLOGY: linear
2 MOLECULE TYPE: peptide
3 SEQUENCE DESCRIPTION: SEQ ID NO: 129:
4 US-09-115-737-129
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6 Query Match 45.5% Score 5; DB 4; Length 10;
7 Best local Similarity 100.0%; Pred. No. 38;
8 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
9
10 QY 6 KKKK 10
11 DB 1 KKKK 5
12
13 RESULT 3
14 US-08-855-531D-47
15 Sequence 47, Application US/08/855531D
16 Patent No. 6110467
17 GENERAL INFORMATION:
18 APPLICANT: PREK, PAUL S.
19 HALBOR, PATRICK G.
20 MENG, XIANGJIN
21 LUM, MELISSA A.
22 LYGG, YOUNG S.
23 TITLE OF INVENTION: VACCINES RAISING AN IMMUNOLOGICAL
24 RESPONSE AGAINST VIRUSES CAUSING PORCINE RESPIRATORY AND
25 REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAINST
26 A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE
27 NUMBER OF SEQUENCES: 47
28 CORRESPONDENCE ADDRESS:
29 ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
30 P.C.
31 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
32 CITY: ARLINGTON
33 STATE: VA
34 COUNTRY: USA
35 ZIP: 22202
36 COMPUTER READABLE FORM:
37 MEDIUM TYPE: Floppy disk
38 COMPUTER: IBM PC compatible
39 OPERATING SYSTEM: PC DOS/MS-DOS
40 SOFTWARE: Patent In Release #1.0, Version #1.0
41 CURRENT APPLICATION DATA:
42 APPLICATION NUMBER: US/08/855,531D
43 FILING DATE: 13-May-1997
44 CLASSIFICATION: Unknown
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: US 07/969,071
47 FILING DATE: 30-OCT-1992
48 ATTORNEY/AGENT INFORMATION:
49 NAME: LAVALLEYE, JEAN-PAUL M.P.
50 REGISTRATION NUMBER: 41,451
51 REFERENCE/DOCKET NUMBER: 4625-038-55X DIV
52 TELECOMMUNICATION INFORMATION:
53 TELEPHONE: 703-413-3000
54 TELEFAX: 703-413-2220
55 TELEX: 248855 SPAT GR
56 INFORMATION FOR SEQ ID NO: 47:
57 SEQUENCE CHARACTERISTICS:
58 LENGTH: 13 amino acids
59 TYPE: amino acid
60 TOPOLOGY: linear
61 MOLECULE TYPE: protein
62 SEQUENCE DESCRIPTION: SEQ ID NO: 47:
63 US-08-855-531D-47
64
65 Query Match 45.5% Score 5; DB 3; Length 13;
66 Best local Similarity 100.0%; Pred. No. 47;
67 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
68
69 QY 6 KKKK 10
70 DB 8 KKKK 12

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RESULT 4
 US 08-855-5268-47
 Sequence 47, Application US/08855268
 Patent No. 6251404
 GENERAL INFORMATION:
 APPLICANT: PREM, PAUL S.
 APPLICANT: BALHUK, PATRICK G.
 APPLICANT: MENG, XIANG-JIN
 APPLICANT: LOM, MELISSA A.
 APPLICANT: LYNG, YOUNG S.
 TITLE OF INVENTION: VACCINES RAISING AN IMMUNOLOGICAL
 RESPONSE AGAINST VIRUSES, MEMBERS OF PROTECTING A PIG AGAINST
 TITLE OF INVENTION: REPRODUCTIVE DISEASES, MEMBERS OF PROTECTING A PIG AGAINST
 TITLE OF INVENTION: A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OHLON, SPIVAK, MCCLELLAND, WATER & NEUSTALT,
 ADDRESSEE: P.C.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/855,5268
 FILING DATE: 13-MAY 1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/969,021
 FILING DATE: 30 OCT-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: LAVALLEYE, JEAN-PAUL M.P.
 REGISTRATION NUMBER: 31,451
 REFERENCE/PROCT NUMBER: 462,046 OX D.V.
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 TELEX: 248855 GRAT GR
 INFORMATION FOR SEQ ID NO:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: linear
 Molecule type: peptide
 US 08-855-5268-47
 Gary Match 45.58% Score % Identity %
 Best local similarity 100.00% Pctid No 47
 Matches 5% conservative 0% Mismatches 0% Indels 0% Gaps 0%
 07 6 KKKKK 10
 11111
 08 8 KKKKK 12
 11111
 RESULT 5
 5304631-9
 Patent No. 5304631
 APPLICANT: STEWART, JOHN M.; BAHN, KARE W.; KILS, WIESLAW A.
 TITLE OF INVENTION: SYNTHETIC HELLYME ENZYME
 NUMBER OF SEQUENCES: 16
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/464,552
 FILING DATE: 16-JAN-1990
 SEQ ID NO: 9

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4  Query Match: 45.5% Score 5: DB 6: Length 14:
5  Best Local Similarity 100.0% Pred. No. 50:
6  Matches 5: Conservative 0: Mismatches 0: Indels
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8  QY 7 LKKA 11
9      11111
10 DB 16 LKKA 14
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```

Query Match      35.4%;   Score 4;   DB 1;   Length 8;
Best Local Similarity 100.0%;   Pred. No. 2.5e+05;
Matches 4;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

QY      6 KKKK 4
IT      4 KKKK 7

```

```

RESULT 7
US-08-434-120-108
: Sequence 107, Application US/08434120
: Patent No. 5635479
: GENERAL INFORMATION:
: APPLICANT: Baker, Margaret A.
: APPLICANT: Jacob, Leonard S.
: APPLICANT: Maloy, W. Leo
: TITLE OF INVENTION: Treatment of Gynecomastia
: TITLE OF INVENTION: Malinquinides with
: TITLE OF INVENTION: Biologically Active Peptides
: NUMBER OF SEQUENCES: 117
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Carelia, Byrne, Bain, Gilliland,
: ADDRESSEE: Cecchi & Stewart
: STREET: 6 Becker Farm Road
: CITY: Roseland
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07068
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch diskette
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: PC-DOS
: SOFTWARE: DM4 V2
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/444,120
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/297,960
: FILING DATE:
: APPLICATION NUMBER: US/08/226,105
: FILING DATE:
: APPLICATION NUMBER: US/07/937,463
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Gieseler, Elliot M.
: REGISTRATION NUMBER: 24,025
: REFERENCE/DACKET NUMBER: 421200 194
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201 994-1700
: TELEFAX: 201-994-1744
: INFORMATION FOR SEQ ID NO: 108:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-434-120-108

Query Match 36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 KLKK 9
Db 111
4 KLKK 7

RESULT 8
US-08-465-325-107
: Sequence 107, Application US/08465425
: Patent No. 5686563
: GENERAL INFORMATION:
: APPLICANT: Madalain Pharmaceuticals Inc.
: APPLICANT: 5110 Campus Drive
: APPLICANT: Plymouth Meeting, PA 19462
: TITLE OF INVENTION: Biologically Active Peptides Having
: TITLE OF INVENTION: N-Terminal Substitutions
: NUMBER OF SEQUENCES: 153

```

```

: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
: ADDRESSEE: Dunner
: STREET: 1400 L Street, N.W. Suite 700
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3315
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/445,325
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 04/186,462
: FILING DATE: 18-JAN-94
: APPLICATION NUMBER: 07/891,261
: FILING DATE: 01-JUN-92
: ATTORNEY/AGENT INFORMATION:
: NAME: Fordis, Jean H.
: REGISTRATION NUMBER: 42,984
: REFERENCE/DACKET NUMBER: 05387-0021 03000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 408-4000
: TELEFAX: (202) 408-4400
: INFORMATION FOR SEQ ID NO: 107:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-465-325-107

Query Match 36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
Db 111
4 KLKK 7

RESULT 9
US-08-621-803-217
: Sequence 237, Application US/08621803
: Patent No. 5851802
: GENERAL INFORMATION:
: APPLICANT: Better, Marc D.
: TITLE OF INVENTION: Methods for Recombinant Microbial Production of
: TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
: NUMBER OF SEQUENCES: 265
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/621,803
: FILING DATE: 22-MAR-1996
: ATTORNEY/AGENT INFORMATION:

```

```

1 NAME: Borum, Michael F.
2 REGISTRATION NUMBER: 25,447
3 REFERENCE/DOCKET NUMBER: 27129/41199
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 312/474-6400
6 TELEFAX: 312/474-0448
7 TELETYPE: 25-4856
8 INFORMATION FOR SEQ ID NO: 2:
9 SEQUENCE CHARACTERISTICS:
10 LENGTH: 8 amino acids
11 TYPE: amino acid
12 TOPOLOGY: linear
13 MOLECULE TYPE: peptide
14 FEATURES:
15 NAME/KEY: misc-feature
16 OTHER INFORMATION: "XMP-412"
17 US 08-621-259A-243
18
19 Query Match: 36.4% Score 4: 08 2: Length 8:
20 Best Local Similarity: 100.0% Prod. No. 2.5e+05:
21 Matches 4: Conservative 0: Mismatches 0: Indels 0:
22
23 QY 7 LKKK 10
24 BL 1 LKKK 4
25
26 RESULT 1:
27 US 08-621-259A-243
28 Sequence 243: Application US/08-621-259A
29 Patent No. 5858974
30 GENERAL INFORMATION:
31 APPLICANT: Little I., Roger G.
32 APPLICANT: Lim, Edward
33 APPLICANT: Padom, Mitchell B.
34 TITLE OF INVENTION: Anti-Fungal Peptides
35 NUMBER OF SEQUENCES: 252
36 CORRESPONDENCE ADDRESS:
37 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
38 STREET: 500 West Madison Street
39 CITY: Chicago
40 STATE: Illinois
41 COUNTRY: United States of America
42 ZIP: 60661
43 COMPUTER READABLE FORM:
44 MEDIUM TYPE: floppy disk
45 OPERATING SYSTEM: PC-DOS/MS-DOS
46 SOFTWARE: Patent In Release #1.0, Version #1.25
47 CURRENT APPLICATION DATA:
48 APPLICATION NUMBER: US/08-621-259A
49 FILING DATE: 21-MAR-1996
50 PRIOR APPLICATION DATA:
51 APPLICATION NUMBER: 08/544,841
52 FILING DATE: 20-JUL-1995
53 ATTORNEY/AGENT INFORMATION:
54 NAME: McNicholas, Janet M.
55 REGISTRATION NUMBER: 32,918
56 REFERENCE/DOCKET NUMBER: 11-21US02
57 TELECOMMUNICATION INFORMATION:
58 TELEPHONE: 312/707-8889
59 TELEFAX: 312/707-9155
60 TELEX:
61 INFORMATION FOR SEQ ID NO: 252:
62 SEQUENCE CHARACTERISTICS:
63 LENGTH: 8 amino acids
64 TYPE: amino acid
65 TOPOLOGY: linear
66 MOLECULE TYPE: peptide
67 FEATURES:
68 NAME/KEY: misc-feature
69 OTHER INFORMATION: "XMP-412"
70 FEATURES:

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1 NAME/KEY: misc-feature
2 OTHER INFORMATION: "Peptide is Cyclized Head to Tail"
3 US 08-621-259A-239
4
5 Query Match: 36.4% Score 4: 08 2: Length 8:
6 Best Local Similarity: 100.0% Prod. No. 2.5e+05:
7 Matches 4: Conservative 0: Mismatches 0: Indels 0:
8
9 QY 7 LKKK 10
10 BL 1 LKKK 4
11
12 RESULT 1:
13 US 08-621-259A-243
14 Sequence 243: Application US/08-621-259A
15 Patent No. 5858974
16 GENERAL INFORMATION:
17 APPLICANT: Little I., Roger G.
18 APPLICANT: Lim, Edward
19 APPLICANT: Padom, Mitchell B.
20 TITLE OF INVENTION: Anti-Fungal Peptides
21 NUMBER OF SEQUENCES: 252
22 CORRESPONDENCE ADDRESS:
23 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
24 STREET: 500 West Madison Street
25 CITY: Chicago
26 STATE: Illinois
27 COUNTRY: United States of America
28 ZIP: 60661
29 COMPUTER READABLE FORM:
30 MEDIUM TYPE: floppy disk
31 OPERATING SYSTEM: PC-DOS/MS-DOS
32 SOFTWARE: Patent In Release #1.0, Version #1.25
33 CURRENT APPLICATION DATA:
34 APPLICATION NUMBER: US/08-621-259A
35 FILING DATE: 21-MAR-1996
36 PRIOR APPLICATION DATA:
37 APPLICATION NUMBER: 08/544,841
38 FILING DATE: 20-JUL-1995
39 ATTORNEY/AGENT INFORMATION:
40 NAME: McNicholas, Janet M.
41 REGISTRATION NUMBER: 32,918
42 REFERENCE/DOCKET NUMBER: 11-21US02
43 TELECOMMUNICATION INFORMATION:
44 TELEPHONE: 312/707-8889
45 TELEFAX: 312/707-9155
46 TELEX:
47 INFORMATION FOR SEQ ID NO: 243:
48 SEQUENCE CHARACTERISTICS:
49 LENGTH: 8 amino acids
50 TYPE: amino acid
51 TOPOLOGY: linear
52 MOLECULE TYPE: peptide
53 FEATURES:
54 NAME/KEY: misc-feature
55 OTHER INFORMATION: "XMP-412"
56 US 08-621-259A-243
57
58 Query Match: 36.4% Score 4: 08 2: Length 8:
59 Best Local Similarity: 100.0% Prod. No. 2.5e+05:
60 Matches 4: Conservative 0: Mismatches 0: Indels 0:
61
62 QY 7 LKKK 10
63 BL 1 LKKK 4
64
65 RESULT 1:
66 US 08-621-259A-243
67 Sequence 243: Application US/08-621-259A
68 Patent No. 5858974
69 GENERAL INFORMATION:
70 APPLICANT: Little I., Roger G.
71 APPLICANT: Lim, Edward
72 APPLICANT: Padom, Mitchell B.
73 TITLE OF INVENTION: Anti-Fungal Peptides
74 NUMBER OF SEQUENCES: 252
75 CORRESPONDENCE ADDRESS:
76 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
77 STREET: 500 West Madison Street
78 CITY: Chicago
79 STATE: Illinois
80 COUNTRY: United States of America
81 ZIP: 60661
82 COMPUTER READABLE FORM:
83 MEDIUM TYPE: floppy disk
84 OPERATING SYSTEM: PC-DOS/MS-DOS
85 SOFTWARE: Patent In Release #1.0, Version #1.25
86 CURRENT APPLICATION DATA:
87 APPLICATION NUMBER: US/08-621-259A
88 FILING DATE: 21-MAR-1996
89 PRIOR APPLICATION DATA:
90 APPLICATION NUMBER: 08/544,841
91 FILING DATE: 20-JUL-1995
92 ATTORNEY/AGENT INFORMATION:
93 NAME: McNicholas, Janet M.
94 REGISTRATION NUMBER: 32,918
95 REFERENCE/DOCKET NUMBER: 11-21US02
96 TELECOMMUNICATION INFORMATION:
97 TELEPHONE: 312/707-8889
98 TELEFAX: 312/707-9155
99 TELEX:
100 INFORMATION FOR SEQ ID NO: 252:
101 SEQUENCE CHARACTERISTICS:
102 LENGTH: 8 amino acids
103 TYPE: amino acid
104 TOPOLOGY: linear
105 MOLECULE TYPE: peptide
106 FEATURES:
107 NAME/KEY: misc-feature
108 OTHER INFORMATION: "XMP-412"
109 FEATURES:

```

```

1  GENERAL INFORMATION:
2  APPLICANT: NALLER, STEVEN G.
3  APPLICANT: CLEVELAND, JEFFREY S.
4  APPLICANT: BLAKE, JAMES
5  APPLICANT: HAFAR, OMAR K.
6  TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PSEUDIN
7  TITLE OF INVENTION: TRANSLATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
8  TITLE OF INVENTION: METHODS OF USE THEREOF
9  NUMBER OF SEQUENCES: 24
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: ROBINS & ASSOCIATES
12 STREET: 90 MIDDLEFIELD ROAD, SUITE 200
13 CITY: MENLO PARK
14 STATE: CA
15 COUNTRY: USA
16 ZIP: 94025
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: PatentIn Release #1.0, Version #1.4
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/928,995#
24 FILING DATE: 12-SEP-1997
25 CLASSIFICATION: 514
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 60/32697#
28 FILING DATE: 20-SEP-1996
29 ATTORNEY/AGENT INFORMATION:
30 NAME: ROBINS, ROBERTA L.
31 REGISTRATION NUMBER: 43,298
32 REFERENCE/DCKET NUMBER: 5948-0611
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (650) 325-7812
35 TELEFAX: (650) 325-7824
36 INFORMATION FOR SEQ ID NO: 17:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 8 amino acids
39 TYPE: amino acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42 MOLECULE TYPE: peptide
43 US-08-928-958-17
44
45 Query Match: 36.4% Score 4: DB 2: Length 8:
46 Best Local Similarity 100.0%: Pct. No. 2.5e+05:
47 Matches 4: Conservative 0: Mismatches 0: Gaps 0:
48
49 QY 6 KLKX 9
50 III
51 DB 2 KLKX 5
52
53 RESULT 14
54 US-09-217-352-237
55 Sequence 237: Application US/09/217352
56 Patent No. 6274344
57 GENERAL INFORMATION:
58 APPLICANT: BOTTORF, MARK D.
59 TITLE OF INVENTION: METHODS FOR RECOMBINANT MICROBIAL PRODUCTION OF
60 TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
61 NUMBER OF SEQUENCES: 255
62 CORRESPONDENCE ADDRESS:
63 ADDRESSEE: Marshall J. Bottorff, Gerstein, Murray & Borun
64 STREET: 600 Sears Tower, 244 South Wacker Drive
65 CITY: Chicago
66 STATE: Illinois
67 COUNTRY: United States of America
68 ZIP: 60606-6402
69 COMPUTER READABLE FORM:
70 MEDIUM TYPE: Floppy disk
71 COMPUTER: IBM PC compatible
72 OPERATING SYSTEM: PC-DOS/MS-DOS
73 SOFTWARE: PatentIn Release #1.0, Version #1.25
74 CURRENT APPLICATION DATA:
75 APPLICATION NUMBER: US/09/217,352
76 FILING DATE:
77 PRIOR APPLICATION DATA:
78 APPLICATION NUMBER: US/621,893
79 FILING DATE: 22-MAR-1996
80 ATTORNEY/AGENT INFORMATION:
81 NAME: Borun, Michael F.
82 REGISTRATION NUMBER: 25,447
83 REFERENCE/DCKET NUMBER: 27129/33199
84 TELECOMMUNICATION INFORMATION:
85 TELEPHONE: 312/474-6300
86 TELEFAX: 312/474-0448
87 TELEX: 253856
88 INFORMATION FOR SEQ ID NO: 257:
89 SEQUENCE CHARACTERISTICS:
90 LENGTH: 6 amino acids
91 TYPE: amino acid
92 TOPOLOGY: linear
93 MOLECULE TYPE: peptide
94 FEATURE:

```

```

1  GENERAL INFORMATION:
2  APPLICANT: NALLER, STEVEN G.
3  APPLICANT: CLEVELAND, JEFFREY S.
4  APPLICANT: BLAKE, JAMES
5  APPLICANT: HAFAR, OMAR K.
6  TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PSEUDIN
7  TITLE OF INVENTION: TRANSLATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
8  TITLE OF INVENTION: METHODS OF USE THEREOF
9  NUMBER OF SEQUENCES: 24
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: ROBINS & ASSOCIATES
12 STREET: 90 MIDDLEFIELD ROAD, SUITE 200
13 CITY: MENLO PARK
14 STATE: CA
15 COUNTRY: USA
16 ZIP: 94025
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: PatentIn Release #1.0, Version #1.4
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/928,995#
24 FILING DATE: 12-SEP-1997
25 CLASSIFICATION: 514
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 60/32697#
28 FILING DATE: 20-SEP-1996
29 ATTORNEY/AGENT INFORMATION:
30 NAME: ROBINS, ROBERTA L.
31 REGISTRATION NUMBER: 43,298
32 REFERENCE/DCKET NUMBER: 5948-0611
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (650) 325-7812
35 TELEFAX: (650) 325-7824
36 INFORMATION FOR SEQ ID NO: 17:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 8 amino acids
39 TYPE: amino acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42 MOLECULE TYPE: peptide
43 US-08-928-958-17
44
45 Query Match: 36.4% Score 4: DB 2: Length 8:
46 Best Local Similarity 100.0%: Pct. No. 2.5e+05:
47 Matches 4: Conservative 0: Mismatches 0: Gaps 0:
48
49 QY 6 KLKX 9
50 III
51 DB 2 KLKX 5
52
53 RESULT 14
54 US-09-217-352-237
55 Sequence 237: Application US/09/217352
56 Patent No. 6274344
57 GENERAL INFORMATION:
58 APPLICANT: BOTTORF, MARK D.
59 TITLE OF INVENTION: METHODS FOR RECOMBINANT MICROBIAL PRODUCTION OF
60 TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
61 NUMBER OF SEQUENCES: 255
62 CORRESPONDENCE ADDRESS:
63 ADDRESSEE: Marshall J. Bottorff, Gerstein, Murray & Borun
64 STREET: 600 Sears Tower, 244 South Wacker Drive
65 CITY: Chicago
66 STATE: Illinois
67 COUNTRY: United States of America
68 ZIP: 60606-6402
69 COMPUTER READABLE FORM:
70 MEDIUM TYPE: Floppy disk
71 COMPUTER: IBM PC compatible
72 OPERATING SYSTEM: PC-DOS/MS-DOS
73 SOFTWARE: PatentIn Release #1.0, Version #1.25
74 CURRENT APPLICATION DATA:
75 APPLICATION NUMBER: US/09/217,352
76 FILING DATE:
77 PRIOR APPLICATION DATA:
78 APPLICATION NUMBER: US/621,893
79 FILING DATE: 22-MAR-1996
80 ATTORNEY/AGENT INFORMATION:
81 NAME: Borun, Michael F.
82 REGISTRATION NUMBER: 25,447
83 REFERENCE/DCKET NUMBER: 27129/33199
84 TELECOMMUNICATION INFORMATION:
85 TELEPHONE: 312/474-6300
86 TELEFAX: 312/474-0448
87 TELEX: 253856
88 INFORMATION FOR SEQ ID NO: 257:
89 SEQUENCE CHARACTERISTICS:
90 LENGTH: 6 amino acids
91 TYPE: amino acid
92 TOPOLOGY: linear
93 MOLECULE TYPE: peptide
94 FEATURE:

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```

1  NAME/KEY:  miss feature
2  OTHER INFORMATION:  "XMP.412"
3
4  US 09 217 052 247
5
6  Query Match: 36.4% Score: 41, 100.0% Ident: 8,
7  Best Local Similarity: 100.0% Ident: 8, 100.0%
8  Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
9
10 QY 1 LKXK 10
11 111
12 Db 1 LKXK 4
13
14 RESULT 15
15 US 09 220 066A-11
16 Sequence 15: Application US/0902066A
17 Patent No. 6347592
18 GENERAL INFORMATION:
19 APPLICANT: TSMGSOND, Robert M.
20 TITLE OF INVENTION: Peptide Molecules of the Tyrosine Receptor Domain
21 TITLE OF INVENTION: Gamma chain and Methods and Compositions for
22 TITLE OF INVENTION: Making and Using the Same
23 NUMBER OF SEQUENCES: 37
24 CORRESPONDENCE ADDRESS:
25 ADDRESSEE: Woodcock Washburn Kelli Macdonald & Neill LLP
26 STREET: One Liberty Place, 40th Floor
27 CITY: Philadelphia
28 STATE: Pennsylvania
29 COUNTRY: USA
30 ZIP: 19103
31 COMPUTER READABLE FORM:
32 MEDIUM TYPE: Floppy disk
33 COMPUTER: IBM PC compatible
34 OPERATING SYSTEM: Windows NT
35 SOFTWARE: WordPerfect V. 6
36 CURRENT APPLICATION DATA:
37 APPLICATION NUMBER: US/09/220,066A
38 FILING DATE:
39 CLASSIFICATION: 540
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 66/290,947
42 FILING DATE: 07-FEB-1997
43 TELECOMMUNICATION INFORMATION:
44 ATTORNEY/AGENT INFORMATION:
45 NAME: Boland, Mark
46 REGISTRATION NUMBER: 35227
47 REFERENCE/CKET NUMBER: T.M. 2,211
48 TELECOMMUNICATION INFORMATION:
49 TELEPHONE: 215 568-4100
50 TELEFAX: 215 568-4439
51 INFORMATION FOR SEQ ID NO: 11:
52 SEQUENCE CHARACTERISTICS:
53 LENGTH: 8 amino acids
54 TYPE: amino acid
55 PRIMARY: Yes
56 MOLECULE TYPE: peptide
57 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
58 US 09 220 066A-11
59
60 Query Match: 36.4% Score: 41, 100.0% Ident: 8,
61 Best Local Similarity: 100.0% Ident: 8, 100.0%
62 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
63
64 QY 1 LKXK 4
65 111
66 Db 1 LKXK 6
67
68 RESULT 16
69 US 09 115-747-107
70 Sequence 16: Application US/09115-747
71 Patent No. 6348445
72 GENERAL INFORMATION:
73 APPLICANT: U. Prasad
74 TITLE OF INVENTION: Biologically Active Peptide
75 TITLE OF INVENTION: Compositions and Uses Therefor
76 NUMBER OF SEQUENCES: 19
77 CORRESPONDENCE ADDRESS:
78 ADDRESSEE: Catala, Byner, Babin, Gillilan,
79 STREET: 4 Becker Farm Road
80 CITY: Roseland
81 STATE: New Jersey
82 COUNTRY: USA
83
84 US 09 193-521-15
85 Sequence 15: Application US/08193521
86 Patent No. 5470950
87 GENERAL INFORMATION:
88 APPLICANT: Maroy, W. Lee
89 APPLICANT: Kari, U. Prasad
90 APPLICANT: Williams, Jon L.
91 TITLE OF INVENTION: Biologically Active Peptide
92 TITLE OF INVENTION: Compositions and Uses Therefor
93 NUMBER OF SEQUENCES: 19
94 CORRESPONDENCE ADDRESS:
95 ADDRESSEE: Catala, Byner, Babin, Gillilan,
96 STREET: 4 Becker Farm Road
97 CITY: Roseland
98 STATE: New Jersey
99 COUNTRY: USA

```

```

1  ZIP: 07068
2  COMPUTER READABLE FORM:
3  MEDIUM TYPE: 3.5 inch diskette
4  COMPUTER: IBM PS/2
5  OPERATING SYSTEM: PC-DOS
6  SOFTWARE: DWA V2
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/08/434,120
9  FILING DATE:
10 CLASSIFICATION: 514
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US/07/870,950
13 FILING DATE:
14 APPLICATION NUMBER: 07/760,354
15 FILING DATE: 13-SEP-1991
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Gisteln, Elliot M.
18 REGISTRATION NUMBER: 24,025
19 REFERENCE/DOCKET NUMBER: 421250-161
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: 201-994-1700
22 TELEFAX: 201-994-1744
23 INFORMATION FOR SEQ ID NO: 15:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 9 amino acids
26 TYPE: amino acid
27 STRANDEDNESS:
28 TOPOLOGY: linear
29 FEATURE:
30 OTHER INFORMATION: May be a terminal amide.
31 OTHER INFORMATION: and/or may be acetylated at
32 OTHER INFORMATION: N-terminus.
33 US-09-787-443-4

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Query Match 36.4% Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 6 KLKK 9
DB 1 11
5 KLKK 8

```

```

RESULT 18
US-08-434 120-109
Sequence 109, Application US/08434120
Patent No. 5645179
GENERAL INFORMATION:
APPLICANT: Baker, Margaret A.
APPLICANT: Jacob, Leonard S.
TITLE OF INVENTION: Treatment of Ovarian Cancer
TITLE OF INVENTION: Malignancies with
TITLE OF INVENTION: Biologically Active Peptides
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bail, Ellington
ADDRESSEE: Cecchi & Stewart
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DWA V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,120
FILING DATE:
CLASSIFICATION: 514

```

```

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/297,950
FILING DATE:
APPLICATION NUMBER: US/08/226,106
FILING DATE:
APPLICATION NUMBER: US/07/937,462
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gisteln, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 421250-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US 08-434-120-109

Query Match 36.4% Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
DB 5 KLKK 8

RESULT 19
US-08-465-425-138
Sequence 108, Application US/08465425
Patent No. 5685563
GENERAL INFORMATION:
APPLICANT: Megalain Pharmaceuticals Inc.
APPLICANT: 5110 Campus Drive
APPLICANT: Plymouth Meeting, PA 19462
TITLE OF INVENTION: Biologically Active Peptides Having
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 L Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-4415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,425
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jeag B
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387-0021-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

```

1 INFORMATION FOR SEQ ID NO: 108:
 2 SEQUENCE CHARACTERISTICS:
 3 LENGTH: 9 amino acids
 4 TYPE: amino acid
 5 STRANDEDNESS: single
 6 TOPOLOGY: linear
 7 MOLECULE TYPE: peptide
 8 US-08-454-207A:108

Query Match: 36.4% Score 4: 10 11 Length 9:
 Best Local Similarity 100.0% Pred. No. 2.5e+05
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

97 6 LKKK 10
 100 1 L
 100 6 LKKK 4

RESULT 20

US-08-454-207A:11

1 Sequence 11: Application US/08454207A
 2 Patent No. 5710123
 3 GENERAL INFORMATION:
 4 APPLICANT: Heavner, George A.
 5 APPLICANT: KRUSZYNSKI, Marian
 6 TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
 7 NUMBER OF SEQUENCES: 70
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP
 10 STREET: One Liberty Place - 46th Floor
 11 CITY: Philadelphia
 12 STATE: PA
 13 COUNTRY: U.S.A.
 14 ZIP: 19103

15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: 3.5 inch disk, 1.44 MB
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: WordPerfect 6.1
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/454-207A
 22 FILING DATE: 09-JUN-1995
 23 CLASSIFICATION: 514
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: PCT/US95/12110
 26 FILING DATE: 13-DEC-1994

27 REFERENCE/DOCKET NUMBER: 08-454-183
 28 TELECOMMUNICATION INFORMATION:
 29 TELEPHONE: 215-568-3100
 30 TELEFAX: 215-568-3439
 31 INFORMATION FOR SEQ ID NO: 11:
 32 SEQUENCE CHARACTERISTICS:
 33 LENGTH: 9 amino acids
 34 TYPE: amino acid
 35 TOPOLOGY: linear
 36 US-08-454-207A:11

Query Match: 36.4% Score 4: 10 11 Length 9:
 Best Local Similarity 100.0% Pred. No. 2.5e+05
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

97 7 LKKK 10
 100 1 L
 100 1 LKKK 4

RESULT 21

US-08-454-207A:12

1 Sequence 12: Application US/08454207A

2 Patent No. 5710123

3 GENERAL INFORMATION:

4 APPLICANT: Heavner, George A.

5 APPLICANT: KRUSZYNSKI, Marian

6 TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING

7 NUMBER OF SEQUENCES: 70

8 CORRESPONDENCE ADDRESS:

9 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP

10 STREET: One Liberty Place - 46th Floor

11 CITY: Philadelphia

12 STATE: PA

13 COUNTRY: U.S.A.

14 ZIP: 19103

15 COMPUTER READABLE FORM:

16 MEDIUM TYPE: 3.5 inch disk, 1.44 MB

17 COMPUTER: IBM PC compatible

18 OPERATING SYSTEM: PC-DOS/MS-DOS

19 SOFTWARE: WordPerfect 6.1

20 CURRENT APPLICATION DATA:

21 APPLICATION NUMBER: US/08/454-207A

22 FILING DATE: 09-JUN-1995

23 CLASSIFICATION: 514

24 PRIOR APPLICATION DATA:

25 APPLICATION NUMBER: PCT/US94/12110

26 FILING DATE: 13-DEC-1994

27 REFERENCE/DOCKET NUMBER: 08-454-183

28 TELECOMMUNICATION INFORMATION:

29 TELEPHONE: 215-568-3100

30 TELEFAX: 215-568-3439

31 INFORMATION FOR SEQ ID NO: 12:

32 SEQUENCE CHARACTERISTICS:

33 LENGTH: 9 amino acids

34 TYPE: amino acid

35 TOPOLOGY: linear

36 US-08-454-207A:12

Query Match: 36.4% Score 4: 10 11 Length 9:
 Best Local Similarity 100.0% Pred. No. 2.5e+05
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

97 7 LKKK 10
 100 1 L
 100 1 LKKK 4

RESULT 22

US-08-454-207A:13

1 Sequence 13: Application US/08454207A

2 Patent No. 5710123

3 GENERAL INFORMATION:

4 APPLICANT: Heavner, George A.

5 APPLICANT: KRUSZYNSKI, Marian

6 TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING

7 NUMBER OF SEQUENCES: 70

8 CORRESPONDENCE ADDRESS:

9 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP

10 STREET: One Liberty Place - 46th Floor

11 CITY: Philadelphia

12 STATE: PA

13 COUNTRY: U.S.A.

14 ZIP: 19103

15 COMPUTER READABLE FORM:

16 MEDIUM TYPE: 3.5 inch disk, 1.44 MB

17 COMPUTER: IBM PC compatible

18 OPERATING SYSTEM: PC-DOS/MS-DOS

19 SOFTWARE: WordPerfect 6.1

20 CURRENT APPLICATION DATA:

21 APPLICATION NUMBER: US/08/454-207A

22 FILING DATE: 09-JUN-1995

23 CLASSIFICATION: 514

24 PRIOR APPLICATION DATA:

25 APPLICATION NUMBER: PCT/US94/12110

26 FILING DATE: 13-DEC-1994

27 REFERENCE/DOCKET NUMBER: 08-454-183

28 TELECOMMUNICATION INFORMATION:

29 TELEPHONE: 215-568-3100

30 TELEFAX: 215-568-3439

31 INFORMATION FOR SEQ ID NO: 13:

32 SEQUENCE CHARACTERISTICS:

33 LENGTH: 9 amino acids

34 TYPE: amino acid

35 TOPOLOGY: linear

36 US-08-454-207A:13

Query Match: 36.4% Score 4: 10 11 Length 9:
 Best Local Similarity 100.0% Pred. No. 2.5e+05
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

97 7 LKKK 10
 100 1 L
 100 1 LKKK 4


```

1  SOFTWARE: Wordperfect 6.1
2  CURRENT APPLICATION DATA:
3  APPLICATION NUMBER: US/08/454,207A
4  FILING DATE: 09-JUN-1995
5  CLASSIFICATION: 514
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER: PCT/US99/12110
8  FILING DATE: 13-DEC-1993
9  PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 07/997,771
11 FILING DATE: 18-DEC-1992
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Dianne B. Elderkin
14 REGISTRATION NUMBER: 28,598
15 REFERENCE/DOCKET NUMBER: COAR 0183
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: 215-568-3100
18 TELEFAX: 215-568-3439
19 INFORMATION FOR SEQ ID NO: 13:
20 SEQUENCE CHARACTERISTICS:
21 LENGTH: 9 amino acids
22 TYPE: amino acid
23 TOPOLOGY: linear
24 US-08 454-207A-13

```

```

Query Match 36.4%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

```

```

QY 7 KKKK 10
DB 1111
   2 KKKK 4

```

```

1  RESULT 25
2  US-08 454-207A-13
3  Sequence 25, Application US/08454207A
4  Patent No. 5710123
5  GENERAL INFORMATION:
6  APPLICANT: Heavner, George A.
7  TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
8  NUMBER OF SEQUENCES: 70
9  CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123ris LLP
11 STREET: One Liberty Place - 46th Floor
12 CITY: Philadelphia
13 STATE: PA
14 COUNTRY: U.S.A.
15 ZIP: 19103
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: 3.5 inch disk, 1.44 MB
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Wordperfect 6.1
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/454,207A
23 FILING DATE: 09-JUN-1995
24 CLASSIFICATION: 514
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: PCT/US99/12110
27 FILING DATE: 13-DEC-1993
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 07/997,771
30 FILING DATE: 18-DEC-1992
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Dianne B. Elderkin
33 REGISTRATION NUMBER: 28,598
34 REFERENCE/DOCKET NUMBER: COAR-0183
35 TELEPHONE: 215-568-3100
36 TELEFAX: 215-568-3439
37 INFORMATION FOR SEQ ID NO: 23:

```

```

1  SOFTWARE: Wordperfect 6.1
2  CURRENT APPLICATION DATA:
3  APPLICATION NUMBER: US/08/454,207A
4  FILING DATE: 09-JUN-1995
5  CLASSIFICATION: 514
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER: PCT/US99/12110
8  FILING DATE: 13-DEC-1993
9  PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 07/997,771
11 FILING DATE: 18-DEC-1992
12 ATTORNEY/AGENT INFORMATION:
13 NAME: Dianne B. Elderkin
14 REGISTRATION NUMBER: 28,598
15 REFERENCE/DOCKET NUMBER: COAR 0183
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: 215-568-3100
18 TELEFAX: 215-568-3439
19 INFORMATION FOR SEQ ID NO: 23:

```

```

Query Match 36.4%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

```

```

1  SEQUENCE CHARACTERISTICS:
2  LENGTH: 9 amino acids
3  TYPE: amino acid
4  TOPOLOGY: linear
5  US-08 454-207A-24

```

```

Query Match 36.4%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

```

```

QY 8 KKKK 11
DB 1111
   2 KKKK 5

```

```

1  RESULT 24
2  US-08 454-207A-24
3  Sequence 24, Application US/08454207A
4  Patent No. 5710123
5  GENERAL INFORMATION:
6  APPLICANT: Heavner, George A.
7  TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
8  NUMBER OF SEQUENCES: 70
9  CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123ris LLP
11 STREET: One Liberty Place - 46th Floor
12 CITY: Philadelphia
13 STATE: PA
14 COUNTRY: U.S.A.
15 ZIP: 19103
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: 3.5 inch disk, 1.44 MB
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Wordperfect 6.1
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/454,207A
23 FILING DATE: 09-JUN-1995
24 CLASSIFICATION: 514
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: PCT/US99/12110
27 FILING DATE: 13-DEC-1993
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: 07/997,771
30 FILING DATE: 18-DEC-1992
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Dianne B. Elderkin
33 REGISTRATION NUMBER: 28,598
34 REFERENCE/DOCKET NUMBER: COAR-0183
35 TELEPHONE: 215-568-3100
36 TELEFAX: 215-568-3439
37 INFORMATION FOR SEQ ID NO: 24:

```

```

Query Match 36.4%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

```

```

QY 8 KKKK 11
DB 1111
   2 KKKK 5

```

```

1  RESULT 25
2  US-08 454-207A-27
3  Sequence 25, Application US/08454207A
4  Patent No. 5756656

```


1 PRIOR APPLICATION DATA: US/07/07/966
 2 FILING DATE: 13-SEP-1991
 3 APPLICATION NUMBER: 07/760,254
 4 FILING DATE: 13-SEP-1991
 5 ATTORNEY/AGENT INFORMATION:
 6 NAME: OLSOVID, ELLIOT M.
 7 REGISTRATION NUMBER: 24,625
 8 REFERENCE/DOCKET NUMBER: 421250-131
 9 TELEPHONE: 201-994-1700
 10 TELEFAX: 201-994-1744
 11 INFORMATION FOR SEQ ID NO: 16:
 12 SEQUENCE CHARACTERISTICS:
 13 LENGTH: 10 amino acids
 14 TYPE: amine acid
 15 STRANDELNESS: linear
 16 MOLECULE TYPE: peptide
 17 OTHER INFORMATION: May be a 10 terminated strand.
 18 OTHER INFORMATION: and/or may be acetylated at
 19 OTHER INFORMATION: N-terminus.
 20 US 09-195 521-16

Query Match 36.4% Score 41 DB 1 Length 10
 Best Local Similarity 100.0% Pred. No. 3.6e+02
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

2Y 6 KLKK 9
 11
 12 6 KLKK 9

1 RESULT 28
 2 US 08-443 429-110
 3 Sequence ID: Application US/08/443/110
 4 Patent No. 565563
 5 GENERAL INFORMATION:
 6 APPLICANT: Baker, Margaret A.
 7 APPLICANT: Jacob, Leonard S.
 8 APPLICANT: Mayo, W. Lee
 9 TITLE OF INVENTION: Treatment of osteoporosis.
 10 TITLE OF INVENTION: Maturation w/o
 11 NUMBER OF SEQUENCES: 117
 12 CORRESPONDENCE ADDRESS:
 13 ADDRESSEE: Carella, Byline, Santa Clara, CA
 14 ADDRESSEE: Jacob, Leonard S.
 15 STREET: 6 Becker Farm Road
 16 CITY: Roseland
 17 STATE: New Jersey
 18 COUNTRY: USA
 19 ZIP: 07068
 20 COMPUTER READABLE FORM:
 21 MEDIUM TYPE: 3.5 inch diskette
 22 COMPUTER: IBM PS/2
 23 OPERATING SYSTEM: PC-DOS
 24 SOFTWARE: DW4 V2
 25 CURRENT APPLICATION DATA:
 26 APPLICATION NUMBER: US/08/443/110
 27 FILING DATE:
 28 CLASSIFICATION: 514
 29 PRIOR APPLICATION DATA:
 30 APPLICATION NUMBER: US/08/297/450
 31 FILING DATE:
 32 APPLICATION NUMBER: US/08/226/108
 33 FILING DATE:
 34 APPLICATION NUMBER: US/07/07/492
 35 FILING DATE:
 36 ATTORNEY/AGENT INFORMATION:
 37 NAME: OLSOVID, ELLIOT M.
 38 REGISTRATION NUMBER: 24,625

1 REFERENCE/DOCKET NUMBER: 421250-134
 2 TELECOMMUNICATION INFORMATION:
 3 TELEPHONE: 201-994-1700
 4 TELEFAX: 201-994-1744
 5 INFORMATION FOR SEQ ID NO: 110:
 6 SEQUENCE CHARACTERISTICS:
 7 LENGTH: 10 amino acids
 8 TYPE: amine acid
 9 STRANDELNESS:
 10 TOPOLOGY: linear
 11 MOLECULE TYPE: peptide
 12 US 09-443-120-110

Query Match 36.4% Score 41 DB 1 Length 10
 Best Local Similarity 100.0% Pred. No. 3.6e+02
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

2Y 6 KLKK 9
 11
 12 6 KLKK 9

1 RESULT 29
 2 US 08 465 425-109
 3 Sequence ID: Application US/08/465/425
 4 Patent No. 565563
 5 GENERAL INFORMATION:
 6 APPLICANT: Matatin Pharmaceuticals Inc.
 7 APPLICANT: 5110 Campus Drive
 8 APPLICANT: Plymouth Meeting, PA 19462
 9 TITLE OF INVENTION: Biologically Active Peptides Having
 10 TITLE OF INVENTION: N-terminal Substitutions
 11 NUMBER OF SEQUENCES: 13
 12 CORRESPONDENCE ADDRESS:
 13 ADDRESSEE: Elnedon, Henderson, Farabow, Garrett &
 14 ADDRESSEE: Turner
 15 STREET: 1400 L Street, N.W. Suite 700
 16 CITY: Washington
 17 STATE: D.C.
 18 COUNTRY: USA
 19 ZIP: 20005-3425
 20 COMPUTER READABLE FORM:
 21 MEDIUM TYPE: Floppy disk
 22 COMPUTER: IBM PC compatible
 23 OPERATING SYSTEM: PC-DOS/MS-DOS
 24 SOFTWARE: Patent In Release #1.0, Version #1.25
 25 CURRENT APPLICATION DATA:
 26 APPLICATION NUMBER: US/08/465/425
 27 FILING DATE: 05 JUN 1995
 28 CLASSIFICATION: 514
 29 PRIOR APPLICATION DATA:
 30 APPLICATION NUMBER: US/184/462
 31 FILING DATE: 18 JAN 94
 32 PRIOR APPLICATION DATA:
 33 APPLICATION NUMBER: 07/891,261
 34 FILING DATE: 01-JUN-92
 35 ATTORNEY/AGENT INFORMATION:
 36 NAME: FORDIS, Sean R.
 37 REGISTRATION NUMBER: 32,984
 38 REFERENCE/DOCKET NUMBER: 05387-0021-03000
 39 TELECOMMUNICATION INFORMATION:
 40 TELEPHONE: (202) 408-4000
 41 TELEFAX: (202) 408-4400
 42 INFORMATION FOR SEQ ID NO: 109:
 43 SEQUENCE CHARACTERISTICS:
 44 LENGTH: 10 amino acids
 45 TYPE: amine acid
 46 STRANDELNESS: single
 47 TOPOLOGY: linear
 48 MOLECULE TYPE: peptide
 49 US 08 465 425 109
 50 Query Match 36.4% Score 41 DB 1 Length 10

Best Local Similarity 100.0%, Seq ID No. 409, 027
Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0

QY 1 KKK 9
DB 1 1
4 KKK 9

RESULT 30
US 08-454-207A-4
Sequence 145, Application US/08454207
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Modatonic Pharmaceuticals Inc.
APPLICANT: 5110 Campus Drive
APPLICANT: Plymouth Meeting, PA 19062
TITLE OF INVENTION: Biologically Active Peptides Having:
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabee &
ADDRESSEE: Dunner
STREET: 1000 F Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-4315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1 B, Ver 3.0, 11/92
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454207
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,432
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/991,421
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: FORDIS, Jean B
REGISTRATION NUMBER: 32,964
REFERENCE/DOCKET NUMBER: 05467-011-000
TELEPHONE: (202) 408-4900
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 145
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US 08-454-207A-4

Query Match 36.4%, Score 4; DB 1; Length 15;
Best Local Similarity 100.0%, Seq ID No. 409, 027
Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0

QY 6 KKK 9
DB 1 KKK 4

RESULT 31
US 08-454-207A-4
Sequence 145, Application US/08454207
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Modatonic Pharmaceuticals Inc.
APPLICANT: 5110 Campus Drive
APPLICANT: Plymouth Meeting, PA 19062
TITLE OF INVENTION: Biologically Active Peptides Having:
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabee &
ADDRESSEE: Dunner
STREET: 1000 F Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-4315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1 B, Ver 3.0, 11/92
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454207
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,432
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/991,421
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: FORDIS, Jean B
REGISTRATION NUMBER: 32,964
REFERENCE/DOCKET NUMBER: 05467-011-000
TELEPHONE: (202) 408-4900
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 146
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US 08-454-207A-4

Query Match 36.4%, Score 4; DB 1; Length 15;
Best Local Similarity 100.0%, Seq ID No. 409, 027
Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0

QY 6 KKK 9
DB 1 KKK 4

Best Local Similarity 100.0%, Seq ID No. 409, 027
Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0

QY 7 LKKK 10
DB 2 LKKK 6

RESULT 32
US 08-454-207A-4
Sequence 145, Application US/08454207A
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Modatonic Pharmaceuticals Inc.
APPLICANT: 5110 Campus Drive
APPLICANT: Plymouth Meeting, PA 19062
TITLE OF INVENTION: Biologically Active Peptides Having:
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabee &
ADDRESSEE: Dunner
STREET: 1000 F Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-4315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1 B, Ver 3.0, 11/92
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454207A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,432
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/991,421
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: FORDIS, Jean B
REGISTRATION NUMBER: 32,964
REFERENCE/DOCKET NUMBER: 05467-011-000
TELEPHONE: (202) 408-4900
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 147
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US 08-454-207A-4

Query Match 36.4%, Score 4; DB 1; Length 10;
Best Local Similarity 100.0%, Seq ID No. 409, 027
Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0

QY 7 LKKK 10
DB 2 LKKK 6

RESULT 33
US 08-454-207A-4
Sequence 145, Application US/08454207A
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Modatonic Pharmaceuticals Inc.
APPLICANT: 5110 Campus Drive
APPLICANT: Plymouth Meeting, PA 19062
TITLE OF INVENTION: Biologically Active Peptides Having:
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabee &
ADDRESSEE: Dunner
STREET: 1000 F Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-4315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1 B, Ver 3.0, 11/92
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454207A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,432
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/991,421
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: FORDIS, Jean B
REGISTRATION NUMBER: 32,964
REFERENCE/DOCKET NUMBER: 05467-011-000
TELEPHONE: (202) 408-4900
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 148
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US 08-454-207A-4

Query Match 36.4%, Score 4; DB 1; Length 15;
Best Local Similarity 100.0%, Seq ID No. 409, 027
Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0

QY 7 LKKK 10
DB 2 LKKK 6

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PUBLICATION DATA:
  APPLICATION NUMBER: PCT/US93/12110
  FILING DATE: 13-DEC-1993
  PUBLICATION DATE: 07/09/97
  APPLICATION NUMBER: 07/997,771
  FILING DATE: 18-DEC-1992
  ATTORNEY/AGENT INFORMATION:
    NAME: Dianne B. ElderKilg
    REGISTRATION NUMBER: 28,598
    REFERENCE/DOCKET NUMBER: 608,183
    TELEPHONE: 215-568-3100
    TELEFAX: 215-568-3439
  INFORMATION FOR SEQ ID NO: 4:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 10 amino acids
      TYPE: amino acid
      TOPOLOGY: circular
  US-08-454,207A-4

Query Match: 36.4%; Score 4: DP 1: Length 10:
Best Local Similarity 100.0%; Pred. No. 3.6e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 KKKK 10
DB 2 KKKK 5

RESULT 44
US-08-418,024-49
  Sequence 39: Application US/8216,426
  Patent No. 5785324
  GENERAL INFORMATION:
    APPLICANT: Gray, Beulah
    APPLICANT: HASEMAN, Judith R.
    APPLICANT: MAYO, Kevin
    TITLE OF INVENTION: Synthesis of peptides with bactericidal
    TITLE OF INVENTION: Activity and Endotoxin Neutralizing Activity for Gram
    NUMBER OF SEQUENCES: 60
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
      STREET: 3100 No. 584066West Center, 90 South Seventh St
      CITY: Minneapolis
      STATE: MN
      COUNTRY: USA
      ZIP: 55402
    COMPUTER READABLE FORM:
      MEDIUM TYPE: Diskette
      OPERATING SYSTEM: IBM Compatible
      SOFTWARE: FASTSEQ Version 1.5
    CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/653,632
      FILING DATE: 24-MAY-1996
      CLASSIFICATION: 514
      PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 08/218026
        FILING DATE: 24-MAR-1994
      ATTORNEY/AGENT INFORMATION:
        NAME: Kelleiborger, Denise M
        REGISTRATION NUMBER: 33,924
        REFERENCE/DOCKET NUMBER: 600,2860811
        TELEPHONE: 612/371-5268
        TELEFAX: 612/342 9081
        TELEX:
      INFORMATION FOR SEQ ID NO: 39:
        SEQUENCE CHARACTERISTICS:
          LENGTH: 10 amino acids
          TYPE: amino acid
          STRANDEDNESS: Single
          TOPOLOGY: Linear
        MOLECULE TYPE: peptide
        HYPOTHETICAL: NO
        ANTI-SENSE: NO
        FRAGMENT TYPE: Internal
        ORIGINAL SOURCE:
          US-08-653-632-39

Query Match: 36.4%; Score 4: DP 2: Length 10:
Best Local Similarity 100.0%; Pred. No. 3.6e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 8 KKKK 11
DB 1 KKKK 4

RESULT 45
US-08-621,803-205
  Sequence 205: Application US/08621803
  Patent No. 5851802
  GENERAL INFORMATION:
    APPLICANT: Better, Marc L.

```



```

1  FILING DATE: 15-MAY-1991
2  PRIOR APPLICATION DATA:
3  APPLICATION NUMBER: US 08/054,414
4  FILING DATE: 15-MAY-1991
5  AGENT/AGENT INFORMATION:
6  NAME: BOYCE LEARY PH.D., KATHRYN
7  REGISTRATION NUMBER: 46,117
8  FILING DATE: 10-JUL-1991
9  PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: PCT/US91/01174
11 FILING DATE: 10-JUL-1991
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: PCT/US91/01174
14 FILING DATE: 15-MAY-1991
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: PCT/US91/01174
17 FILING DATE: 24-MAR-1991
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 08/150,462
20 FILING DATE: 31-MAR-1994
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: PCT/US94/00175
23 FILING DATE: 24-MAR-1995
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/307,113
26 FILING DATE: 16-SEP-1994
27 AGENT/AGENT INFORMATION:
28 NAME: CLOUGH, David W
29 REGISTRATION NUMBER: 46,107
30 REFERENCE/Docket NUMBER: 291,172,632
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 312 474-5400
33 INFORMATION FOR SEQ ID NO: 447:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 10 amino acids
36 TYPE: amino acid
37 STRANDEDNESS: single
38 FEATURE: linear
39 US 08/059 260A 447

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```

Query Match 35.4% Score 4.05 4 Length 10
Best Local Similarity 100.0% Pct. No. 3.6e+02
Matches 4 Conservative 0 Mismatches 0 Gaps 0
QY 2 GSAY 5
LE 111
7 GSAY 10

```

```

1  Sequence 49: Application US/08547414
2  Patent No. 4,274,544
3  GENERAL INFORMATION:
4  APPLICANT: KAZAKIAN, J. R. DATE: B
5  APPLICANT: BEKE, G. D.
6  APPLICANT: MORAN, JOHN V.
7  APPLICANT: COMBROSKI, BETH A.
8  TITLE OF INVENTION: COMPARISONS AND METHODS FOR
9  NUMBER OF SEQUENCES: 137
10 REFERENCE/Docket NUMBER: 291,172,632
11 ADDRESS: PANITCH SCHWARTZ JACOBS & SODI
12 CITY: PHILADELPHIA
13 STATE: PA
14 COUNTRY: U.S.A.
15 ZIP: 19103 7086
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 OPERATING SYSTEM: PC DOS/MS DOS
19 SOFTWARE: Patent In Release #10, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/647,844A
22 FILING DATE: 28-APR-1997
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 08/749,800
25 FILING DATE: 10-MAY-1996

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1  PRIOR APPLICATION DATA:
2  APPLICATION NUMBER: US 09/055,841
3  FILING DATE: 10-MAY-1996
4  AGENT/AGENT INFORMATION:
5  NAME: BOYCE LEARY PH.D., KATHRYN
6  REGISTRATION NUMBER: 46,117
7  REFERENCE/Docket NUMBER: 291,172,632
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: 312-567-2420
10 TELEFAX: 312-567-2491
11 INFORMATION FOR SEQ ID NO: 447:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 10 amino acids
14 TYPE: amino acid
15 STRANDEDNESS: single
16 FEATURE: linear
17 MOLECULE TYPE: protein
18 US 08/647-844A-48

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Query Match 35.4% Score 4.05 4 Length 10
Best Local Similarity 100.0% Pct. No. 3.6e+02
Matches 4 Conservative 0 Mismatches 0 Gaps 0
QY 2 GSAY 5
LE 111
7 GSAY 10

```

```

1  Sequence 49: Application US/9274542
2  Patent No. 4,274,544
3  GENERAL INFORMATION:
4  APPLICANT: Better, Marc B.
5  TITLE OF INVENTION: Methods for Recombinant Microbial Production of
6  NUMBER OF SEQUENCES: 265
7  REFERENCE/Docket NUMBER: 291,172,632
8  ADDRESS: Marshall, Thomas, Gerstein, Murray & Burns
9  STREET: 6400 Sears Tower, 24th South Wacker Drive
10 CITY: Chicago
11 STATE: Illinois
12 COUNTRY: United States of America
13 ZIP: 60606-6402
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 OPERATING SYSTEM: PC DOS/MS DOS
17 SOFTWARE: Patent In Release #10, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/09/217,454
20 FILING DATE:
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/621,803
23 FILING DATE: 22-MAR-1996
24 AGENT/AGENT INFORMATION:
25 NAME: Boron, Michael E.
26 REGISTRATION NUMBER: 25,447
27 REFERENCE/Docket NUMBER: 271,297,409
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 312/474-6400
30 TELEFAX: 312/474-6448
31 INDEX: 25,447
32 INFORMATION FOR SEQ ID NO: 405:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 10 amino acids
35 TYPE: amino acid
36 STRANDEDNESS: single
37 FEATURE: linear
38 NAME/KEY: 312 474-6400
39 US 08/647-844A-48

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NAME/KEY: Modified site
 LOCATION: 3 Regions
 OTHER INFORMATION: /label: Activated
 OTHER INFORMATION: /note: "The 3 Regions of Activated"
 US 09 787 443 4 205

Query Match: 96.4% Score 4: 100.0% Length 10:
 Best Local Similarity: 100.0% Pat. No. 6:45445
 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 7 KKK 10
 111
 DC 7 KKK 10

RESULT 4:
 US 09 720 05A 28
 Sequence 28: Application US/0902005A
 Patent No. 6:45402
 GENERAL INFORMATION:
 APPLICANT: Townsend, Robert M.
 APPLICANT: Korosold, Robert
 TITLE OF INVENTION: Peptide Methods of the Tyrosine Receptor Domain
 TITLE OF INVENTION: Gamma Chain and Methods and Compositions for
 TITLE OF INVENTION: Making and Using the Same
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Karl M. Lawton & M. 6:4540212 10P
 STREET: One Liberty Place, 4th Floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Wordperfect V. 8
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/020,05A
 FILING DATE: 07 FEB 1997
 PRIORITY APPLICATION NUMBER: US 6:454030, 41
 ATTORNEY/AGENT INFORMATION:
 NAME: Andrew, Mark
 REGISTRATION NUMBER: 539
 REFERENCE/AGENT NUMBER: 100.0%
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215 568-3100
 TELEFAX: 215 568-3439
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 TOPOLOGY: circular
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: peptide
 US 09 720 05A 28

Query Match: 36.4% Score 4: 100.0% Length 10:
 Best Local Similarity: 100.0% Pat. No. 6:45445
 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 1 AGA 4
 111
 DC 4 AGA 7

RESULT 4:
 US 09 115 730 104
 Sequence 109: Application US/09115730
 Patent No. 6:45445
 GENERAL INFORMATION:
 APPLICANT: G. Prasad Kuri
 APPLICANT: Tally J. Williams
 APPLICANT: Michael McNamee
 TITLE OF INVENTION: Biologically Active Peptides With Reduced
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Emerson, Paradows, Garrett &
 STREET: 1401 Street, N.W. Suite 700
 CITY: Washington

GENERAL INFORMATION:
 APPLICANT: G. Prasad Kuri
 APPLICANT: Michael McNamee
 TITLE OF INVENTION: Biologically Active Peptides With Reduced
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Emerson, Paradows, Garrett &
 STREET: 1401 Street, N.W. Suite 700
 CITY: Washington

Query Match: 96.4% Score 4: 100.0% Length 10:
 Best Local Similarity: 100.0% Pat. No. 6:45402
 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 6 KKK 9
 111
 DC 6 KKK 9

RESULT 4:
 US 09 115 730 104
 Sequence 148: Application US/09115730
 Patent No. 6:45445
 GENERAL INFORMATION:
 APPLICANT: G. Prasad Kuri
 APPLICANT: Tally J. Williams
 APPLICANT: Michael McNamee
 TITLE OF INVENTION: Biologically Active Peptides With Reduced
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Emerson, Paradows, Garrett &
 STREET: 1401 Street, N.W. Suite 700
 CITY: Washington


```

1  STATE: D.C.
2  COUNTRY: USA
3  ZIP: 20005-3515
4  COMPUTER READABLE FORM:
5  MEDIUM TYPE: Floppy disk
6  OPERATING SYSTEM: IBM PC compatible
7  SOFTWARE: Patent in Release #1.0, Version #1.30
8
9  CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/97/03437A
11 FILING DATE: 15-JUL-1997
12 CLASSIFICATION: Unknown
13
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: 08/445,440
16 FILING DATE: 05-JUN-1995
17 APPLICATION NUMBER: 08/144,462
18 FILING DATE: 18-JAN '94
19 APPLICATION NUMBER: 07/441,201
20 FILING DATE: 01-JUN '92
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Fordis, Jean B
23 REGISTRATION NUMBER: 42,494
24 REFERENCE/DOCKET NUMBER: 05/06/0021 Patent
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (202) 408-4300
27 TELEFAX: (202) 408-4409
28 INFORMATION FOR SEQ ID NO: 148:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 10 amino acids
31 TYPE: amino acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 N-TERMINUS TYPE: peptide
35 SEQUENCE DESCRIPTION: SEQ ID NO: 148:
36
37 US-09-115 737 148
38
39 Query Match 36.4% Score 47 DB 47 Length 107
40 Best Local Similarity 100.0% Pref No. 3,6e+02
41 Matches 4: Conservative 0: Mismatches 62 Indels 0
42
43 QY 6 KKKK 9
44 1 1 1
45 1 KKKK 4
46
47 RESULT 44
48 US-09-104 437A 437
49 Sequence 147, Application US/99/04437A
50 Patent No. 6492160
51 GENERAL INFORMATION:
52 APPLICANT: Winter, Gregory Paul
53 Griffiths, Andrew David
54 Williams, Samuel Cameron
55 Waterhouse, Peter
56 Nissim, Ahava
57 Johnson, Kevin Stuart
58 Smith, Andrew John Hammond
59 TITLE OF INVENTION: Methods for predicting members of species
60 binding pairs
61
62 NUMBER OF SEQUENCES: 600
63 CORRESPONDENCE ADDRESS:
64 ADDRESSEE: Audrey L. Battinicki
65 STREET: Marshall, Gerstein & Board
66 6300 Sears Tower, 23rd South Wacker Drive
67 CITY: Chicago
68 STATE: Illinois
69 COUNTRY: USA
70 ZIP: 60606-8402
71 COMPUTER READABLE FORM:
72 MEDIUM TYPE: Floppy disk
73 OPERATING SYSTEM: IBM PC compatible
74 SOFTWARE: Patent in Release #1.0, Version #1.24, #1.3

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1  CURRENT APPLICATION DATA:
2  APPLICATION NUMBER: US/99/104,337A
3  FILING DATE: 25-JAN-1998
4  PRIOR APPLICATION DATA:
5  APPLICATION NUMBER: US 08/350,260
6  FILING DATE: 05-DEC-1994
7  APPLICATION NUMBER: 08-410,549.4
8  FILING DATE: 15-MAY-1994
9  APPLICATION NUMBER: 08-520,618.9
10 FILING DATE: 24-MAR-1994
11 APPLICATION NUMBER: PCI/3894/C0883
12 FILING DATE: 15-MAY-1992
13 APPLICATION NUMBER: PCI/3894/C0609
14 FILING DATE: 28-MAR-1994
15 APPLICATION NUMBER: US 08/156,002
16 FILING DATE: 31-MAR-1994
17 APPLICATION NUMBER: US 08/307,619
18 FILING DATE: 16-SEP-1994
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Battinicki, Audrey L.
21 REGISTRATION NUMBER: 40,499
22 REFERENCE/DOCKET NUMBER: 28111/32372A
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 312-474-6300
25 INFORMATION FOR SEQ ID NO: 437:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 10 amino acids
28 TYPE: amino acid
29 STRANDEDNESS: single
30 TOPOLOGY: linear
31 SEQUENCE DESCRIPTION: SEQ ID NO: 437:
32
33 US-09-104 437A 437
34
35 Query Match 36.4% Score 47 DB 47 Length 107
36 Best Local Similarity 100.0% Pref No. 3,6e+02
37 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
38
39 QY 2 GSAY 5
40 1 1 1
41 1 GSAY 10
42
43 RESULT 44
44 US-08-983-157B 17
45 Sequence 17, Application US/08964157B
46 Patent No. 6479848
47 GENERAL INFORMATION:
48 APPLICANT: HEARING, Vincent J., Jr.
49 TITLE OF INVENTION: Protein and Peptides Thereof
50
51 NUMBER OF SEQUENCES: 28
52 CORRESPONDENCE ADDRESS:
53 ADDRESSEE: Needle & Rosenberg, P.C.
54 STREET: 127 Peachtree St., N.E.
55 CITY: Atlanta
56 STATE: GA
57 COUNTRY: USA
58 ZIP: 30303-1811
59 COMPUTER READABLE FORM:
60 MEDIUM TYPE: Floppy disk
61 OPERATING SYSTEM: IBM PC compatible
62 SOFTWARE: Patent in Release #1.0, Version #1.30
63 CURRENT APPLICATION DATA:
64 APPLICATION NUMBER: US/08/983,157B
65 FILING DATE: 22-DEC-1997
66 CLASSIFICATION: Unknown
67 PRIOR APPLICATION DATA:
68 APPLICATION NUMBER: PCI/US96/10695
69 FILING DATE: 21-JUN-1996
70 APPLICATION NUMBER: 60/000,436
71 FILING DATE: 23-JUN-1995
72 ATTORNEY/AGENT INFORMATION:

```

NAME: Spratt, Wendell
 REGISTRATION NUMBER: 36,516
 REFERENCE/DOCKET NUMBER: 14014, 5, 19
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 688-0770
 TELEFAX: (404) 688-9869
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 STRAIGHTNESS: not relevant
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US 09-787-443-4

Query Match 36.4% Score 4; DP 12; Length 10;
 Best Local Similarity 100.0%, Prod. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKKA 11
 LB 2 KKKA 5

RESULT 45
 PCT US95-09262-140
 Sequence 180, Application PC/TIS/6092/2
 GENERAL INFORMATION:
 APPLICANT:
 NUMBER OF SEQUENCES: 206
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, C/O Sears, Roebuck & Co.
 STREET: 6000 Sears Tower, 2nd South Wacker Dr SW
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Ver 0.0 #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/09262
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/472,100
 FILING DATE: 13-JAN-95
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/406,474
 FILING DATE: 15-SEP-94
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/213,540
 FILING DATE: 11-JUL-94
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/209,762
 FILING DATE: 11-MAR-94
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/183,222
 FILING DATE: 14-JAN-94
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/093,202
 FILING DATE: 15-JUL-93
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/040,644
 FILING DATE: 12-MAR-93
 ATTORNEY/AGENT INFORMATION:
 NAME: Sorub, Michael F.
 REGISTRATION NUMBER: 25,447
 REFERENCE/DOCKET NUMBER: 27129/1, 40
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6309
 TELEFAX: 312/474-6448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 180:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: "XMP-359"
 NAME/KEY: Modified site
 LOCATION: C-Terminal
 OTHER INFORMATION: /note: "The C-Terminus is Amidated"
 PCT-US95-09262-180

Query Match 36.4% Score 4; DP 5; Length 10;
 Best Local Similarity 100.0%, Prod. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKKK 10
 LB 7 LKKK 10

RESULT 46
 US-07-725-331-67
 Sequence 67, Application US/07725331
 Patent No. 5294565
 GENERAL INFORMATION:
 APPLICANT: Houghton, Richard
 APPLICANT: Bendelie, Sylvie
 TITLE OF INVENTION: Amphiphilic Peptide Compositions and
 TITLE OF INVENTION: Analogues Thereof
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dressler, Goldsmith, Sutter, Shore,
 ADDRESS: 6 Midway
 STREET: 180 No. 5294565th Stetson
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/725,331
 FILING DATE:
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/554,422
 FILING DATE: 19-JUL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Gamsou, Edward P.
 REGISTRATION NUMBER: 29,381
 REFERENCE/DOCKET NUMBER: 421250-80
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/6165416
 TELEFAX: 312/6165450
 INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRAIGHTNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:

OTHER INFORMATION: C-terminal amide, may be
OTHER INFORMATION: acetylated at N-terminus
US-07-725-931-67

Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KLKK 9
III
LB 3 KLKK 6

RESULT 47
US-08-193-521-17
Sequence 17, Application US/08193521
Patent No. 5470950
GENERAL INFORMATION:
APPLICANT: Maloy, W. Lee
APPLICANT: Williams, Jon I.
TITLE OF INVENTION: Biologically Active Peptide
TITLE OF INVENTION: Compositions and Uses Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn, Byrne, Bait, Gilligan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08193521
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07870960
FILING DATE:
APPLICATION NUMBER: 07/760,054
FILING DATE: 13 SEP 1991
ATTORNEY/AGENT INFORMATION:
NAME: Glstein, Elliot M.
REGISTRATION NUMBER: 24,026
REFERENCE/DOCKET NUMBER: 421250-191
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide,
OTHER INFORMATION: and/or may be acetylated at
OTHER INFORMATION: N-terminus.

Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
III
LB 3 KLKK 6

RESULT 48
US-08-193-521-17
Sequence 17, Application US/08193521
Patent No. 5470950
GENERAL INFORMATION:
APPLICANT: Maloy, W. Lee
APPLICANT: Williams, Jon I.
TITLE OF INVENTION: Biologically Active Peptide
TITLE OF INVENTION: Compositions and Uses Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn, Byrne, Bait, Gilligan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08193521
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07870960
FILING DATE:
APPLICATION NUMBER: 07/760,054
FILING DATE: 13 SEP 1991
ATTORNEY/AGENT INFORMATION:
NAME: Glstein, Elliot M.
REGISTRATION NUMBER: 24,026
REFERENCE/DOCKET NUMBER: 421250-191
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide,
OTHER INFORMATION: and/or may be acetylated at
OTHER INFORMATION: N-terminus.

Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
III
LB 3 KLKK 6

RESULT 49
US-08-193-521-18
Sequence 18, Application US/08193521
Patent No. 5470950
GENERAL INFORMATION:
APPLICANT: Maloy, W. Lee
APPLICANT: Williams, Jon I.
TITLE OF INVENTION: Biologically Active Peptide
TITLE OF INVENTION: Compositions and Uses Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn, Byrne, Bait, Gilligan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08193521
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07870960
FILING DATE:
APPLICATION NUMBER: 07/760,054
FILING DATE: 13 SEP 1991
ATTORNEY/AGENT INFORMATION:
NAME: Glstein, Elliot M.
REGISTRATION NUMBER: 24,026
REFERENCE/DOCKET NUMBER: 421250-191
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide,
OTHER INFORMATION: and/or may be acetylated at
OTHER INFORMATION: N-terminus.

QY 6 KLKK 9
III
LB 3 KLKK 6

Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 48
US-08-193-521-17
Sequence 17, Application US/08193521
Patent No. 5470950
GENERAL INFORMATION:
APPLICANT: Maloy, W. Lee
APPLICANT: Williams, Jon I.
TITLE OF INVENTION: Biologically Active Peptide
TITLE OF INVENTION: Compositions and Uses Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn, Byrne, Bait, Gilligan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08193521
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07870960
FILING DATE:
APPLICATION NUMBER: 07/760,054
FILING DATE: 13 SEP 1991
ATTORNEY/AGENT INFORMATION:
NAME: Glstein, Elliot M.
REGISTRATION NUMBER: 24,026
REFERENCE/DOCKET NUMBER: 421250-191
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide,
OTHER INFORMATION: and/or may be acetylated at
OTHER INFORMATION: N-terminus.

Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
III
LB 7 KLKK 10

RESULT 49
US-08-193-521-18
Sequence 18, Application US/08193521
Patent No. 5470950
GENERAL INFORMATION:
APPLICANT: Maloy, W. Lee
APPLICANT: Williams, Jon I.
TITLE OF INVENTION: Biologically Active Peptide
TITLE OF INVENTION: Compositions and Uses Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn, Byrne, Bait, Gilligan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08193521
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07870960
FILING DATE:
APPLICATION NUMBER: 07/760,054
FILING DATE: 13 SEP 1991
ATTORNEY/AGENT INFORMATION:
NAME: Glstein, Elliot M.
REGISTRATION NUMBER: 24,026
REFERENCE/DOCKET NUMBER: 421250-191
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide,
OTHER INFORMATION: and/or may be acetylated at
OTHER INFORMATION: N-terminus.

Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
III
LB 7 KLKK 10

RESULT 49
US-08-193-521-18
Sequence 18, Application US/08193521
Patent No. 5470950
GENERAL INFORMATION:
APPLICANT: Maloy, W. Lee
APPLICANT: Williams, Jon I.
TITLE OF INVENTION: Biologically Active Peptide
TITLE OF INVENTION: Compositions and Uses Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn, Byrne, Bait, Gilligan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08193521
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07870960
FILING DATE:
APPLICATION NUMBER: 07/760,054
FILING DATE: 13 SEP 1991
ATTORNEY/AGENT INFORMATION:
NAME: Glstein, Elliot M.
REGISTRATION NUMBER: 24,026
REFERENCE/DOCKET NUMBER: 421250-191
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide,
OTHER INFORMATION: and/or may be acetylated at
OTHER INFORMATION: N-terminus.

Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
III
LB 7 KLKK 10

RESULT 49
US-08-193-521-18
Sequence 18, Application US/08193521
Patent No. 5470950
GENERAL INFORMATION:
APPLICANT: Maloy, W. Lee
APPLICANT: Williams, Jon I.
TITLE OF INVENTION: Biologically Active Peptide
TITLE OF INVENTION: Compositions and Uses Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn, Byrne, Bait, Gilligan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08193521
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07870960
FILING DATE:
APPLICATION NUMBER: 07/760,054
FILING DATE: 13 SEP 1991
ATTORNEY/AGENT INFORMATION:
NAME: Glstein, Elliot M.
REGISTRATION NUMBER: 24,026
REFERENCE/DOCKET NUMBER: 421250-191
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide,
OTHER INFORMATION: and/or may be acetylated at
OTHER INFORMATION: N-terminus.

Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1  TITLE OF INVENTION: Compositions and Uses Involving
2  NUMBER OF SEQUENCES: 19
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE: Carella, Byrne, Rabin, Sullivan,
5  ADDRESSEE: Carella & Stewart
6  STREET: 6 Hooker Farm Road
7  CITY: Roseland
8  STATE: New Jersey
9  COUNTRY: USA
10 ZIP: 07068
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: 3.5 inch diskette
13 COMPUTER: IBM PS/2
14 OPERATING SYSTEM: PC-DOS
15 SOFTWARE: DM4 V2
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/06/143,521
18 FILING DATE:
19 CLASSIFICATION: 514
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US/01/870,319
22 FILING DATE:
23 ATTENTION NUMBER: 07/760,054
24 FILING DATE: 13-SEP-1991
25 ATTORNEY/AGENT INFORMATION:
26 NAME: OLSOIN, ELLIOT M.
27 REGISTRATION NUMBER: 24,025
28 REFERENCE/DCKET NUMBER: 42,200-10,
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 201-994 1700
31 TELEFAX: 201-994-1744
32 INFORMATION FOR SEQ ID NO: 1:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 11 amino acids
35 TYPE: amino acid
36 STRANDEDNESS:
37 NUCLEIC ACID: linear
38 MOLECULE TYPE: peptide
39 FEATURES:
40 OTHER INFORMATION: May be a C-terminal amino
41 OTHER INFORMATION: and/or may be acetylated
42 OTHER INFORMATION: N-terminus.
43 US 06/143 521-19
44
45 Query Match: 6,440, Score 4, DB 1, Length 17,
46 Best Local Similarity: 100.0%, Pred. No. 3.9e+02,
47 Matches: 4, Conservative: 0, Mismatches: 0, Gaps: 0;
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49 Q7: 8 KKKK 11
50 DB: 111
51 8 KKKK 11
52
53 Sequences completed: September 30, 2003, 10:28:38
54 Job time: 14.9167 secs
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1  SOFTWARE: ASCII text
2  CURRENT APPLICATION DATA:
3  APPLICATION NUMBER: US/06/178,570
4  FILING DATE: JANUARY 7, 1994
5  CLASSIFICATION: 515
6  ATTORNEY/AGENT INFORMATION:
7  NAME: DEGGRELL, GILBERT A., JR.
8  REGISTRATION NUMBER: 61,505
9  REFERENCE/DCKET NUMBER: HPI 104
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (517) 427-7400
12 TELEFAX: (517) 427-5941
13 INFORMATION FOR SEQ ID NO: 75:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 11 amino acids
16 TYPE: amino acid
17 TOPOLOGY: linear
18 MOLECULE TYPE: peptide
19 FRAGMENT TYPE: internal
20 US-06 178-570-75
21
22 Query Match: 6,440, Score 4, DB 1, Length 17,
23 Best Local Similarity: 100.0%, Pred. No. 3.9e+02,
24 Matches: 4, Conservative: 0, Mismatches: 0, Gaps: 0;
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26 Q7: 8 KKKK 11
27 DB: 111
28 8 KKKK 11
29
30 Sequences completed: September 30, 2003, 10:28:38
31 Job time: 14.9167 secs
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382	3	27.3	9	11	US 09-787-443-4-2	Sequence 52, Appl	455	3	27.3	9	12	US-10-022-066-441	Sequence 441, App
383	3	27.3	9	11	US 09-787-443-4-3	Sequence 53, Appl	456	3	27.3	9	12	US-10-022-066-534	Sequence 534, App
384	3	27.3	9	11	US 09-787-443-4-4	Sequence 54, Appl	457	3	27.3	9	12	US-10-022-066-570	Sequence 570, App
385	3	27.3	9	11	US 09-787-443-4-5	Sequence 55, Appl	458	3	27.3	9	12	US-10-022-066-616	Sequence 616, App
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387	3	27.3	9	11	US 09-787-443-4-7	Sequence 57, Appl	460	3	27.3	9	12	US-10-022-066-616	Sequence 284, App
388	3	27.3	9	11	US 09-787-443-4-8	Sequence 58, Appl	461	3	27.3	9	12	US-10-022-066-616	Sequence 662, App
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394	3	27.3	9	11	US 09-787-443-4-14	Sequence 64, Appl	467	3	27.3	9	12	US-10-022-066-616	Sequence 16, Appl
395	3	27.3	9	11	US 09-787-443-4-15	Sequence 65, Appl	468	3	27.3	9	12	US-10-022-066-616	Sequence 17, Appl
396	3	27.3	9	11	US 09-787-443-4-16	Sequence 66, Appl	469	3	27.3	9	12	US-10-022-066-616	Sequence 18, Appl
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416	3	27.3	9	11	US 09-787-443-4-36	Sequence 86, Appl	489	3	27.3	9	12	US-10-022-066-616	Sequence 9, Appl
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453	3	27.3	9	11	US 09-787-443-4-73	Sequence 123, Appl							

ALIGNMENTS

RESULT 1
US-09-572-270A-434
Sequence 434, Applicant: US/09572270A
Publication No. US20030148368A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Inter complementary peptide listing
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09572270A
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 1144
SOFTWARE: Pro: Patent version 1.0
SEQ ID NO 434
LENGTH: 10
TYPE: PPT
ORGANISM: Arabidopsis thaliana
OTHER INFORMATION: Sequence located in HMGI, at 443-452 and may interact with
US-09-572-270A-434
Query Match: 45.5%, Score 57, DP 127, Length 10;
Best Local Similarity: 100.0%, Pctd. No. 90;

Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AGSAV 5
11111
2 AGSAV 6

RESULT 2
US-10-424 125 6
Sequence 5, Application US/10224125
Publication No. US2003016184A1
GENERAL INFORMATION:
APPLICANT: REID, ROBERT H.
APPLICANT: BOELEKER, EUGAR C.
APPLICANT: VAN HAMONT, JOHN
APPLICANT: SEIFERSTROM, JEAN A.
APPLICANT: MCCUEEN, CHARLES
APPLICANT: CASSELLS, FREDERICK
TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENDOCRINOGENIC
TITLE OF INVENTION: ORGANISMS USING ANTIGENS FROM INFLUENZA WITHIN
TITLE OF INVENTION: B-CELL-DEPENDENT HYPOCOMPATIBILITY MIMIC-SPEAKERS
FILE REFERENCE: Army 108
CURRENT APPLICATION NUMBER: US/10/224,125
CURRENT FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: 08/789,734
PRIOR FILING DATE: 1997-01-27
PRIOR APPLICATION NUMBER: 08/452,944
PRIOR FILING DATE: 1994-12-06
PRIOR APPLICATION NUMBER: 06/034,947
PRIOR FILING DATE: 1993-03-22
PRIOR APPLICATION NUMBER: 07/467,403
PRIOR FILING DATE: 1992-04-10
PRIOR APPLICATION NUMBER: 07/805,724
PRIOR FILING DATE: 1991-11-21
PRIOR APPLICATION NUMBER: 07/690,195
PRIOR FILING DATE: 1991-04-24
PRIOR APPLICATION NUMBER: 07/521,445
PRIOR FILING DATE: 1990-05-11
PRIOR APPLICATION NUMBER: 07/495,537
PRIOR FILING DATE: 1990-03-15
PRIOR APPLICATION NUMBER: 06/540,608
PRIOR FILING DATE: 1984-03-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 10
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthesized
US 10-224 125 6

Quality Match 45.5% Score 5: 100.0% Pred. No. 100.0%
Best Local Similarity 100.0% Conservative 0: Mismatches 0: Indels 0: Gaps 0:
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 SAVKL 7
11111
2 SAVKL 6

RESULT 3
US-10-156-570A-15
Sequence 15, Application US/10156570A
Publication No. US20030125242A1
GENERAL INFORMATION:
APPLICANT: ROSENHECKER, JOSEPH
APPLICANT: RUTTER, WOLFGANG
APPLICANT: KULUPF, CARSTEN MARTIN
APPLICANT: FRANK, CHRISTIAN
TITLE OF INVENTION: POLYPEPTIDES COMBINING MULTIMERS OF NOCTURNAL
TITLE OF INVENTION: LOCALIZATION SIGNALS FOR PROTEIN TRANSLOCATION DOMAINS

1 TITLE OF INVENTION: ARTIFICIAL USE FOR TRANSFERRING NUCLEIC ACID MOLECULES
2 FILE REFERENCE: US/09-787-443-4-oli.rapb
3 CURRENT APPLICATION NUMBER: US/10/156,570A
4 CURRENT FILING DATE: 2002-09-24
5 PRIOR APPLICATION NUMBER: 09/47700/11690
6 PRIOR FILING DATE: 2000-11-23
7 NUMBER OF SEQ ID NOS: 32
8 SOFTWARE: Patent In Ver. 2.1
9 SEQ ID NO 15
10 LENGTH: 10
11 TYPE: PRI
12 ORGANISM: Artificial Sequence
13 FEATURE:
14 OTHER INFORMATION: Description of Artificial Sequence: hepatitis virus
15 OTHER INFORMATION: Delta antigen nuclear localization sequence
US 10-156-570A-15

Quality Match 45.5% Score 5: 100.0% Pred. No. 100.0%
Best Local Similarity 100.0% Conservative 0: Mismatches 0: Indels 0: Gaps 0:
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 6 KKKKK 10
11111
2 KKKKK 9

RESULT 4
US-09-992 665-27
Sequence 27, Application US/09992665
Publication No. US2003039209A1
GENERAL INFORMATION:
APPLICANT: KARP, PAUL
TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: GENENTEX, 002A
CURRENT APPLICATION NUMBER: US/09/992,665
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: 09/249,508
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 15
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Probe
US 09-992-665 27

Quality Match 45.5% Score 5: 100.0% Pred. No. 100.0%
Best Local Similarity 100.0% Conservative 0: Mismatches 0: Indels 0: Gaps 0:
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 6 KKKKK 10
11111
5 KKKKK 9

RESULT 5
US-10-014-322A 92
Sequence 92, Application US/10014322A
Publication No. US20030162129A1
GENERAL INFORMATION:
APPLICANT: NESTOR, J. John
APPLICANT: WILSON, CAROL
APPLICANT: TAN BEHR, CHRISTINA
APPLICANT: KATES, STEVEN
APPLICANT: KISTENBERG, JOHN
TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compou
FILE REFERENCE: CNS 068
CURRENT APPLICATION NUMBER: US/10/014,322A
CURRENT FILING DATE: 2002-07-09


```

Best Local Similarity 100.0%  Score 4: DB 15: Length 8;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

SY 7 LKXX 10
II 111
IB 2 LKXX 5

RESULT 9
US-10-133-210-174
? Sequence 174, Application US/10/133-210
? Publication No. US2004016964A1
? GENERAL INFORMATION:
? APPLICANT: Belzitsky, Jay
? APPLICANT: Gilukota, Kamalakar
? APPLICANT: Vaccaro, Dennis
? APPLICANT: Wong, Zhiping
? TITLE OF INVENTION: FLUORESCENT LIMER PROTEINS AND PEPTIDES
? FILE REFERENCE: CLON-077CIP
? CURRENT APPLICATION NUMBER: US/10/133-210
? PRIOR FILING DATE: 2002-04-26
? PRIOR FILING DATE: 2000-06-14
? PRIOR FILING DATE: 2001-06-14
? NUMBER OF SEQ ID NOS: 22
? SOFTWARE: FastSeq for Windows Version 1.1
? SEQ ID NO 14
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-174

Query Match 36.4%  Score 4: DB 15: Length 8;
Best Local Similarity 100.0%  Score 4: DB 15: Length 8;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

SY 7 LKXX 9
II 111
IB 2 LKXX 5

RESULT 10
US-10-133-210-174
? Sequence 174, Application US/10/133-210
? Publication No. US2004016964A1
? GENERAL INFORMATION:
? APPLICANT: Belzitsky, Jay
? APPLICANT: Gilukota, Kamalakar
? APPLICANT: Vaccaro, Dennis
? APPLICANT: Wong, Zhiping
? TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
? FILE REFERENCE: HU-035AX
? CURRENT APPLICATION NUMBER: US/10/133-210
? PRIOR FILING DATE: 2002-04-26
? PRIOR FILING DATE: 2001-06-14
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 146
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-174

Query Match 36.4%  Score 4: DB 15: Length 8;
Best Local Similarity 100.0%  Score 4: DB 15: Length 8;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

```

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SY 5 LKXX 8
II 111
IB 2 LKXX 5

RESULT 11
US-10-133-210-172
? Sequence 172, Application US/10/133-210
? Publication No. US2004016964A1
? GENERAL INFORMATION:
? APPLICANT: Belzitsky, Jay
? APPLICANT: Gilukota, Kamalakar
? APPLICANT: Vaccaro, Dennis
? APPLICANT: Wong, Zhiping
? TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
? FILE REFERENCE: HU-035AX
? CURRENT APPLICATION NUMBER: US/10/133-210
? PRIOR FILING DATE: 2002-04-26
? PRIOR FILING DATE: 2001-06-14
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 172
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-172

Query Match 36.4%  Score 4: DB 15: Length 8;
Best Local Similarity 100.0%  Score 4: DB 15: Length 8;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

SY 7 LKXX 10
II 111
IB 2 LKXX 5

RESULT 12
US-10-133-210-173
? Sequence 173, Application US/10/133-210
? Publication No. US2004016964A1
? GENERAL INFORMATION:
? APPLICANT: Belzitsky, Jay
? APPLICANT: Gilukota, Kamalakar
? APPLICANT: Vaccaro, Dennis
? APPLICANT: Wong, Zhiping
? TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
? FILE REFERENCE: HU-035AX
? CURRENT APPLICATION NUMBER: US/10/133-210
? PRIOR FILING DATE: 2002-04-26
? PRIOR FILING DATE: 2001-06-14
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 173
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-173

Query Match 36.4%  Score 4: DB 15: Length 8;
Best Local Similarity 100.0%  Score 4: DB 15: Length 8;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

SY 7 LKXX 10
II 111
IB 2 LKXX 5

```

```

1  TYPE: PWT
2  ORGANISM: N. rustica
3  US-09-826-177-12
4
5  Query Match
6  Best Local Similarity: 100.0%, Score: 4, DB: 9, Length: 9,
7  Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0,
8
9  QY 4 AVKL 7
10 111
11 2 AVKL 5
12
13 RESULT 15
14 US-09-826-177-14
15 1 Sequence: 14, Application: US/09/826-177
16 2 Patent No.: US2002022024A1
17 3 GENERAL INFORMATION:
18 4 APPLICANT: BAIG, Salim
19 5 TITLE OF INVENTION: Homocysteine Inhibitors and Methods of Use
20 6 FILE REFERENCE: 245,0038-0101
21 7 CURRENT APPLICATION NUMBER: US/09/826-177
22 8 CURRENT FILING DATE: 2001-09-18
23 9 PRIOR APPLICATION NUMBER: US-60/144,426
24 10 PRIOR FILING DATE: 2000-04-04
25 11 NUMBER OF SEQ ID NOS: 97
26 12 SOFTWARE: Patent in version 3.1
27 13 SEQ ID NO: 14
28 14 LENGTH: 9
29 15 TYPE: PWT
30 16 ORGANISM: L. aestivum
31 17 US-09-826-177-14
32
33 Query Match
34 Best Local Similarity: 100.0%, Score: 4, DB: 9, Length: 9,
35 Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0,
36
37 QY 4 AVKL 7
38 111
39 2 AVKL 5
40
41 RESULT 16
42 US-09-826-177-36
43 1 Sequence: 42, Application: US/09/826-177
44 2 Patent No.: US2002022024A1
45 3 GENERAL INFORMATION:
46 4 APPLICANT: BAIG, Salim
47 5 TITLE OF INVENTION: Homocysteine Inhibitors and Methods of Use
48 6 FILE REFERENCE: 245,0038-0101
49 7 CURRENT APPLICATION NUMBER: US/09/826-177
50 8 CURRENT FILING DATE: 2001-09-18
51 9 PRIOR APPLICATION NUMBER: US-60/194,426
52 10 PRIOR FILING DATE: 2000-04-04
53 11 NUMBER OF SEQ ID NOS: 97
54 12 SOFTWARE: Patent in version 3.1
55 13 SEQ ID NO: 14
56 14 LENGTH: 9
57 15 TYPE: PWT
58 16 ORGANISM: A. thaliana
59 17 US-09-826-177-36
60
61 Query Match
62 Best Local Similarity: 100.0%, Score: 4, DB: 9, Length: 9,
63 Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0,
64
65 QY 4 AVKL 8
66 111
67 5 AVKL 4
68
69 RESULT 14
70 US-09-826-177-32
71 1 Sequence: 42, Application: US/09/826-177
72 2 Patent No.: US2002022024A1
73 3 GENERAL INFORMATION:
74 4 APPLICANT: BAIG, Salim
75 5 TITLE OF INVENTION: Homocysteine Inhibitors and Methods of Use
76 6 FILE REFERENCE: 245,0038-0101
77 7 CURRENT APPLICATION NUMBER: US/09/826-177
78 8 CURRENT FILING DATE: 2001-09-18
79 9 PRIOR APPLICATION NUMBER: US-60/144,426
80 10 PRIOR FILING DATE: 2000-04-04
81 11 NUMBER OF SEQ ID NOS: 97
82 12 SOFTWARE: Patent in version 3.1
83 13 SEQ ID NO: 12
84 14 LENGTH: 9

```

```
RESULT 17
US-09-826-177-46
? Sequence 46, Application US/09826177
? Patent No. US2002022024A1
? GENERAL INFORMATION:
? APPLICANT: BAIG, Salman
? APPLICANT: PETERSON, David
? TITLE OF INVENTION: Hemoglobinase Inhibitors and Methods of Use
? FILE REFERENCE: 235,0038,0101
? CURRENT APPLICATION NUMBER: US/09/826,177
? CURRENT FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: US 60/194,426
? PRIOR FILING DATE: 2000-04-04
? NUMBER OF SEQ ID NOS: 97
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 46
? LENGTH: 9
? TYPE: PRT
? ORGANISM: C. elegans
US-09-826-177-46

Query Match      36.4%, Score 4, DB 9, Length 9;
Best Local Similarity 100.0%, Pred. No. 5, Le+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      4 AVKL 7
DB      1111
        2 AVKL 5

RESULT 18
US-09-826-177-44
? Sequence 48, Application US/09826177
? Patent No. US2002022024A1
? GENERAL INFORMATION:
? APPLICANT: BAIG, Salman
? APPLICANT: PETERSON, David
? TITLE OF INVENTION: Hemoglobinase Inhibitors and Methods of Use
? FILE REFERENCE: 235,0038,0101
? CURRENT APPLICATION NUMBER: US/09/826,177
? CURRENT FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: US 60/194,426
? PRIOR FILING DATE: 2000-04-04
? NUMBER OF SEQ ID NOS: 97
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 48
? LENGTH: 9
? TYPE: PRT
? ORGANISM: C. elegans
US-09-826-177-48

Query Match      36.4%, Score 4, DB 9, Length 9;
Best Local Similarity 100.0%, Pred. No. 5, Le+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      4 AVKL 7
DB      1111
        2 AVKL 5

RESULT 19
US-09-826-177-52
? Sequence 54, Application US/09826177
? Patent No. US2002022024A1
? GENERAL INFORMATION:
? APPLICANT: BAIG, Salman
? APPLICANT: PETERSON, David
? TITLE OF INVENTION: Hemoglobinase Inhibitors and Methods of Use
? FILE REFERENCE: 235,0038,0101
? CURRENT APPLICATION NUMBER: US/09/826,177
? CURRENT FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: US 60/194,426
? PRIOR FILING DATE: 2000-04-04
? NUMBER OF SEQ ID NOS: 97
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 52
? LENGTH: 9
? TYPE: PRT
? ORGANISM: Aedes aegypti
US-09-826-177-62

Query Match      36.4%, Score 4, DB 9, Length 9;
Best Local Similarity 100.0%, Pred. No. 5, Le+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      4 AVKL 7
DB      1111
        2 AVKL 5
```

```
RESULT 20
US-09-826-177-54
? Sequence 54, Application US/09826177
? Patent No. US2002022024A1
? GENERAL INFORMATION:
? APPLICANT: BAIG, Salman
? APPLICANT: PETERSON, David
? TITLE OF INVENTION: Hemoglobinase Inhibitors and Methods of Use
? FILE REFERENCE: 235,0038,0101
? CURRENT APPLICATION NUMBER: US/09/826,177
? CURRENT FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: US 60/194,426
? PRIOR FILING DATE: 2000-04-04
? NUMBER OF SEQ ID NOS: 97
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 54
? LENGTH: 9
? TYPE: PRT
? ORGANISM: L. major
US-09-826-177-54

Query Match      36.4%, Score 4, DB 9, Length 9;
Best Local Similarity 100.0%, Pred. No. 5, Le+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      4 AVKL 7
DB      1111
        2 AVKL 5

RESULT 21
US-09-826-177-62
? Sequence 62, Application US/09826177
? Patent No. US2002022024A1
? GENERAL INFORMATION:
? APPLICANT: BAIG, Salman
? APPLICANT: PETERSON, David
? TITLE OF INVENTION: Hemoglobinase Inhibitors and Methods of Use
? FILE REFERENCE: 235,0038,0101
? CURRENT APPLICATION NUMBER: US/09/826,177
? CURRENT FILING DATE: 2001-09-18
? PRIOR APPLICATION NUMBER: US 60/194,426
? PRIOR FILING DATE: 2000-04-04
? NUMBER OF SEQ ID NOS: 97
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 62
? LENGTH: 9
? TYPE: PRT
? ORGANISM: Aedes aegypti
US-09-826-177-62

Query Match      36.4%, Score 4, DB 9, Length 9;
Best Local Similarity 100.0%, Pred. No. 5, Le+05;
Matches      4; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      4 AVKL 7
DB      1111
        2 AVKL 5
```

```

111
2 AVKL 5

RESULT 22
US-09-876-604A-589
1 Sequence 136, Application US/0987604A
2 Patent No. US20020365138A
3 GENERAL INFORMATION:
4 APPLICANT: Ward, Peter A.
5 APPLICANT: Haber Jacq, Markus
6 APPLICANT: Salma, Vidya
7 APPLICANT: Cerniak, Boris
8 TITLE OF INVENTION: Compositions and Methods for the Treatment of Seters
9 FILE REFERENCE: US-0783
10 CURRENT APPLICATION NUMBER: US/09/876,604
11 CURRENT FILING DATE: 2001-06-11
12 PRIOR APPLICATION NUMBER: 09/487,471
13 PRIOR FILING DATE: 1999-08-31
14 NUMBER OF SEQ ID NOS: 74
15 SOFTWARE: Patent In Ver. 2.0
16 SEQ ID NO: 21
17 LENGTH: 9
18 TYPE: PRT
19 ORGANISM: Artificialia, Sequence
20 FEATURE:
21 OTHER INFORMATION: Description of Artificialia, Sequence, Synthetic
US-09-878-603-21

Query Match: 36.4%, Score 4, DB 11, Length 9,
Best Local Similarity: 100.0%, Pred. No. 5, 1e-05,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 SAVK 5
LB 111
5 SAVK 8

RESULT 23
US-09-876-904A-589
1 Sequence 589, Application US/0987604A
2 Patent No. US20020372794A
3 GENERAL INFORMATION:
4 APPLICANT: BOLLIGAS, TENI
5 TITLE OF INVENTION: ENCAPSULATION OF PLASMA AND CELL-GENES AND IMMUNOPROTEIN
6 TITLE OF INVENTION: AGENTS WITH NO CLEARLY DEFINED CATALYTIC, STIMULATING, OR PEPTIDIC
7 TITLE OF INVENTION: CONJUGATES AND TARGETED DELIVERY OF PROTEINS
8 FILE REFERENCE: JP 2002-00
9 CURRENT APPLICATION NUMBER: US/09/876,904A
10 CURRENT FILING DATE: 2001-06-09
11 PRIOR APPLICATION NUMBER: US 60/210,000
12 PRIOR FILING DATE: 2000-06-09
13 NUMBER OF SEQ ID NOS: 629
14 SOFTWARE: Patent In Ver. 2.1
15 SEQ ID NO: 586
16 LENGTH: 9
17 TYPE: PRT
18 ORGANISM: Unknown Organism
19 FEATURE:
20 OTHER INFORMATION: Description of Unknown Organism, Protein Testis II (194 aa)
US-09-876-904A-589

Query Match: 36.4%, Score 4, DB 11, Length 9,
Best Local Similarity: 100.0%, Pred. No. 5, 1e-05,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 8 KKKA 11
LB 111
6 KKKA 9

RESULT 24
US-09-995-529-136

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```

1 Sequence 136, Application US/0995529
2 Patent No. US200200995529A1
3 GENERAL INFORMATION:
4 APPLICANT: Watkins, Jeffery L.
5 APPLICANT: Buse, William L.
6 APPLICANT: Tang, Yim
7 TITLE OF INVENTION: Humanized Celladen Antibodies and
8 TITLE OF INVENTION: Related Methods
9 FILE REFERENCE: P IX 4576
10 CURRENT APPLICATION NUMBER: US/09/995,529
11 CURRENT FILING DATE: 2001-11-26
12 NUMBER OF SEQ ID NOS: 358
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO: 136
15 LENGTH: 9
16 TYPE: PRT
17 ORGANISM: Artificialia, Sequence
18 FEATURE:
19 OTHER INFORMATION: Synthetic antibody mutation
US-09-995-529-136

Query Match: 36.4%, Score 4, DB 11, Length 9,
Best Local Similarity: 100.0%, Pred. No. 5, 1e-05,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 2 GSAY 5
LB 111
5 GSAY 6

RESULT 25
US-09-715-527-565
1 Sequence 295, Application US/09765527
2 Patent No. US20020066638A
3 GENERAL INFORMATION:
4 APPLICANT: Better, Marc C.
5 TITLE OF INVENTION: Methods for Recombinant Microbial Production of
6 TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
7 NUMBER OF SEQUENCES: 265
8 CORRESPONDENCE ADDRESS:
9 ADDRESS: Marstad, O'Toole, Gerstein, Murray & Horn
10 STREET: 6400 Sears Tower, 233 South Wacker Drive
11 CITY: Chicago
12 STATE: Illinois
13 COUNTRY: United States of America
14 ZIP: 60606-6432
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS DOS
19 SOFTWARE: Patent In Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/09/765,527
22 FILING DATE: 18 Jan-2003
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 08/621,803
25 FILING DATE: <Unknown>
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Borum, Michael E.
28 REGISTRATION NUMBER: 25,447
29 REFERENCE/DOCUMENT NUMBER: 27129/33199
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 312/474-6100
32 TELEFAX: 312/474-0448
33 TELEX: 25-4856
34 INFORMATION FOR SEQ ID NO: 205:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 10 amino acids
37 TYPE: amino acid
38 TOPOLOGY: linear
39 MOLECULE TYPE: peptide
40 FEATURE:
41 NAME/KEY: misc_feature

```


: CURRENT FILING DATE: 2000-05-17
 : NUMBER OF SEQ ID NOS: 4203
 : SOFTWARE: Protolent version 1.0
 : SEQ ID NO 2308
 : LENGTH: 10
 : TYPE: PRT
 : ORGANISM: Homo Sapiens
 : FEATURES:
 : OTHER INFORMATION: Sequence located in MYK or MTK at 1354-1367 and may interact with
 : OTHER INFORMATION: Sequence 2307 in this patent
 US-09-572-404B-2908

Query Match 36.4% Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Prod. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSAV 5
 DB 3 GSAV 6

RESULT 49
 US-09-572-404B-3280
 : Sequence 3280, Application US/09/572404B
 : Publication No. US20030078374A1
 : GENERAL INFORMATION:
 : APPLICANT: Proteom Ltd
 : TITLE OF INVENTION: Complementary peptide fragments from the human genome
 : FILE REFERENCE: Human patent
 : CURRENT APPLICATION NUMBER: US/09/572-404B
 : CURRENT FILING DATE: 2000-05-17
 : NUMBER OF SEQ ID NOS: 4203
 : SOFTWARE: Protolent version 1.0
 : SEQ ID NO 3280
 : LENGTH: 10
 : TYPE: PRT
 : ORGANISM: Homo Sapiens
 : FEATURES:
 : OTHER INFORMATION: Sequence located in GSAV at 1360-1369 and may interact with
 : OTHER INFORMATION: Sequence 3279 in this patent
 US-09-572-404B-3289

Query Match 36.4% Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Prod. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AASA 4
 DB 5 AASA 6

RESULT 40
 US-09-572-404B-142
 : Sequence 142, Application US/09/572-055A
 : Publication No. US20030083243A1
 : GENERAL INFORMATION:
 : APPLICANT: Owen, Donald K.
 : TITLE OF INVENTION: SHORT REACTIVE Peptides
 : FILE REFERENCE: HELX027
 : CURRENT APPLICATION NUMBER: US/09/572-055A
 : CURRENT FILING DATE: 2001-03-28
 : NUMBER OF SEQ ID NOS: 165
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 142
 : LENGTH: 10
 : TYPE: PRT
 : ORGANISM: ARTIFICIAL SEQUENCE
 : FEATURES:
 : OTHER INFORMATION: SYNTHETIC SEQUENCE
 : NAME/KEY: K10-RES
 : LOCATION: (10)
 : OTHER INFORMATION: AMIDATION
 US-09-572-055A-142

Query Match 36.4% Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Prod. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKKA 9
 DB 6 KKKA 9

RESULT 41
 US-09-572-270A-318
 : Sequence 318, Application US/09/572270A
 : Publication No. US20030148568A1
 : GENERAL INFORMATION:
 : APPLICANT: Proteom Ltd
 : TITLE OF INVENTION: Inter complementary peptide listing
 : FILE REFERENCE:
 : CURRENT APPLICATION NUMBER: US/09/572,270A
 : CURRENT FILING DATE: 2000-05-17
 : NUMBER OF SEQ ID NOS: 1144
 : SOFTWARE: Protolent version 1.0
 : SEQ ID NO 318
 : LENGTH: 10
 : TYPE: PRT
 : ORGANISM: Arabidopsis thaliana
 : OTHER INFORMATION: Sequence located in TOP2, at 1249-1258 and may interact with
 US-09-572-270A-318

Query Match 36.4% Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Prod. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKKA 11
 DB 2 KKKA 5

RESULT 42
 US-09-572-270A-320
 : Sequence 320, Application US/09/572270A
 : Publication No. US20030148568A1
 : GENERAL INFORMATION:
 : APPLICANT: Proteom Ltd
 : TITLE OF INVENTION: Inter complementary peptide listing
 : FILE REFERENCE:
 : CURRENT APPLICATION NUMBER: US/09/572,270A
 : CURRENT FILING DATE: 2000-05-17
 : NUMBER OF SEQ ID NOS: 1144
 : SOFTWARE: Protolent version 1.0
 : SEQ ID NO 320
 : LENGTH: 10
 : TYPE: PRT
 : ORGANISM: Arabidopsis thaliana
 : OTHER INFORMATION: Sequence located in TOP2, at 1248-1257 and may interact with
 US-09-572-270A-320

Query Match 36.4% Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Prod. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKKA 11
 DB 3 KKKA 6

RESULT 43
 US-09-572-270A-629
 : Sequence 629, Application US/09/572270A
 : Publication No. US20030148568A1
 : GENERAL INFORMATION:
 : APPLICANT: Proteom Ltd
 : TITLE OF INVENTION: Inter complementary peptide listing

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1 FILE REFERENCE:
2 CURRENT APPLICATION NUMBER: US/09/572-270A
3 CURRENT FILING DATE: 2000-05-17
4 NUMBER OF SEQ ID NOS: 1144
5 SOFTWARE: Protolent version 1.0
6 SEQ ID NO 629
7 LENGTH: 10
8 TYPE: PRT
9 ORGANISM: Arabidopsis Thaliana
10 OTHER INFORMATION: Sequence located in Genbank at 79-87 and may interact with
US 09 572-270A-629

Query Match 36.4% Score 4: DB 12: Length 10:
Best Local Similarity 100.0%: Prid. No. 8e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 GSAY 5
DB 1 GSAY 4

RESULT 44
US-09-572-270A-631
1 Sequence 631, Application US/09/572-270A
2 Publication No. US20030148368A1
3 GENERAL INFORMATION:
4 APPLICANT: Proteom Ltd
5 TITLE OF INVENTION: Inter complementary peptide listing
6 FILE REFERENCE:
7 CURRENT APPLICATION NUMBER: US/09/572-270A
8 CURRENT FILING DATE: 2000-05-17
9 NUMBER OF SEQ ID NOS: 1144
10 SOFTWARE: Protolent version 1.0
11 SEQ ID NO 631
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Arabidopsis Thaliana
15 OTHER INFORMATION: Sequence located in Unknown at 79-84 and may interact with
US-09-572-270A-631

Query Match 36.4% Score 4: DB 12: Length 10:
Best Local Similarity 100.0%: Prid. No. 8e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 GSAY 5
DB 2 GSAY 5

RESULT 45
US-09-572-270A-840
1 Sequence 840, Application US/09/572-270A
2 Publication No. US20030148368A1
3 GENERAL INFORMATION:
4 APPLICANT: Proteom Ltd
5 TITLE OF INVENTION: Inter complementary peptide listing
6 FILE REFERENCE:
7 CURRENT APPLICATION NUMBER: US/09/572-270A
8 CURRENT FILING DATE: 2000-05-17
9 NUMBER OF SEQ ID NOS: 1144
10 SOFTWARE: Protolent version 1.0
11 SEQ ID NO 840
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Arabidopsis Thaliana
15 OTHER INFORMATION: Sequence located in RPL44 at 79-86, 89 and may interact with
US-09-572-270A-840

Query Match 36.4% Score 4: DB 12: Length 10:
Best Local Similarity 100.0%: Prid. No. 8e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 GSAY 5

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1 APPLICANT: Seattle, Ernest S
2 TITLE OF INVENTION: Targeted Vaccine Delivery Systems
3 FILE REFERENCE: 1821-0020001
4 CURRENT APPLICATION NUMBER: US/09/344,243
5 PRIOR FILING DATE: 2001-04-22
6 PRIOR APPLICATION NUMBER: US/00/196,472
7 PRIOR FILING DATE: 2000-04-12
8 NUMBER OF SEQ ID NOS: 6
9 SOFTWARE: Patent version 4.0
10 SEQ ID NO 46
11 LENGTH: 10
12 TYPE: PRT
13 ORGANISM: Artificial Sequence
14 NAME/KEY: miscellaneous
15 OTHER INFORMATION: c35 peptides
US-09-533-203-46

Query Match: 36.4%, Score 47, DB 12, Length 10,
Best Local Similarity: 100.0%, Pred. No. 86-02,
Matches 4, Conservative 0, Mismatches 0, Gaps 0,

QY 4 SAVK 6
111
DB 1 SAVK 4

RESULT 49
US 17 022 506 406
1 Sequence 406: Application US/17/022,006
2 Publication No.: US20030166057A1
3 GENERAL INFORMATION:
4 APPLICANT: HILLERMAN, WILLIAM R.
5 APPLICANT: HILLERMAN, KILEY RAE
6 TITLE OF INVENTION: METHOD AND APPARATUS FOR DELIVERING ANTIBODIES AND
7 FILE REFERENCE: 6680-034
8 CURRENT APPLICATION NUMBER: US/02/2,106
9 PRIOR FILING DATE: 2002-09-09
10 PRIOR APPLICATION NUMBER: 69/256,413
11 PRIOR FILING DATE: 2000-12-18
12 PRIOR APPLICATION NUMBER: 63/296,439
13 PRIOR FILING DATE: 2000-12-18
14 PRIOR APPLICATION NUMBER: 59/403,102
15 PRIOR FILING DATE: 1999-12-17
16 PRIOR APPLICATION NUMBER: 69/994,300
17 PRIOR FILING DATE: 2001-11-10
18 NUMBER OF SEQ ID NOS: 548
19 SOFTWARE: Patent Vcr. 2.1
20 SEQ ID NO 466
21 LENGTH: 10
22 TYPE: PRT
23 ORGANISM: Artificial Sequence
24 NAME/KEY: miscellaneous
25 OTHER INFORMATION: Description of Artificial Sequence of Synthetic
26 FEATURES:
27 NAME/KEY: N-TERMINUS
28 LOCATION: (27-113)
29 OTHER INFORMATION: Unknown amino acid
US 17 022 506 406

Query Match: 36.4%, Score 47, DB 12, Length 10,
Best Local Similarity: 100.0%, Pred. No. 86-02,
Matches 4, Conservative 0, Mismatches 0, Gaps 0,

QY 1 AGSA 4
111
DB 6 AGSA 9

RESULT 50
US 10 168 185 11

1 Sequence 11: Application US/10/168,185
2 Publication No.: US20030175802A1
3 GENERAL INFORMATION:
4 APPLICANT: Ambrust, Edgar Paul
5 APPLICANT: Mussbacher, Albert
6 APPLICANT: Schmidt, Gayk, Heinrich
7 TITLE OF INVENTION: Method for Determining Parathormone
8 TITLE OF INVENTION: Activity in a Human Sample
9 FILE REFERENCE: HLA 00408
10 CURRENT APPLICATION NUMBER: US/10/168,185
11 PRIOR FILING DATE: 2002-06-17
12 PRIOR APPLICATION NUMBER: PCT/EP02/12911
13 PRIOR FILING DATE: 2000-12-18
14 PRIOR APPLICATION NUMBER: DE 19961350
15 PRIOR FILING DATE: 1999-12-17
16 NUMBER OF SEQ ID NOS: 11
17 SOFTWARE: FastSeq for Windows Version 4.0
18 SEQ ID NO 11
19 LENGTH: 10
20 TYPE: PRT
21 ORGANISM: Homo Sapiens
22 US 10-168-185-11

Query Match: 36.4%, Score 47, DB 12, Length 10,
Best Local Similarity: 100.0%, Pred. No. 86-02,
Matches 4, Conservative 0, Mismatches 0, Gaps 0,

QY 4 KKKA 11
111
DB 7 KKKA 10

Search completed: September 30, 2003, 10:52:56
Job Time: 25.5 secs

227	4	36.4	10	22	AAH9772	Human C35 peptide	302	4	36.4	10	22	AAGB7481	Saccharomyces cere
230	4	36.4	10	22	ABH12522	Human C35 peptide	303	4	36.4	10	22	AAGH7696	Saccharomyces cere
231	4	36.4	10	22	ABH12524	Human C35 peptide	304	4	36.4	10	22	AAGH7697	Saccharomyces cere
242	4	36.4	10	22	ABH12566	Human C35 peptide	305	4	36.4	10	22	AAG93375	Procollagen alpha
243	4	36.4	10	22	ABH12570	Human C35 peptide	306	4	36.4	10	22	AAG93376	Procollagen alpha
244	4	36.4	10	22	ABH12575	Human C35 peptide	307	4	36.4	10	22	AAG65480	Anti-tungal peptid
245	4	36.4	10	22	ABH12665	Human C35 peptide	308	4	36.4	10	22	AAB57730	D. teissieri IDM pe
246	4	36.4	10	22	ABH12669	Human C35 peptide	309	4	36.4	10	23	ABJ15176	Immunogenic HIV pe
247	4	36.4	10	22	ABH12674	Human C35 peptide	310	4	36.4	10	24	ABG91987	Human antibody fra
248	4	36.4	10	22	ABH12676	Human C35 peptide	311	4	36.4	10	24	ABG78296	Human Fv molecule
249	4	36.4	10	22	ABH12678	Human C35 peptide	312	4	36.4	10	23	AAJ99697	Vectors pcDNA3.2+
240	4	36.4	10	22	ABH13011	Human C35 peptide	313	4	36.4	10	23	AAE22461	Biologically activ
241	4	36.4	10	22	ABH13050	Human C35 peptide	314	4	36.4	10	23	AAE22500	Biologically activ
242	4	36.4	10	22	ABH13094	Human C35 peptide	315	4	36.4	10	23	ABH96947	Human tumour antig
243	4	36.4	10	22	ABH13139	Human C35 peptide	316	4	36.4	10	23	ABH97135	Human tumour antig
244	4	36.4	10	22	ABH13142	Human C35 peptide	317	4	36.4	10	23	ABH44681	Human protective s
245	4	36.4	10	22	ABH13274	Human C35 peptide	318	4	36.4	10	24	ABH69724	Human immunodefici
246	4	36.4	10	22	ABH13313	Human C35 peptide	319	4	36.4	10	24	ABH69729	Human immunodefici
247	4	36.4	10	22	ABH13386	Human C35 peptide	320	4	36.4	10	24	ABH69752	Human immunodefici
248	4	36.4	10	22	ABH13387	Human C35 peptide	321	4	36.4	10	24	ABH69801	Human immunodefici
249	4	36.4	10	22	ABH13425	Human C35 peptide	322	4	36.4	10	24	ABH69929	Human immunodefici
250	4	36.4	10	22	ABH13471	Human C35 peptide	323	4	36.4	10	24	ABH69935	Human immunodefici
251	4	36.4	10	22	ABH13516	Human C35 peptide	324	4	36.4	10	24	ABH70021	Human immunodefici
252	4	36.4	10	22	ABH13592	Human C35 peptide	325	4	36.4	10	24	ABH70168	Human immunodefici
253	4	36.4	10	22	ABH13617	Human C35 peptide	326	4	36.4	10	24	ABH70324	Human immunodefici
254	4	36.4	10	22	ABH13667	Human C35 peptide	327	4	36.4	10	24	ABH70342	Human immunodefici
255	4	36.4	10	22	ABH13719	Human C35 peptide	328	4	36.4	10	24	ABH70348	Human immunodefici
256	4	36.4	10	22	ABH13743	Human C35 peptide	329	4	36.4	10	24	ABH70624	Human cancer-relat
257	4	36.4	10	22	ABH13747	Human C35 peptide	330	4	36.4	10	24	ABH707631	Human cancer-relat
258	4	36.4	10	22	ABH13747	Human C35 peptide	331	4	36.4	10	24	ABH707647	Human cancer-relat
259	4	36.4	10	22	ABH13811	Human C35 peptide	332	4	36.4	10	24	ABH70779	Human cancer-relat
260	4	36.4	10	22	ABH13846	Human C35 peptide	333	4	36.4	10	24	ABH70811	Human cancer-relat
261	4	36.4	10	22	ABH13972	Human C35 peptide	334	4	36.4	10	24	ABH70823	Human cancer-relat
262	4	36.4	10	22	ABH13978	Human C35 peptide	335	4	36.4	10	24	ABH70853	Human cancer-relat
263	4	36.4	10	22	ABH14017	Human C35 peptide	336	4	36.4	10	24	ABH808029	Human cancer-relat
264	4	36.4	10	22	ABH14047	Human C35 peptide	337	4	36.4	10	24	ABH808035	Human cancer-relat
265	4	36.4	10	22	ABH14057	Human C35 peptide	338	4	36.4	10	24	ABH808064	Human cancer-relat
266	4	36.4	10	22	ABH14108	Human C35 peptide	339	4	36.4	10	24	ABH808204	Human cancer-relat
267	4	36.4	10	22	ABH14114	Human C35 peptide	340	4	36.4	10	24	ABH808393	Human cancer-relat
268	4	36.4	10	22	ABH14147	Human C35 peptide	341	4	36.4	10	24	ABH808440	Human cancer-relat
269	4	36.4	10	22	ABH14196	Human C35 peptide	342	4	36.4	10	24	ABH808451	Human cancer-relat
270	4	36.4	10	22	ABH14234	Human C35 peptide	343	4	36.4	10	24	ABH808460	Human cancer-relat
271	4	36.4	10	22	ABH14317	Human C35 peptide	344	4	36.4	10	24	ABH808590	Human cancer-relat
272	4	36.4	10	22	ABH14328	Human C35 peptide	345	4	36.4	10	24	ABH808608	Human cancer-relat
273	4	36.4	10	22	ABH14415	Human C35 peptide	346	4	36.4	10	24	ABH808610	Human cancer-relat
274	4	36.4	10	22	ABH14554	Human C35 peptide	347	4	36.4	10	24	ABH808615	Human cancer-relat
275	4	36.4	10	22	ABH14565	Human C35 peptide	348	4	36.4	10	24	ABH808620	Human cancer-relat
276	4	36.4	10	22	ABH14577	Human C35 peptide	349	4	36.4	10	24	ABH808783	Human cancer-relat
277	4	36.4	10	22	ABH14612	Human C35 peptide	350	4	36.4	10	24	ABH808795	Human cancer-relat
278	4	36.4	10	22	ABH14613	Human C35 peptide	351	4	36.4	10	24	ABH808825	Human cancer-relat
279	4	36.4	10	22	ABH14642	Human C35 peptide	352	4	36.4	10	24	ABH808835	Human cancer-relat
280	4	36.4	10	22	ABH14657	Human C35 peptide	353	4	36.4	10	24	ABH808863	Human cancer-relat
281	4	36.4	10	22	AAH03431	Neisseria meningit	354	4	36.4	10	24	ABH808883	Human cancer-relat
282	4	36.4	10	22	AAG94713	Human complementar	355	4	36.4	10	24	ABH808895	Human cancer-relat
283	4	36.4	10	22	AAG94712	Human complementar	356	4	36.4	10	24	ABH808925	Human cancer-relat
284	4	36.4	10	22	AAG94714	Human complementar	357	4	36.4	10	24	ABH808935	Human cancer-relat
285	4	36.4	10	22	AAG94716	Human complementar	358	4	36.4	10	24	ABH808961	Human cancer-relat
286	4	36.4	10	22	AAG94722	Human complementar	359	4	36.4	10	24	ABH16359	Human cancer-relat
287	4	36.4	10	22	AAG94740	Human complementar	360	4	36.4	10	24	ABH16363	Human cancer-relat
288	4	36.4	10	22	AAG94742	Human complementar	361	4	36.4	10	24	ABH16467	Human cancer-relat
289	4	36.4	10	22	AAG94744	Human complementar	362	4	36.4	10	24	ABH16483	Human cancer-relat
290	4	36.4	10	22	AAG94752	Human complementar	363	4	36.4	10	24	ABH16530	Human cancer-relat
291	4	36.4	10	22	AAG94767	Human complementar	364	4	36.4	10	24	ABH16546	Human cancer-relat
292	4	36.4	10	22	AAG94768	Human complementar	365	4	36.4	10	24	ABH16667	Human cancer-relat
293	4	36.4	10	22	AAG94768	Human complementar	366	4	36.4	10	24	ABH16677	Human cancer-relat
294	4	36.4	10	22	AAG94768	Human complementar	367	4	36.4	10	24	ABH16686	Human cancer-relat
295	4	36.4	10	22	AAG94768	Human complementar	368	4	36.4	10	24	ABH16759	Human cancer-relat
296	4	36.4	10	22	AAG94768	Human complementar	369	4	36.4	10	24	ABH16916	Human cancer-relat
297	4	36.4	10	22	AAG94768	Human complementar	370	4	36.4	10	24	ABH17071	Human cancer-relat
298	4	36.4	10	22	AAG94768	Human complementar	371	4	36.4	10	24	ABH17278	Human cancer-relat
299	4	36.4	10	22	AAG94768	Human complementar	372	4	36.4	10	24	ABH17305	Human cancer-relat
300	4	36.4	10	22	AAG94768	Human complementar	373	4	36.4	10	24	ABH17322	Human cancer-relat
301	4	36.4	10	22	AAG94768	Human complementar	374	4	36.4	10	24	ABH17352	Human cancer-relat

376	1	45.4	10	24	ABR27509	Human cancer-relat	448	4	36.4	11	20	AAV0733	Peptide used to ma
377	2	45.4	10	24	ABR27521	Human cancer-relat	449	4	36.4	11	21	ABR26808	Phosphoryl group a
378	3	46.4	10	24	ABR27951	Human cancer-relat	450	4	36.4	11	21	AAV55530	Transactivator of
379	4	36.4	10	24	ABR28117	Human cancer-relat	451	4	36.4	11	21	ABR8559	NCAM Igl binding p
380	5	36.4	10	24	ABR28259	Human cancer-relat	452	4	36.4	11	21	AAV7919	Cyclin containing
381	6	36.4	10	24	ABR28418	Human cancer-relat	453	4	36.4	11	22	ABR34031	Human DNA derived
382	7	46.4	10	24	ABR28506	Human cancer-relat	454	4	36.4	11	22	ABP13794	HIV A02 super moti
383	8	46.4	10	24	ABR28506	Human cancer-relat	455	4	36.4	11	22	ABP13804	HIV A02 super moti
384	9	46.4	11	5	AAV2439	Biological syntheti	456	4	36.4	11	22	ABP1805	HIV B58 super moti
385	10	46.4	11	5	AAV2439	Biological syntheti	457	4	36.4	11	22	ABP18275	HIV B58 super moti
386	11	46.4	11	13	AAV2439	Sequence of peptid	458	4	36.4	11	22	ABP19373	HIV B62 super moti
387	12	46.4	11	13	AAV2439	Sequence of peptid	459	4	36.4	11	22	AAU06690	Thymosin beta fami
388	13	46.4	11	13	AAV2439	Amphiphilic peptid	460	4	36.4	11	22	AAU06690	Anti-fungal peptid
389	14	46.4	11	13	AAV2439	Amphiphilic peptid	461	4	36.4	11	23	ABP55000	Cyclin dependent p
390	15	46.4	11	13	AAV2439	Amphiphilic peptid	462	4	36.4	11	23	AAE24225	Human HIF-1 protei
391	16	46.4	11	14	AAV2439	Amphiphilic peptid	463	4	36.4	11	23	AAE23798	Peptide encoded by
392	17	46.4	11	14	AAV2439	Amphiphilic peptid	464	4	36.4	11	23	AAU97241	Thymosin-beta-10-1
393	18	46.4	11	14	AAV2439	Amphiphilic peptid	465	4	36.4	11	23	ABP50826	Hyaluronan (HA) b
394	19	46.4	11	14	AAV2439	Amphiphilic peptid	466	4	36.4	11	23	AAE22462	Biologically activ
395	20	46.4	11	14	AAV2439	C-terminal subst	467	4	36.4	11	23	AAE22462	Biologically activ
396	21	46.4	11	14	AAV2439	C-terminal subst	468	4	36.4	11	23	AAE22463	Biologically activ
397	22	46.4	11	14	AAV2439	C-terminal subst	469	4	36.4	11	23	AAE22464	Biologically activ
398	23	46.4	11	14	AAV2439	Amphiphilic peptid	470	4	36.4	11	23	AAE22479	Biologically activ
399	24	46.4	11	14	AAV2439	Amphiphilic peptid	471	4	36.4	11	23	AAE22480	Biologically activ
400	25	46.4	11	14	AAV2439	Amphiphilic peptid	472	4	36.4	11	23	AAE22482	Biologically activ
401	26	46.4	11	14	AAV2439	Biologically activ	473	4	36.4	11	23	AAE22493	Biologically activ
402	27	46.4	11	15	AAV2439	Ion channel formi	474	4	36.4	11	23	AAE22498	Biologically activ
403	28	46.4	11	15	AAV2439	Ion channel formi	475	4	36.4	11	23	AAU75185	Amino acid sequenc
404	29	46.4	11	15	AAV2439	Ion channel formi	476	4	36.4	11	23	ABR74482	DNA repair protein
405	30	46.4	11	15	AAV2439	Amphiphilic pepti	477	4	36.4	11	23	ABR74670	Transcription fact
406	31	46.4	11	15	AAV2439	Amphiphilic pepti	478	4	36.4	11	23	ABR74780	Nuclear protein nu
407	32	46.4	11	15	AAV2439	Amphiphilic pepti	479	4	36.4	11	23	ABR74833	Nuclear protein nu
408	33	46.4	11	15	AAV2439	Amphiphilic peptid	480	4	36.4	11	24	AAE54316	Human opsin recept
409	34	46.4	11	15	AAV2439	Amphiphilic peptid	481	4	36.4	11	24	ABJ36811	G protein coupled
410	35	46.4	11	15	AAV2439	Peptide which neut	482	4	36.4	11	24	ABJ36897	G protein coupled
411	36	46.4	11	15	AAV2439	Peptide which neut	483	4	36.4	11	24	ABR99794	Peptide used as ph
412	37	46.4	11	15	AAV2439	Peptide which neut	484	4	36.4	11	24	ABP56629	Cyclin dependent p
413	38	46.4	11	15	AAV2439	Cancer treating, a	485	4	36.4	11	24	ABR99485	Phosphoryl group a
414	39	46.4	11	15	AAV2439	Cancer treating, a	486	4	36.4	11	24	ABP55028	Cyclin dependent p
415	40	46.4	11	15	AAV2439	Cancer treating, a	487	4	36.4	12	10	AAV22222	Peptide stabilised
416	41	46.4	11	15	AAV2439	Peptide used to ma	488	4	36.4	12	13	AAV2396	Sequence of amphip
417	42	46.4	11	16	AAV2439	Ion-channel formi	489	4	36.4	12	14	AAV45116	Amphiphilic peptid
418	43	46.4	11	16	AAV2439	Ion-channel formi	490	4	36.4	12	14	AAV45114	Amphiphilic peptid
419	44	46.4	11	16	AAV2439	Ion-channel formi	491	4	36.4	12	14	AAV36372	Amphiphilic ion ch
420	45	46.4	11	16	AAV2439	Ion-channel formi	492	4	36.4	12	14	AAV33957	Amphiphilic peptid
421	46	46.4	11	16	AAV2439	Ion-channel formi	493	4	36.4	12	14	AAV31147	C-terminal subst
422	47	46.4	11	16	AAV2439	Ion-channel formi	494	4	36.4	12	14	AAV35365	Amphiphilic peptid
423	48	46.4	11	16	AAV2439	Ion-channel formi	495	4	36.4	12	14	AAV39075	Biologically activ
424	49	46.4	11	16	AAV2439	Ion-channel formi	496	4	36.4	12	14	AAV35971	Ion channel formi
425	50	46.4	11	16	AAV2439	Ion-channel formi	497	4	36.4	12	15	AAV50547	Amphiphilic peptid
426	51	46.4	11	16	AAV2439	Ion-channel formi	498	4	36.4	12	15	AAV50432	Amphiphilic peptid
427	52	46.4	11	17	AAV2439	Amphiphilic peptid	499	4	36.4	12	15	AAV56932	Peptide which neut
428	53	46.4	11	17	AAV2439	Anti-fungal peptid	500	4	36.4	12	15	AAV60702	N-terminal a.a. of
429	54	46.4	11	17	AAV2439	Magainin-derived a							
430	55	46.4	11	17	AAV2439	Magainin-derived a							
431	56	46.4	11	18	AAV44589	Anti-fungal peptid							
432	57	46.4	11	18	AAV44589	NCAM binding doma							
433	58	46.4	11	18	AAV43762	Bactericidal/pepti							
434	59	46.4	11	19	AAV5190	Fragment of human							
435	60	46.4	11	19	AAV5482	Amphiphilic peptid							
436	61	46.4	11	19	AAV5522	Amphiphilic peptid							
437	62	46.4	11	19	AAV5522	Amphiphilic peptid							
438	63	46.4	11	19	AAV5554	Amphiphilic peptid							
439	64	46.4	11	20	AAV10780	Multiply branched							
440	65	46.4	11	20	AAV10780	Peptide used to ma							
441	66	46.4	11	20	AAV10780	Peptide used to ma							
442	67	46.4	11	20	AAV10780	Peptide used to ma							
443	68	46.4	11	20	AAV10780	Peptide used to ma							
444	69	46.4	11	20	AAV10780	Peptide used to ma							
445	70	46.4	11	20	AAV10780	Peptide used to ma							
446	71	46.4	11	20	AAV10780	Peptide used to ma							
447	72	46.4	11	20	AAV10780	Peptide used to ma							

ALIGNMENTS

RESULT :
 ID: AAV85532 standard: peptide; 11 AA.
 XX
 AC AAV85532:
 XX
 DT 07-AUG-2000 (first entry)
 XX
 DE NCAM Igl binding peptide #4.
 XX
 KW NCAM: neural cell adhesion molecule; Igl: immunoglobulin domain 1;
 KW neurite outgrowth promoter; proliferation: nerve damage; sclerosis;
 KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
 KW treatment: prosthetic nerve guide; treatment: nervous system.

DE 11-SEP-2001 (first entry)
DE Arabidopsis thaliana peptide library #434
XX Plant peptide pesticides: peptide-bioinsecticide patent and drug research
XX Arabidopsis thaliana
XX W200142279-A2
XX 14-JUN-2001
XX 1-SEP-2001: 2000WO-G804773.
XX 13-DEC-1999: 99GB-0029471.
XX (PRT) PROTEAM LTD.
XX ROBERTS GW, Heat Jk;
XX WPI: 2001-983629/40.
DE A set of peptide ligands for antigenic drug research and development of
PT therapeutic agents comprise specific complementary peptides to proteins
PT encoded by genes of plant genomes
XX Encapsule 4; Page 92; 20pp; English.
XX The present invention relates to a set of peptide ligands consisting of
XX specific complementary peptides to proteins encoded by genes of plant
XX genomes. The present sequence is one such peptide from Arabidopsis
XX thaliana. The peptides of the present invention are useful in an assay to
XX identify a peptide, especially a peptide polypeptide or herbicide. The
XX peptides are also useful for drugs for antigenic drug research and
XX development.
XX Sequence: 10 AA:
DE Query Match: 45.9%; Score 5; DB 22; Length 10;
DE Best Local Similarity: 100.0%; Pred. No. 1e-02;
DE Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DE
DE 1 AASAV 5
DE III
DE 2 AASAV 6
DE
DE RESULT #
DE AA36029 Standard: Peptide, 10 AA
DE AA36029
DE 11-SEP-2001 (first entry)
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 1374
DE Saccharomyces cerevisiae complementary peptide: drug design
DE Saccharomyces cerevisiae
DE W0200442276-A1
DE 14-JUN-2001
DE 1-SEP-2001: 2000WO-G804773.
DE 13-DEC-1999: 99GB-0029471.
DE (PRT) PROTEAM LTD.
DE ROBERTS GW, Heat Jk;
DE

XX WPI: 2001-967867/38.
XX Identify complementary peptides by analysis of protein and
XX nucleotide sequence databases, useful in drug design -
XX Example 1; Page 247; 488pp; English.
XX The invention relates to the identification of complementary peptides
XX by analysis of protein and nucleotide sequence databases from either
XX eukaryotic genomes, excluding human and plants. The specific
XX complementary peptides interact with their relevant target proteins
XX encoded in the eukaryotic genome. The peptides may be used as reagents
XX and drugs for drug discovery and as lead ligands for drug design and
XX development. The present sequence is a complementary peptide from
XX Saccharomyces cerevisiae.
XX Sequence: 10 AA:
XX
XX Query Match: 45.9%; Score 5; DB 22; Length 10;
XX Best Local Similarity: 100.0%; Pred. No. 1e-02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 7 LKKKA 11
XX I L I I
XX 5 LKKKA 9
XX
XX RESULT 9
XX AAE02968
XX 10-AAE02968 Standard: Peptide, 10 AA
XX
XX AAE02968
XX 10-AUG-2001 (first entry)
XX Nucleic acid localisation: Sequence #14 of hepatitis virus delta antigen.
XX Peptide monomer, nuclear localisation sequence; NLS;
XX protein transduction domain; PTD; molecule transfer; delta antigen.
XX Hepatitis virus.
XX W020010647-A2
XX 11-MAY-2001
XX 24-NOV-2000: 2000WO-G811600.
XX 24-NOV-1999: 99EP-0126423.
XX (ROSE) ROSENHECKER J.
XX (RITT) RITTER W.
XX (RUDN) RUDOLPH C M.
XX (PLAN) PLANK C.
XX ROSENHECKER J, RITTER W, RUDOLPH CM, PLANK C;
XX WPI: 2001-967866/38.
XX Novel polypeptides comprising at least two monomers which comprise a
XX nuclear localisation sequence and protein transduction domain,
XX respectively useful for transferring nucleic acid molecules into
XX eukaryotic cells.
XX Disclosure: Page 4; 68pp; English.
XX The present invention relates to a polypeptide comprising at least two
XX peptide monomers, in which each peptide monomer comprises an amino acid
XX sequence which serves as a nuclear localisation sequence (NLS) or an
XX amino acid sequence which serves as protein transduction domain (PTD) in
XX eukaryotic cells. The polypeptide of the invention is used for
XX transferring a molecule into eukaryotic cells. The use of a polypeptide

CC comprising NLS or PTD drastically increases the efficiency of the transfer of attached molecules, preferably negatively charged molecules into the nucleus or cytoplasm of a eukaryotic cell. The present sequence is NLS of the hepatitis virus delta antigen.

XX Sequence 10 AA:

SQ Sequence 10 AA: 45.5% Score 5; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKKK 10
1111
Z KLKKK 5

RESULT 11

ABJ01182

ID AAE22481 standard; Peptide: 10 AA;

AC AAE22481;

DT 25 JUL 2002 (first entry)

DE Biologically active peptide #13

XX Biologically active peptide; toxicity: antimicrobial and tumor; methan sulphinate derivative; wound healing; burn therapy; sepsis; eye infection; cyst; spore; trophozoite; tumor; lung infection; cystic fibrosis; septic shock; bacterial endotoxin; cytostatic; antibacterial; immunosuppressive;

XX Unidentified.

CS Key location/qualifiers

XX Modified site 1

FI Modified site 10 /note "Linked to octanoyl group"

FI Modified site 10 /note "N-terminal amino"

XX US644845-B1

XX 19 FEB 2002

XX 15 JUL 1996; 98US-0115747

XX 18 JAN 1994; 94US-0144462

XX 01 JUN 1992; 92US-0591207

XX 05 JUN 1995; 95US-0465339

XX 15 JUL 1997; 97US-0891006

XX (MAGNA) MAGNANIN PHARM INC.

XX Karl CP, Williams TJ, Meliane M

XX WPI: 2002-350076/38

XX Reducing toxicity of unsubstituted or N-terminal substituted peptide having antimicrobial and antitumor activity useful in treating eye infections and tumor, by forming methan sulphinate derivative or analog of peptide

XX Example 1; Column 107-108; 78pp; English.

XX The invention relates to biologically active peptides with reduced toxicity and methods of preparing them. The peptides and proteins of the invention have improved antimicrobial and anti tumor activity while exhibiting reduced toxicity. The method of reducing toxicity involves the formation of related methan sulphinate derivatives or analogues. The method is useful for reducing the toxicity of an unsubstituted peptide or an N-terminal substituted peptide which is utilized in promoting or stimulating healing of a wound in a host. Treatment of external burns, prevention of treatment of eye infections

CC caused by bacteria or fungi, in killing cysts, spores, or trophozoites of infection-causing organisms, and may also be employed in the treatment of tumors, serious lung infections such as those occurring in cystic fibrosis, for treating sepsis, septic shock, and other related ailments, and for neutralising bacterial endotoxins. The present sequence is a biologically active peptide of the invention.

SQ Sequence 10 AA:

Query Match 45.5% Score 5; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKKK 10

1111

Z KLKKK 5

RESULT 11

ABJ01182

ID ABJ01182 standard; Peptide: 14 AA;

AC ARJ01182;

DT 13 SEP 2002 (first entry)

DE Human Ebf-1 transcriptional regulator peptide fragment.

XX Human; cancer; neoplastic disease; tumour specific marker; cytostatic; transcription factor.

XX Bore sapiens.

XX W0200240716-A2.

XX 23 MAY 2002

XX 14 NOV 2001; 2001WO-US43461

XX 16 NOV 2000; 2000US-249508P

XX (CEMI) CEMINES LLC

XX Pat K

XX WPI: 2002-57346/57

XX Determining the presence of neoplastic molecular markers, by identifying the presence of markers in host test sample using array of neoplastic molecular marker specific reagents and analyzing the array of the reagents

XX Example 3; Page 11; 41pp; English.

XX The present invention relates to a method for determining the presence of neoplastic molecular markers in a host, involving the use of neoplastic molecular marker specific reagents to detect such markers and analyzing the array of reagents, allowing the identification of the neoplastic disease present. This can be used to determine the best treatment for cancers, in particular neural cell, lung and prostate tumours. The present sequence is a peptide derived from a transcription factor capable of acting as a marker of the invention.

XX Sequence 14 AA:

Query Match 45.5% Score 5; DB 23; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKKK 10

1111

Z KLKKK 9

```

RESULTS 12
AA097612
ID AA097612 standard; peptide: 14 AA.
XX
XX
AC AA097612
XX
PT 24 JAN 2002 (first entry)
XX
XX Human peptide #887 encoded by a SNT gene transcript.
XX
XX Immunosuppressive; antimicrobial; gene therapy; vaccine; enzyme; cancer;
XX neuroprotective; angiopoietin; apoptosis related protein; cadherin;
XX amyloid protein; polypeptide; sepsis; related protein; cadherin;
XX cyclo; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytokine; kinase; cytokine; interferon;
XX interleukin; G-protein coupled receptor; kinase; kinase; inflammation;
XX multifactorial; disease; autoimmune disease; infection;
XX nervous system disease.
XX
XX Homo sapiens.
XX
XX W0200134744 A2.
XX
XX 05 JUL 2001.
XX
XX 28 DEC 2001; 2000W-US45498.
XX
XX 28 DEC 1999; 9905-0173419.
XX
XX 27 DEC 2000; 2000US-0173419.
XX
XX (CRA) CURAGEN CORP.
XX
XX Shinkels SA, Leuch M.
XX
XX WPI: 2001-016494/53.
XX
XX Polysaccharide nucleic acids oxidized (A), amylase, cyclase, polymerase,
XX oligonucleotides and histones, used for diagnosing and treating, e.g.,
XX cancer, autoimmune diseases and infectious.
XX
XX Disclosure: Page 3862; 414 pp; English.
XX
XX The present invention relates to oligonucleotides (see AA097612 AAL466)
XX encoding polymorphic variants of proteins related to amylases, amylase
XX proteins, endopeptidase, angiotensin, angiotensin related proteins, angiotensin,
XX polymerase, oligonucleotides, histone, kinase, cytokine, colony stimulating factor,
XX complement related proteins, G-protein coupled receptor, kinase,
XX interleukin, interleukin, G-protein coupled receptor, kinase,
XX the present sequence is a peptide encoded by the SNT gene, which may be used in the
XX the oligonucleotides and the peptides encoded by the SNT gene may be used in the
XX prevention, diagnosis and treatment of diseases associated with
XX inappropriate expression of the proteins listed above. Disorders that may
XX be prevented, diagnosed and/or treated include multi-factorial diseases
XX with a genetic component, such as autoimmune diseases (e.g., rheumatoid
XX arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
XX and Grave's disease), inflammatory cancer (e.g., cancers of the bladder,
XX brain, breast, colon and kidney, leukaemia), diseases of the nervous
XX system, and an infection of pathogenic organisms.
XX
XX Sequence 14 AA:
XX
XX Query Match 45.5% Score 50.1 E 2e-06 Match 14
XX Best Local Similarity 100.0% Pos: 1-14-21
XX Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
XX
XX 5 KKKK 10
XX
XX 10 KKKK 14
XX
XX
XX RESULTS 13
AA097613

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ID AA097613 standard; peptide: 14 AA.
XX
XX AA097613;
XX
XX 17 JUL 2001 (first entry)
XX
XX Human gene 1 encoded secreted protein fragment, SEQ ID NO:91.
XX
XX Human secreted protein; proliferative disorder; cancer; tumour;
XX foetal abnormality; developmental abnormality; haematopoietic disorder;
XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX inflammation; allergy; neurological disorder; Alzheimer's disease;
XX Parkinson's disease; cognitive disorder; schizophrenia; asthma;
XX skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
XX cardiovascular disorder; angioneurotic disorder; kidney disorder;
XX gastrointestinal disorder; pregnancy-related disorder; gene therapy;
XX endocrine disorder; infection; wound healing; vulnary;
XX cell culture; chemotaxis; food additive;
XX binding partner identification.
XX
XX Homo sapiens.
XX
XX W0200134759 A1.
XX
XX 17 MAY 2001.
XX
XX 05 NOV 2000; 2000W-US 00657.
XX
XX 12 NOV 1999; 9905-0164741.
XX
XX 30 JUN 2000; 2000US-025132.
XX
XX (HMA) HUMAN GENE SEI INC.
XX
XX Ruben SM, Katzsonis GA, Ni J, Soppet DR.
XX
XX WPI: 2001-016494/53.
XX
XX New nucleic acid molecules encoding human secreted proteins, used in
XX preventing, treating or ameliorating a disorder, e.g., Alzheimer's and
XX Parkinson's diseases and cancers.
XX
XX Disclosure: Page 7; 95pp; English.
XX
XX AA097613-AA097614 represent cDNAs corresponding to 6 human secreted
XX protein genes, and AA097613-AA097614 represent the proteins they encode.
XX AA097613-AA097614 represent human secreted protein fragments/variants.
XX The secreted proteins and their genes are useful for preventing,
XX treating or ameliorating medical conditions, e.g., by protein or gene
XX therapy. Pathological conditions can be diagnosed by determining the
XX amount of the new protein in a sample or by determining the presence of
XX mutations in the new genes. Specific uses are described for each of the
XX 6 genes, based on the tissues in which they are most highly expressed,
XX and include developing products for the diagnosis or treatment of
XX proliferative disorders, cancer, tumours, foetal and developmental
XX abnormalities, haematopoietic disorders, diseases of the immune system,
XX AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
XX allergies, neurological disorders (e.g., Alzheimer's disease,
XX Parkinson's disease), cognitive disorders, schizophrenia, asthma,
XX skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
XX cardiovascular disorders, angioneurotic disorders, kidney disorders,
XX gastrointestinal disorders, pregnancy-related disorders, endocrine
XX disorders, and infections. The proteins can also be used to aid wound
XX healing and epithelial cell proliferation, to prevent skin aging due to
XX sunburn, to maintain organs before transplantation, for supporting cell
XX culture of primary tissues, to regenerate tissues, to identify their
XX cognate ligands or binding partners, and in chemotaxis, and can be used
XX as a food additive or preservative to modify storage properties.
XX Antibodies specific for a protein of the invention can be used in
XX alleviating symptoms associated with the disorders mentioned above, and
XX in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
XX immunosorbent assay (ELISA). The present disclosure represents a human
XX secreted protein fragment referred to in the disclosure of the invention.
XX
XX

```

SQ Sequence 14 AA:
 Query Match 45.5% Score 5, DB 220, length 14;
 Best Local Similarity 100.0% (red. No. 1.4e-02);
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKSAV 5
 DE 4 AKSAV 8
 PS
 RESUME 14
 AAR76704
 DE AAR76704 standard, peptide: 15 AA.
 XX
 AC AAR76704
 XX
 DE 1 JAN 1996 (first entry)
 XX
 DE tetra- branched signal peptide, 1996;
 XX
 DE tetra- branched; membrane, signal, peptide, core, hormones;
 KW polylysine core; drug delivery.
 XX
 GS Synthetic.
 XX
 FH Key location/qualifiers
 FT Modified site 5
 FT /label branch site
 FT /note "omiga amino group in the signal peptide
 Lys(5) forms a peptide bond with the
 C-terminus of the tetrapeptide
 Arg-Lys-Lys-Lys"
 FT
 FT Modified site 6
 FT /label branch site
 FT /note "omiga amino group in the signal peptide
 Lys(6) forms a peptide bond with the
 C-terminus of the peptide
 Arg-Lys-Lys-Lys-Lys
 FT
 FT Modified site 7
 FT /label branch site
 FT /note "omiga amino group in the signal peptide
 Lys(7) is a peptide bond with the
 C-terminus of the tetrapeptide
 Arg-Lys-Lys-Lys-Lys-Lys"
 FT
 PS JPL024597 A.
 XX
 DE 10 MAR 1996;
 FT
 FT 05 MAR 1996; 94JP-0276912;
 FT
 FT 05 MAR 1996; 94JP-0276912;
 FT (FUGIT) 20011 1;
 XX
 DE 1995-212054/28;
 XX
 DE Membrane localizing signal peptide, used for the production
 of drugs into cells, particularly in the treatment of AIDS.
 XX
 PS LUSC0506, Fig 1: 4pp; Japanese
 XX
 DE AAR76704 is a polylysine core peptide of 15 amino acids (10 Arginine, 5
 Lysine-Lys-Lys-Lys-Ala-Ala-Lys-Lys-Lys-Lys-Lys-Lys-Lys-Lys-Lys-Lys)
 XX
 DE signal peptide which when conjugated to a protein, allows the
 XX
 DE passage through the cell membrane and allows drug delivery.
 XX
 PS Sequence 15 AA.
 XX

Query Match 45.5% Score 5, DB 16, length 15;
 Best Local Similarity 100.0% (red. No. 1.4e-02);
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 AKKA 11
 DE 4 AKKA 8
 PS
 RESUME 15
 AAW71415
 DE AAW71415 standard, peptide: 15 AA.
 XX
 AC AAW71415
 XX
 DE 27 DEC 1998 (first entry)
 XX
 DE peptide forming a helix structure.
 XX
 DE Helix structure; alpha-helical coiled coil; enzyme inhibitor;
 KW receptor agonist; antagonist.
 XX
 GS Synthetic.
 XX
 PN JPL024597 A.
 XX
 DE 14 SEP 1998;
 FT
 FT 05 MAR 1997; 97JP-0047504;
 XX
 DE 03 MAR 1997; 97JP-0047504;
 XX
 PA (SEH-) SEIBUTSU HONSHI KODAKU KENKYUSHO KK.
 XX
 DE WPI, 1998-551189/47.
 XX
 DE peptide having alpha helical coiled structure - useful as enzyme
 FT inhibitor etc.
 FT
 PS Claim 4, Page 2; 1999; Japanese
 XX
 DE AAW71415-20 represent peptides that form helix structures. They are part
 of a peptide of the formula A-H-C, where parts A (see AAW71415-15) and
 C form helix structures, and H is a linker portion linking A and C with
 covalent bonds. The whole peptide A-H-C (see AAW71421-5) for specific
 examples) has an alpha helical coiled coil structure. The peptide
 A-H-C can be used as an enzyme inhibitor, a receptor agonist and a
 receptor antagonist.
 XX
 PS Sequence 15 AA:
 Query Match 45.5% Score 5, DB 19, length 15;
 Best Local Similarity 100.0% (red. No. 1.4e-02);
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 KKKK 10
 DE 4 KKKK 8
 PS
 RESUME 15
 AAW80544
 DE AAW80544 standard, peptide: 15 AA.
 XX
 AC AAW80544;
 XX
 DE 06 DEC 1998 (first entry)
 XX
 DE beta-sheet structure forming peptide fragment.
 XX
 DE beta-sheet structure forming peptide fragment.
 XX
 DE beta-sheet structure forming peptide fragment.
 XX
 PS Sequence 15 AA.
 XX

XX Claim 10; Page 7; spp: English.
 XX Attached to the last AA (Ala) is a water soluble or copolymer of
 XX diethylacrylamide and N-ethyl-1,6-diaminohexane substituted with
 XX bisallylamine. This peptide is part of a polymer
 XX addition product (1) which comprises a non-pharmaceutical backbone of
 XX macrom. at least 5,000 (preferably 500,000) to which this
 XX peptide pendant is chemically bonded. (1) are used as highly
 XX efficient adsorbents for bile pigment and bile acid (cholesterol
 XX acid), and are particularly useful for the treatment of
 XX hyperbilirubinemia by adsorption or elimination from blood plasma and
 XX gastro intestinal tract. (1) can also be used to reduce
 XX hypercholesterolemia. See also AAR6154; 6; AAR6148-99.
 XX (Updated on 25-MAR-2003 to correct PA field.)
 XX (Updated on 25-MAR-2003 to correct P1 field.)
 XX Sequence: B AA:
 SQ

Query Match: 56.4%; Score 4; Db 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKA 11
 DB 111
 1 KKA 6

RESULT 19
 AAR45126
 10 AAR45126 standard; peptide: B AA.
 XX
 AC AAR45126:
 XX
 XX 25-MAR-2003 (updated)
 DI 25-MAR-1993 (first entry)
 XX
 XX Amphipathic peptide for N-terminal, lipophilic substituted, Lysine
 XX Ion channel: mutagenic; Polar: X; Non-polar: 100%; 100%; 100%; 100%;
 KW amphipathic hydrophobic; hydrophobic; 100%; 100%; 100%; 100%;
 KW inhibition target cell; virus; virally infected cell;
 KW antimicrobial; antiviral; antitumor; anti-infective;
 KW spermicide; wound healing; burn; infection;
 XX
 CS Synthesis:
 XX
 XX W 942415g Ala
 FI Modified site: /Note: "May be acetylated"
 FI Modified site: /Note: "May be acetylated"
 FI
 XX 27 MAY 1993; 93WO-US051942.
 XX
 XX 01 JUN 1992; 92US-0891201.
 XX
 XX (MAGA) MAGAININ PHARM INC.
 PA
 FI Kari U.
 XX
 XX WPI: 1993-405419/50.
 XX
 XX Peptide(s) or proteins with an N-terminal, lipophilic subst.,
 FI used for inhibiting growth of target cell; virus of
 FI virally-infected cell
 XX
 XX Disclosure; Page 97-103; 113pp; English.
 XX
 XX A novel, compn. for inhibiting growth of a target cell; virus of
 XX virally infected cell comprises a peptide of formula 1 N(N) X (1).
 XX X is a biologically active amphipathic ion channel-forming peptide
 XX or protein; pref. a magainin peptide; a beta peptide; a XPP
 XX peptide; a CFP peptide; a decapeptide of a sarcophagin
 XX N is the nitrogen of the N-terminal amino group.

XX T is a lipophilic moiety; pref. R CO, where R is a 2-16C
 XX hydrocarbon (alkyl or aromatic or alkylaromatic).
 XX T is pref. an octanoyl group.
 XX W is T or hydroxyl.
 XX Amphipathic peptides as examples of X are given in AAR45115-134.
 XX The N-terminal subst. peptides and proteins have increased
 XX biological activity as compared with unsubst. peptides or proteins
 XX or peptides subst. at the N terminal with an acetyl gp.
 XX They can be used as antimicrobial agents, antiviral agents,
 XX antitumor agents, antiparasitic agents or spermicides and
 XX can also exhibit other bioactive functions. They can also be
 XX used in promoting or stimulating wound healing, for the treatment
 XX of external burns and to treat and/or prevent skin and burn
 XX infections or eye infections.
 XX (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence: B AA:
 SQ

Query Match: 56.4%; Score 4; Db 14; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKK 9
 DB 111
 4 KKK 7

RESULT 20
 AAR33569
 10 AAR33569 standard; peptide: B AA.
 XX
 AC AAR33569:
 XX
 XX 25-MAR-2003 (updated)
 DI 25-MAR-1993 (first entry)
 XX
 XX Amphipathic peptide (b).
 XX
 KW Hydrophobic; hydrophilic; neutral; (b); ionophore; channel-forming;
 KW human virus; antimicrobial; antiviral; antibacterial; antitumor;
 KW antiparasitic; spermicide; preservative; sterilant; disinfectant;
 KW wound healing; burn; infection; eye; cysts; spores; trophozoites;
 KW plants; contamination;
 XX
 CS Synthesis:
 XX
 XX Key: Local/Qty/Qualifiers
 FI Modified site: /Note: "May be acetylated"
 FI Modified site: /Note: "May be acetylated"
 FI
 XX W09125802-A1
 XX
 XX 01 APR 1994.
 PD
 XX 04-SEP-1992; 92WO-US07622.
 XX
 XX 13-SEP-1991; 91US-0760054.
 PR 20-APR-1992; 92US-0870960.
 XX
 XX (MAGA) MAGAININ PHARM INC.
 PA
 XX Kari U., Mary W., Williams J.
 FI
 XX WPI: 1993-117245/14.
 XX
 XX New biologically active amphipathic peptide cpds. having ion
 XX channel-forming properties used for inhibiting growth of target
 XX cells, virus or viral-infected cells
 XX
 XX Claim 27; Page 41; 45pp; English.
 XX

CC useful against bacteria associated with dental implant infections and
 CC the peptides can stimulate the healing of wounds to the oral cavity.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA:
 Query Match 36.4% Score 4; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
 1 1 1
 DB 4 KLKK 7

RESULT 24
 AAR50559 standard; peptide: 8 AA.

XX AC AAR50598;
 XX 25 MAR 2003 (updated)
 XX DT 19-DEC-1994 (first entry)
 XX XX Ion channel forming peptide
 XX XX Ion channel forming peptide; 4 month skin disease malignancy;
 XX melanoma; carcinoma; basal cell squamous cell; madainin; PGLa;
 XX CPP peptides; sarcotoxin; melittin; apidaecin; defensin;
 XX major basic protein; bactericidal permeability increasing protein;
 XX porfobin.

XX CS Synthetic.
 XX PN W09405313-A1.
 XX DT 01-JUN-1994.

XX PF 23-DEC-1994; 94WO-0511885.
 XX PR 03-SEP-1992; 92US-0984957.
 XX XX (MAGNIN) MAGAININ PHARM INC.

XX DT Jacob LS, Maloy WL;
 XX WPI: 1994-199965/24.

XX PT Treating skin cancer with ion channel (base peptide(s)) e.g.
 XX madainin, melittin etc., specifically for treating melanoma

XX PS Disclosure: Page 119; 146pp; English.

XX CC The peptide is used to treat dermatological malignancies. It
 CC may be used to treat especially melanoma but also basal cell and
 CC squamous cell carcinomas. It can be used together with an ion which
 CC also inhibits/prevents growth of the target cells. Peptides used for
 CC such therapy/prevents growth of the target cells. Peptides used for
 CC sarcotoxins, melittin, apidaecins, defensins, major basic protein of
 CC eosinophils; bactericidal permeability increasing protein and porfobin.
 CC See also AAR505976-Q5597.

XX CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA:

Query Match 36.4% Score 4; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
 1 1 1
 DB 4 KLKK 7

RESULT 24
 AAR50559 standard; peptide: 8 AA.

XX AC AAR50559;
 XX 25 MAR 2003 (updated)
 XX DT 18-OCT-1994 (first entry)
 XX XX Amphiphilic peptide #109.

XX XX Amphiphilic ion forming quaternary malignancy; madainin; PGLa;
 XX XPF; CPP; cerropin; sarcotoxin; melittin; apidaecin; defensin;
 XX major basic protein; eosinophils; uterine; cervical; cancer;
 XX bacterial permeability increasing protein; ovarian; stage IC.

XX CS Synthetic.

XX PN W09405313-A1.

XX DT 17-MAR-1994

XX PF 16-AUG-1993; 94WO-0507798.

XX PR 31 AUG-1992; 92US-0937452

XX XX (MAGNIN) MAGAININ PHARM INC.

XX DT Baker MA, Jacob LS, Maloy WL;

XX WPI: 1994-100451/12.

XX PT Treating quaternary malignancies with amphiphilic peptide(s) -
 XX which form ion channels, e.g. madainin or PGLa peptide(s),
 XX partic. for treating ovarian, uterine or cervical cancers.

XX PS Disclosure: Page 114; 130pp; English.

XX CC The sequences given in AAR50452-568 represent amphiphilic ion forming
 CC peptides which may be used to treat quaternary malignancy.

XX CC These peptides are based on magainin, PGLa, XPF or CPP, a cerropin, a
 CC sarcotoxin, melittin, an apidaecin, a defensin, major basic protein of
 CC eosinophils or a bacterial permeability increasing protein. These
 CC peptides are esp. used to treat ovarian, esp. stage IC, uterine or
 CC cervical cancers.

XX CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA:

Query Match 36.4% Score 4; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
 1 1 1 1 1
 DB 4 KLKK 7

RESULT 25
 AAR50444 standard; peptide: 8 AA.

XX AC AAR50444;

XX 25-MAR-2003 (updated)

XX DT 17-OCT-1994 (first entry)

XX XX Amphiphilic peptide #109.

XX XX Amphiphilic peptide; aprotic organic solvent; alcohol; antitumour;
 XX antimicrobial; antifungal; antiparasitic; anticancer;
 XX antiviral; human; animal; plant; ion-channel; forming peptide.

used in combination with one or more protease inhibitors
 on other alphaherpesviruses forming peptides
 or proteins, they are effective in the treatment of cancer
 growths. In particular, they are effective in the treatment of melanoma
 they may be useful in inhibiting, preventing, and/or destroying
 potential "tumor" malignant cells capable of metastasizing
 sites.
 (Updated on 25-MAR-2003 to correct EN field.)

Query Match: 36.4%, Score 41, DB 10, Length 8;
 Best Local Similarity: 100.0%, Pred. No. 9, 3e+05;
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query: 6 KKKK
 ID: 4 KKKK

Result 28
 AAK90255 Standard; peptide: 8 AA.

AAK90255
 10 JUN 1996 (first entry)
 Ion channel forming peptide #107 with cationic N-terminal group.
 Ion channel forming peptides, comprising a N-terminal cationic
 mediator; inhibition; cell death; viral replication; membrane
 membrane permeability; antimicrobial; anti-bacterial; anti-viral;
 anti-cancer; anti-viral; spectrophotometry; tumor; and parasitic.
 Synthetic.

Key: location/sequence
 Modified site: /note: "N-terminal cationic group is modified
 at site 10 by the peptide sequence
 octanoyl"

W0957570-AL
 20 APR 1995
 18 JAN 1995 95W035037.4
 18 JAN 1994 94US018442.2
 (MAGNIN PHARM INC)
 Kar, JP, McLane M, Williams TJ
 W01 1995 253826/34
 Ion channel forming amphipathic peptide with a cationic
 lipophilic lipophilic group as an antiviral and bactericidal
 antiparasitic or antitumor agent

Claim 28; Page 107; 139pp; English

The present peptide is a specific cationic amphipathic ion channel
 specific formula for ion channel forming peptide (independent)
 These receptors are known to have a cationic lipidic lipidic
 antitumor activity against microorganisms including gram negative
 and gram positive bacteria, fungi, viruses, protozoa and parasites
 N-terminal modification (proline, amino acids, hydrophobicity) to produce
 an ion channel forming peptide having a lipophilic N-terminus
 increases the biological activity of the peptides against target cells,
 viruses and virally-infected cells compared to peptides substituted with
 an acetyl group at the N-terminus. Compounds comprising the peptides

with lipophilic modifications are claimed for inhibiting growth of a
 target cell, virus or virally infected cell.

Query Match: 36.4%, Score 41, DB 10, Length 8;
 Best Local Similarity: 100.0%, Pred. No. 9, 3e+05;
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query: 6 KKKK
 ID: 4 KKKK

Result 29
 AAK47993 Standard; peptide: 8 AA.

AAK47993
 20 APR 1998 (first entry)
 Bactericidal/permeability increasing peptide XMP-412.
 Bactericidal/permeability increasing peptide; BPI; fusion protein;
 bacterial infection; fungal infection; endotoxin; heparin;
 angiogenesis; angiogenic; angiogenic; angiogenic; angiogenic;
 Home synthesis;
 Synthetic.

W0974509 AL
 20-SEP-1997
 18-MAR-1997 97W03053287.1
 22-MAR-1996 96US052180.1
 (X-MA) X-MA 1000
 Section MD
 W01 1997 48 215/14
 Recombinant production of bactericidal/permeability increasing
 protein by expression as a fusion protein in microbial host cells,
 then cleaving the BPI peptide from the carrier
 Claim for page 142; 140pp; English

A new recombinant DNA vector construct has been developed which encodes
 a fusion protein and is suitable for introduction into a bacterial host.
 The vector comprises: (a) DNA encoding at least one cationic
 bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
 carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
 located between (a) and (b). The present sequence represents a
 specifically claimed BPI peptide. The peptides have many uses including
 the treatment of bacterial and fungal infections. BPI peptides also
 bind to endotoxins and heparin, neutralising their effects. The
 peptides have further been shown to inhibit angiogenesis (partly due to
 heparin binding activity). The fusion proteins have been found to be
 expressed in large amounts without significant proteolysis, and in some
 cases are actually secreted from the host cells. This allows the
 indirect production of antimicrobial BPI peptides in microbial hosts.

Query Match: 36.4%, Score 41, DB 18, Length 8;
 Best Local Similarity: 100.0%, Pred. No. 9, 3e+05;
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query: 6 KKKK
 ID: 4 KKKK

XX (MAGALIN) MAGALIN PHARM INC.
 XX P: Magoy WLL
 XX WPI: 1998 456190/39.
 XX Magalidin peptide analogues useful as immunomodulators of an antigen
 XX agents, etc.
 XX Disclosure: Column 20; 25pp; English.
 XX The invention relates to analogues of a mutation of or D- or L- form
 XX analogues, deletion analogues of related peptides. It also relates
 XX to basic polypeptides having at least 16 amino acids, including at least
 XX 8 hydrophobic amino acids and at least a hydrophilic amino acids. The
 XX peptides may be used as anticancer agents, antiviral agents,
 XX antibiotics, antitumor agents, antiparasitic agents, spermicides,
 XX preservatives or sterilants, or agents for promoting wound healing. The
 XX present sequence represents a specific example of a peptide disclosed in
 XX the specification.
 XX Sequence: 8 AA:
 Query Match: 36.4%; Score 4; DB 19; Length 8;
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 KKKK 9
 DB 1 1 1
 3 4 KKKK 7

RESULTS 1
 IC AAW61744 standard; peptide: 8 AA.
 AC AAW61744;
 DI 09 NOV 1998 (first entry)
 DE Peptide mimetic of cytokine receptor gamma chain 11.
 KW Peptide mimetic gamma-chain; cytokine receptor; signal transduction;
 KW autoimmune disease; graft vs. host disease; transplant rejection;
 KW graft rejection; interleukin; immunosuppressants; T cells; B cells.
 XS Synthetic.
 PN WO834141-A1.
 PZ 13 AUG 1998.
 XX 06 FEB 1998; 95WO-052335.
 XX 07 FEB 1997; 97US-0036941.
 XX (DRJER) UNIV JEFFERSON THOMAS.
 XX Kornfeld W, Townsend RM;
 WPI: 1998 446544/38.
 XX New peptide(s) mimicking a loop in the gamma chain of cytokine
 XX receptors inhibit signal transduction through these receptors,
 XX useful as immunosuppressants for treatment or prevention of
 XX leukaemia, autoimmune disease, graft rejection
 XX Claim 2; page 28; 54pp; English.
 XX The peptide mimetics AAW61734-W61736 and AAW75001-W77014 mimic a loop on
 XX the gamma-chain of cytokine receptors, and interact with a cytokine or
 XX a gamma-chain partner receptor chain of a heterodimeric cytokine

CC receptor. They inhibit signal transduction mediated by cytokine receptor
 CC binding (of cytokines that bind to receptors with a gamma-chain). They
 CC are used to inhibit or suppress cytokine-mediated immune responses.
 CC growth, proliferation, function and activity of cells. Particularly they
 CC are used for treatment or prevention of lymphoma, leukaemia, allergy
 CC (e.g. asthma), autoimmune disease (e.g. rheumatoid arthritis, lupus,
 CC multiple sclerosis or myasthenia gravis), graft vs. host disease and
 CC transplant or graft rejection. They inhibit function of interleukin
 CC (IL) 2, 4, 7, 9, 13 and 15 (the receptors for which include a
 CC common gamma chain), so function as immunosuppressants by reducing
 CC proliferation of T and B cells.
 XX Sequence: 8 AA:
 Query Match: 36.4%; Score 4; DB 19; Length 8;
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGSA 4
 DB 1 1 1
 3 AGSA 6

RESULTS 44
 AAW56407
 IC AAW56407 standard; peptide: 8 AA.
 AC AAW56407;
 DI 05 AUG 1998 (first entry)
 DE Nuclear localisation signal (NLS).
 XX Signal peptide; nuclear localisation signal; NLS;
 KW immunosuppressive activity; inhibition; nuclear translocation; inhibitor;
 KW nuclear translocation; treatment; immune disorder; autoimmune disease;
 KW hypersensitivity; sepsis; prevention; septic shock; antiviral agent;
 KW tumour growth; suppressor.
 XX Unidentified.
 OS WC9811907-A.
 PN 26 MAR 1998
 PD 15 SEP 1997; 97WO-0516217.
 XX 12 SEP 1997; 97US-0928958.
 XX 20 SEP 1996; 96US-0029378.
 XX (BRIM) BRISTOL-MYERS Squibb Co.
 XX Blake J, Cleveland JS, Baffa OK, Nadler SG;
 WPI: 1998-237028/19.
 XX Nuclear translocation inhibitor polypeptides comprising signal
 XX sequence for delivery through the cytoplasmic membrane and at least
 XX 2 nuclear localisation sequences
 XX Claim 10; Page 44; 69pp; English.
 XX Peptides AAW56400-13 represent nuclear localisation signals (NLSs). The
 XX sequence is used to construct the nuclear translocation inhibitor
 XX polypeptide of the invention. Nuclear translocation inhibitor
 XX polypeptides comprise a signal sequence peptide capable of delivering
 XX the polypeptide through the cytoplasmic membrane into a cell, and at
 XX least 2 NLSs. The polypeptides can be used to inhibit nuclear
 XX translocation of a cellular protein. In addition, since the nuclear
 XX translocation of certain cellular peptides is required for the host
 XX organism to mount an immune response, the polypeptide inhibitors are
 XX useful as immunosuppression agents. The polypeptides can therefore be
 XX used for the treatment of immune disorders including autoimmune

CC diseases. The polypeptides can also be used for treating physical
 CC symptoms manifested by responses to antigens which can initiate a state
 CC of hypersensitivity, for the treatment of sepsis and in the prevention
 CC of septic shock, antiviral agents, tumor growth suppressors, and for
 CC transcriptionally modulating the expression of cellular genes.

XX Sequence: # AA;

Query Match: 36.4%; Score 4; DB 20; Length 8;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKKK 9

DB 2 LKKK 6

RESULT 46

AAAY09619

ID AAAY09619 standard; Peptide: # AA

XX AAAY09615;

XX 07-MAY-1999 (first entry)

XX Antifungal peptide XMP-408

XX Antifungal; BPI; bactericidal/permeability increasing protein;

XX Candida infection;

XX Synthetic;

XX US5658974-A;

XX 12-JAN-1999;

XX 21-MAR-1996; 96US-0621259;

XX 21-MAR-1996; 96US-0621259;

XX 20-JUL-1995; 95US-0504841;

XX (XOMA) XOMA CORP;

XX Faden MS; Lum E; Little RG;

XX WPI; 1999-119956/10;

XX Antifungal peptides comprising part of bactericidal or

XX permeability-increasing protein sequence or related sequence

XX Claim 2; Columns 221-222; 134pp; English;

XX New peptides are provided which are based on Domain III (amino acids

XX 142-169) of human bactericidal/permeability-increasing protein (BPI).

XX The peptides all have a C-terminal amide. More particularly, the claims

XX relate to: (1) a peptide that has an amino acid sequence of human BPI

XX from position 148 to position 161 (KSKVGLQLQFHKK) and variants of the

XX sequence having antifungal activity; and (2) an antifungal peptide

XX having 6-14 amino acids comprising (a) a core sequence selected from

XX LQL, LQIF, WLQL, LIQLF and WLQIF and (b) one or more cationic amino

XX acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric

XX acid) at the N and/or C terminus of the core sequence. The new peptides

XX are used for killing or inhibiting replication of fungi in vitro; and

XX for treating fungal infections in vivo, in particular infections of

XX Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.

XX krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide

XX can be administered topically, intravenously, orally or as an aerosol,

XX optionally together with a non-peptide antifungal agent.

XX Sequence: # AA;

Query Match: 36.4%; Score 4; DB 20; Length 8;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKKK 10

DB 1 LKKK 4

RESULT 47

AAAY0744

ID AAAY0744 standard; Peptide: # AA

XX AAAY0744;

XX 07-MAY-1999 (first entry)

XX Antifungal peptide XMP-408

XX Antifungal; BPI; bactericidal/permeability increasing protein;

XX Candida infection;

XX Synthetic;

XX US5658974-A;

XX 12-JAN-1999;

XX 21-MAR-1996; 96US-0621259;

XX 20-JUL-1995; 95US-0504841;

XX (XOMA) XOMA CORP;

XX Faden MS; Lum E; Little RG;

XX WPI; 1999-119956/10;

XX Antifungal peptides comprising part of bactericidal or

XX permeability-increasing protein sequence or related sequence

XX Claim 2; Columns 221-222; 134pp; English;

XX New peptides are provided which are based on Domain III (amino acids

XX 142-169) of human bactericidal/permeability-increasing protein (BPI).

XX The peptides all have a C-terminal amide. More particularly, the claims

XX relate to: (1) a peptide that has an amino acid sequence of human BPI

XX from position 148 to position 161 (KSKVGLQLQFHKK) and variants of the

XX sequence having antifungal activity; and (2) an antifungal peptide

XX having 6-14 amino acids comprising (a) a core sequence selected from

XX LQL, LQIF, WLQL, LIQLF and WLQIF and (b) one or more cationic amino

XX acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric

XX acid) at the N and/or C terminus of the core sequence. The new peptides

XX are used for killing or inhibiting replication of fungi in vitro; and

XX for treating fungal infections in vivo, in particular infections of

XX Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.

XX krusei, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide

XX can be administered topically, intravenously, orally or as an aerosol,

XX optionally together with a non-peptide antifungal agent.

XX Sequence: # AA;

XX AAY07461
XX 11-MAY 1999 (first entry)
XX Peptide used to make biologically active peptides
XX Septic shock; pseudomonas aeruginosa, typhoid fever, shis;
XX antimicrobial; antiviral; antibacterial; antitumor; antiparasitic;
XX antiparasitic; spectinomide; preservative; sterilant; disinfectant;
XX wound healing; burn; skin infection; eye infection; solid tumor;
XX leukemia; non-small cell lung cancer; adenocarcinoma; flat infection;
XX peritoneal disease; plaque; quaternary cationic streptococcus; actin;
XX Synthesized
XX W09903400 A2
XX 26 JAN 1999
XX 15 JUL 1998 98WO-US14612
XX 15 JUL 1997 97US-0893026
XX (MAGNA) MAGALIN PHARM INC.
XX Karl UP, McEane M, Williams TJ
XX W1: 1999 13:859/11
XX Treatment of septic shock with a modification of recombinant tetraol
XX peptide - or its methane sulphonic derivative of reduced toxicity,
XX also generally useful as antimicrobial and antitumor agents
XX Example 1: Page 184; 202pp; English
XX AAY0640-795 represent peptides used in the production of biologically
XX active peptides with reduced toxicity, the biologically active peptides
XX are used to treat sepsis or septic shock, and comprise the formula:
XX I-(NW)-X, where X = biologically active amphiphilic ion channel
XX forming peptide or protein; I = lipophilic group; and W = hydrogen or 1,
XX the peptides are particularly used to treat infections by pseudomonas
XX aeruginosa in patients with cystic fibrosis, for more generally as
XX antimicrobial, antiviral, antibacterial, antifungal, antitumor or
XX antiparasitic agents, and also as storage stabilizers as preservatives,
XX sterilants, and disinfectants in human and veterinary medicine, they
XX can be used to stimulate wound healing, treat burns and/or skin and
XX burn infections, eye infections, solid tumors, and leukodermas
XX (particularly non-small cell lung cancer and adenocarcinoma), including
XX those resistant to other antitumor agents, and also for treatment of
XX infections in plants, and, when formulated in a biologically tolerable
XX for treating or preventing periodontal diseases, plaque, gingivitis and/or
XX caries (specifically by action on streptococcus strains)
XX Sequence: 8 AA:
XX Query Match: 36.4%; Score 4; DB 21; Length 8;
XX Best Local Similarity: 100.0%; Pred. No. 9.4e-05;
XX Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 6 KKKK 9
XX ID 1111
XX DB 2 KKKK 5
XX RESULT 49
XX AAY66377
XX ID AAY66377 standard; peptide: 8 AA.
XX AC AAY66377;
XX 22-FEB 2000 (first entry)
XX B2A-B8 binding HIV 1 Pol peptide #179.
XX HIV-1; MHC; major histocompatibility complex; Class I; HLA;
XX human leukocyte antigen; allele; binding; conserved; genome;
XX peptide; targeting; toxic; drug; antibody; antigen; antiviral;
XX molecular conjugate therapeutic; diagnosis; treatment; pathogen;
XX localization; quantification; detection; infection; drug resistance;
XX immune response.
XX Human immunodeficiency virus type 1.
XX

DE Human or rat androgen receptor NLS sequence.
XX Cellular protein; nuclear translocation; nuclear localization signal;
XX immunosuppressant; immune response; viral infection; immune disorder;
XX rheumatoid arthritis; multiple sclerosis; juvenile-onset diabetes; NLS;
XX systemic lupus erythematosus; SLE; asthma; sepsis; tumor growth; human;
XX fibroblast growth factor; androgen receptor.
XX Homo sapiens.
XX Rattus sp.
XX W09957.0 A1
XX 11 NOV 1999
XX 25-APR 1999 99WO-US08984
XX 04 MAY 1998 98US-0072429
XX (BRM) BRISTOL-MYERS SQUIBB CO.
XX Nadler SG
XX WPI: 2000-062141/05
XX Novel composition comprising a nuclear localization signal and an
XX inhibitor of nuclear translocation, useful for preventing transplanted
XX organ or tissue rejection.
XX Claim 8; Page 42; 68pp; English.
XX The invention provides a composition comprising an isolated polypeptide
XX (1) (polypeptide inhibitor of a cellular protein nuclear translocation)
XX which comprises a signal sequence peptide capable of delivering (1)
XX through a cytoplasmic membrane into the cell; and a nuclear localization
XX signal sequence (NLS) present along with an immunosuppressant, (2) or
XX its derivatives provide useful tools for introducing an exogenous
XX polypeptide comprising an NLS into an intact cell to inhibit nuclear
XX translocation of a cellular protein, for studying the role of nuclear
XX translocation in the regulation of cellular processes. See AAY55812 for
XX detailed uses of (1) and compositions containing (1). The present
XX sequence represents a NLS sequence from human or rat androgen receptor.
XX Sequence: 6 AA:
XX Query Match: 36.4%; Score 4; DB 21; Length 8;
XX Best Local Similarity: 100.0%; Pred. No. 9.4e-05;
XX Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 6 KKKK 9
XX ID 1111
XX DB 2 KKKK 5
XX RESULT 49
XX AAY66377
XX ID AAY66377 standard; peptide: 8 AA.
XX AC AAY66377;
XX 22-FEB 2000 (first entry)
XX B2A-B8 binding HIV 1 Pol peptide #179.
XX HIV-1; MHC; major histocompatibility complex; Class I; HLA;
XX human leukocyte antigen; allele; binding; conserved; genome;
XX peptide; targeting; toxic; drug; antibody; antigen; antiviral;
XX molecular conjugate therapeutic; diagnosis; treatment; pathogen;
XX localization; quantification; detection; infection; drug resistance;
XX immune response.
XX Human immunodeficiency virus type 1.
XX

KW molecular conjugate therapeutic, diagnostic, treatment, pathogen
 KW neutralisation, quantification, detection, infection, drug resistance,
 KW immune response
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810 A1.
 XX
 PP 07-03-1999.
 XX
 PP 01 MAR 1999; 95W0 0507111.
 XX
 PP 01 MAR 1998; 96S-0052580.
 XX
 PA (USP) UNIV BOSTON.
 XX
 PI ZARISA C, BORZUTSKY J, GAIKATA S, VACCARIO G, WONG Z, ZHANG C.
 XX
 PP WO/ 2000 038361/03.
 XX
 PP Novel methods for designing polypeptide therapeutics which are
 used for diagnosis, imaging and treatment against pathogens.
 XX
 PP Example 5, Page 46; 62pp; English.
 XX
 CC AAV6199-96413 are peptides derived from conserved portions of the
 CC HIV-1 genome which bind to different HLA classes (I, II, and III).
 CC These peptides are used to
 CC construct targeting antigens comprising one or more peptides bound to
 CC the corresponding MHC Class I molecule, which can be used to raise
 CC antibodies. The antibody may then be used as a targeting vehicle to
 CC deliver a potentially toxic drug to its target site of action, rather
 CC than administering it systemically, which may result in adverse side
 CC effects. The invention relates to improved methods for the design of
 CC molecular conjugate therapeutics for the diagnosis and treatment of
 CC infections caused by pathogens with a high mutation rate (such as
 CC HIV-1). This method involves identifying conserved peptide-encoding
 CC regions among the genomes of multiple variants of a pathogen, identifying
 CC the Class I MHC molecules which occur with greatest frequency in a
 CC population of interest (e.g., human sub-populations), and determining
 CC which of the peptides bind to the Class I MHC molecules. The MHC-binding
 CC peptides and the corresponding Class I MHC molecules are selected and
 CC used to construct targeting antigens, which are in turn used to produce
 CC targeted antibodies. The methods may be used in two ways:
 CC identification and in situ detection of specific peptide-MHC class I
 CC complexes and also to detect and treat viral infection by the methods of
 CC the invention. Antigens against the peptide-MHC complex are resistant to
 CC drugs and to the immune response, as well as being in a situation for
 CC targeting toxic compounds to destroy cells and suppress the virus and
 CC accessible to T cells. In addition, the peptide-MHC complexes
 CC whereas current therapies only affect viral replication.

XX Query Match: 36.4%; Score 4; DR 22; Length 8;
 XX Best Local Similarity: 100.0%; Pred. No. 9, 3e-05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 7 VKKK 10
 XX 1 VKKK 4
 XX
 XX RESULT 4:
 XX ABP13128
 XX ID ABP13128 standard; Peptide: 8 AA;
 XX AC ABP13143;
 XX U: 15 JUL 2002 (first entry)
 XX
 XX HIV A02 super motif pol peptide #58.
 XX
 XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
 XX vpr; tat; cytochrome T lymphocyte; C1; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.

KW HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
 KW vpr; tat; cytochrome T lymphocyte; C1; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810 A1.
 XX
 PP 12-APR-2001.
 XX
 PP 05-03-2000; 2000W 052766.
 XX
 PP 05-03-1999; 96S 0412869.
 XX
 PA (EP) EP1006NE INC.
 XX
 PI Sette A, Stacey J, Southwood S, Livingston BD, Chestnut R;
 PI Bako DM, Cellis E, Kubo RT, Grey HM;
 XX
 PP WPI: 2001-054887/47.
 XX
 PP Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 XX peptide groups, useful for vaccinating against HIV-1.
 XX
 PP Claim 32; Page 137; 448pp; English.
 XX
 CC The present invention describes a composition (1) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (AB25347 to
 CC AB25397). (1) has virucide activity and can be used in vaccines. (1)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumor-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of a group-based vaccine approach is the ability
 CC to combine selected groups (C1L and H1L), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX
 XX Sequence # AA;
 XX Query Match: 36.4%; Score 4; DR 22; Length 8;
 XX Best Local Similarity: 100.0%; Pred. No. 9, 3e-05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 5 VKKK 6
 XX 1 VKKK 5
 XX
 XX RESULT 4:
 XX ABP13143
 XX ID ABP13143 standard; Peptide: 8 AA;
 XX AC ABP13143;
 XX U: 15 JUL 2002 (first entry)
 XX
 XX HIV A02 super motif pol peptide #58.
 XX
 XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
 KW vpr; tat; cytochrome T lymphocyte; C1; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.

XX human immunodeficiency virus type 1.
 XX W12-001-24810 A1.
 XX 12 APR 2001.
 XX 05 OCT 2000: 2000W0-0527266.
 XX 05 OCT 1999: 99US-0412866.
 XX (EPIV) EPIMUNE IN.
 XX Settle A, Sidney J, Southwood S, Livingston RD, Chesnut R;
 Baker EM, Tellez E, Kuhn RT, Grey HM;
 W12-001-24810 A1.
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)
 peptide groups, useful for vaccinating against HIV-1.
 XX Claim 32: Page 137: 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 human immunodeficiency virus-1 (HIV-1) or gp comprising an amino acid
 sequence selected from 51 defined amino acid sequences (AB25347 to
 AB25397). (I) has virucide activity and can be used in vaccines. (I)
 may be used for immunising subjects against HIV-1 infections. The use of
 group-based vaccines has several advantages over traditional vaccines,
 particularly when compared to the use of whole antigens in vaccine
 compositions. There is evidence that the immune response to whole
 antigens is directed largely toward variable regions of the antigen,
 allowing for immune escape due to mutations. The groups for inclusion in
 an group-based vaccine may be selected from conserved regions of viral or
 tumour associated antigens, which therefore reduces the likelihood of
 escape mutants. Furthermore, immunosuppressive groups that may be present
 in whole antigens can be avoided with the use of group-based vaccines.
 An additional advantage of an group-based vaccine approach is the ability
 to combine selected groups (C11 and H11), and further, to modify the
 composition of the groups, achieving, for example, enhanced
 immunogenicity. Accordingly, the immune response can be modulated, as
 appropriate, for the target disease. Similar engineering of the response
 is not possible with traditional approaches. AB25347 to AB25412
 represent peptide sequences used in the exemplification of the present
 invention.

XX Sequence: 8 AA.
 XX Query Match: 0.4%, Score 47, 58 22; Length 8;
 Best Local Similarity: 100.0%, Ident. No. 9, 3e-05;
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 QY 9 VKKK W
 ID 1
 2 18KK 5
 111
 2 18KK 5
 RES001 44
 AB14646
 ID AB14646 standard; Peptide: 8 AA.
 XX AB14646
 AC AB14646
 XX 15 JUL 2002 (first entry)
 XX HIV A63 super motif pol peptide #18.
 XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
 vpr; vti; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
 anti-aids; vaccine; HIV infection; immunisation; virucide.
 XX Human immunodeficiency virus type 1.
 XX W12-001-24810 A1.
 XX 12 APR 2001

PN W12-001-24810 A1.
 XX 12 APR 2001.
 XX 05 OCT 2000: 2000W0-0527266.
 XX 05 OCT 1999: 99US-0412866.
 XX (EPIV) EPIMUNE IN.
 XX Settle A, Sidney J, Southwood S, Livingston RD, Chesnut R;
 Baker EM, Tellez E, Kuhn RT, Grey HM;
 W12-001-24810 A1.
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)
 peptide groups, useful for vaccinating against HIV-1.
 XX Claim 32: Page 168: 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 sequence selected from 51 defined amino acid sequences (AB25347 to
 AB25397). (I) has virucide activity and can be used in vaccines. (I)
 may be used for immunising subjects against HIV-1 infections. The use of
 group-based vaccines has several advantages over traditional vaccines,
 particularly when compared to the use of whole antigens in vaccine
 compositions. There is evidence that the immune response to whole
 antigens is directed largely toward variable regions of the antigen,
 allowing for immune escape due to mutations. The groups for inclusion in
 an group-based vaccine may be selected from conserved regions of viral or
 tumour associated antigens, which therefore reduces the likelihood of
 escape mutants. Furthermore, immunosuppressive groups that may be present
 in whole antigens can be avoided with the use of group-based vaccines.
 An additional advantage of an group-based vaccine approach is the ability
 to combine selected groups (C11 and H11), and further, to modify the
 composition of the groups, achieving, for example, enhanced
 immunogenicity. Accordingly, the immune response can be modulated, as
 appropriate, for the target disease. Similar engineering of the response
 is not possible with traditional approaches. AB25347 to AB25412
 represent peptide sequences used in the exemplification of the present
 invention.

XX Sequence: 8 AA.
 XX Query Match: 0.4%, Score 47, 58 22; Length 8;
 Best Local Similarity: 100.0%, Ident. No. 9, 3e-05;
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 QY 9 VKKK W
 ID 1
 2 18KK 5
 111
 2 18KK 5
 RES001 45
 AB14644
 ID AB14644 standard; Peptide: 8 AA.
 XX AB14644
 AC AB14644
 XX 15 JUL 2002 (first entry)
 XX HIV A63 super motif pol peptide #18.
 XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
 vpr; vti; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
 anti-aids; vaccine; HIV infection; immunisation; virucide.
 XX Human immunodeficiency virus type 1.
 XX W12-001-24810 A1.
 XX 12 APR 2001

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XX 05-OCT-1999; 2000WO-US27766.
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XX
XX 05-OCT-1999; 99US 0412863.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut K;
XX Baker DM, Collins E, Kubo RT, Grey BM;
XX
XX WP: 2001-054887/57.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.
XX
XX Claim 32: Page 168; 448pp; English.
XX
XX The present invention describes a composition (1) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (AB25347 to
XX AB25357). (1) has virucide activity and can be used in vaccines. (1)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX
XX Query Match 36.4%, Score 4, DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 7 LKKK 10
XX DB 4 LKKK 7
XX
XX RESULT 46
XX ABP15845
XX ID ABP15845 standard; Peptide: 8 AA.
XX
XX Ac ABP15845;
XX
XX 15-JUL-2002 (first entry)
XX
XX HIV A24 super motif pol peptide #25
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
XX vpr; vpr; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus type 1.
XX
XX WO200124810-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-1999; 2000WO-US27766.
XX
XX (EPIM-) EPIMMUNE INC.

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PR 05-OCT-1999; 99US 0412863.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut K;
XX Baker DM, Collins E, Kubo RT, Grey BM;
XX
XX WP: 2001-054887/57.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.
XX
XX Claim 32: Page 168; 448pp; English.
XX
XX The present invention describes a composition (1) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (AB25347 to
XX AB25357). (1) has virucide activity and can be used in vaccines. (1)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX
XX Query Match 36.4%, Score 4, DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 VKLK 8
XX DB 2 VKLK 5
XX
XX RESULT 47
XX ABP19387
XX ID ABP19387 standard; Peptide: 8 AA.
XX
XX Ac ABP19387;
XX
XX 15-JUL-2002 (first entry)
XX
XX HIV B62 super motif pol peptide #393.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
XX vpr; vpr; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus type 1.
XX
XX WO200124810-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-1999; 2000WO-US27766.
XX
XX 05-OCT-1999; 99US 0412863.
XX
XX (EPIM-) EPIMMUNE INC.

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XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;
 XX WPI: 2001 454887/47;
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)
 PI peptide groups, useful for vaccinating against HIV 1;
 XX Claim 32: Page 266; 448pp; English;
 XX The present invention describes a composition (i) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (i) has virucide activity and can be used in vaccines. (i)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX Sequence 8 AA;
 SQ Query Match 46.4%, Score 4; DH 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 VKKK 10
 DL III
 2 VKKK 5
 RESULT 49
 ABP19423
 XX ABP19423 Standard; Peptide: R AA;
 XX ABP19423;
 XX 15-JUL-2002 (first entry)
 XX HIV H62 super motif pol peptide #429
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX Human immunodeficiency virus type 1.
 XX W0200124810-A1.
 XX 12-APR-2001.
 XX 05-OCT-2000; 2000W0-US27766.
 XX 05-OCT-1999; 99US-0412863.
 XX (EPIM) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;
 XX WPI: 2001 454887/47;

XX WPI: 2001 454887/47;
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)
 PI peptide groups, useful for vaccinating against HIV-1;
 XX Claim 32: Page 266; 448pp; English;
 XX The present invention describes a composition (i) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to
 CC ABP25397). (i) has virucide activity and can be used in vaccines. (i)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.
 XX Sequence 8 AA;
 SQ Query Match 46.4%, Score 4; DH 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 VKLK 8
 JB III
 2 VKLK 5
 RESULT 49
 ABP21678
 XX ABP21678 Standard; Peptide: R AA;
 XX ABP21678;
 XX 15-JUL-2002 (first entry)
 XX HIV AG3 motif pol peptide #673
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX Human immunodeficiency virus type 1.
 XX W0200124810-A1.
 XX 12-APR-2001.
 XX 05-OCT-2000; 2000W0-US27766.
 XX 05-OCT-1999; 99US-0412863.
 XX (EPIM) EPIMUNE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cellis E, Kubo RT, Grey HM;
 XX WPI: 2001 454887/47;

The present invention describes a composition (*C*) comprising a preferred human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (APP2947 to APP2997). (*D*) has virulence activity and can be used as vaccines. (*E*) may be used for immunising subjects against HIV-1 infections; the use of group based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens or vaccine compositions. There is evidence that the immune response to vaccine antagons is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore requires the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CII_L, CIII_L, and RII), and further to modify the composition of the groups, allowing, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar evaluation of the response is not possible with traditional approaches. Appendix A, APP2947-2997 represent peptide sequences used in the optimization of the present invention.

Sequence B AA;

Serely Matrix 30.4%; Score 41; bit 24; Length 6
Best local similarity 100.0%, Pred No. of gaps:
Matches 41 Conservative 0% Mismatches 5% Indels 0%

ZV Z I KKK LQ
IU IUU
LH 4 IKK 7

RIS L L G
AAR L V D
LE APP L V D standard; Peptide = SA
XX XX
AF App 2776;
XX XX
XJ JY 276, 2002 (first entry)
XX XX
GE HIV AAA edit; pol peptide #1
XX XX
KW HIV-1 Human Immunodeficiency Virus Type 1 (HIV-1) gp120 glycoprotein surface protein, cytotoxic T lymphocyte associated virus type 1 receptor binding site, group 1
SW HIV-1 HXB2/HXBc2 isolate cytochrome b gene product, full length
XX XX
XX Human immunodeficiency virus type 1
XX W 258125-H1-A1
XX XX
XL 12-Aug-2001.
XX XX
XX PDB ID# 2000; 2000W-JS2776B,
IR PDB ID# 1999; 99CS-041286A,
XX XX
LA (EPM) EPIMUNE INC.,
XX Saito A, Sakurai Y, Sawakoshi N, et al. (1999) Characterization
F Baker DM, Cellis E, Kubo RT, Gray GR,
XX Baker DM, Cellis E, Kubo RT, Gray GR,
IR WUII 2001 AS4887/SZ
XX XX
XX Vaccine compositions comprising heteromeric and/or homomeric epitope fragments
IL Peptide groups useful for vaccination against HIV-1

CS Anticarpus heterophyllus.
 XX
 PR Key Location/Qualifiers
 FI Misc Difference 1
 FI Note "unchanged hydrophobic amino acid
 FI - opt. absent"
 XX
 XX W09222574-A1.
 XX
 XX 28-DEC-1992.
 XX
 XX 05-JUN-1992. 92MO-PR00510.
 XX
 XX 15-JUN-1992. 91PR-0005043.
 XX
 XX 31-JAN-1992. 92PR-0001127.
 XX
 XX (INRM) INSEK INS1 NAT SANIE & BEIH MED.
 XX
 XX Gauthier P., Bevaux G., Bernard G., Rivest S., Nicolas M.,
 FI Linaud J.
 XX
 XX W011993-018076/02.
 XX
 XX Jacalin and its new peptide fragments for treating HIV
 FI interacting with the CD4 receptor and specifically preventing
 FI infection of lymphocytes
 XX
 XX Claim 2, Page 14: 27pp; French.
 XX
 XX This fragment of Jacalin interacts with the T4 receptor and is
 CC analogous with the sequence of the HIV protein gp120. The peptide
 CC and other peptides with biological activity equivalent to that of
 CC Jacalin are useful in treatment of diseases caused by HIV. They
 CC specifically inhibit infection of lymphocytes by HIV, do not affect
 CC normal lymphocyte function and (unlike Jacalin itself) do not
 CC deactivate cells.
 CC (Updated on 25-MAR-2003 to correct FN 11034.)
 XX
 XX Sequence 15 AA:
 XX
 XX Query Match 45.5%; Score 4; DB 14; Length 15;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 XX Matches 6; Conservative 2; Mismatches 0; Indels 0; Caps 0;
 XX
 XX 2 INKK1 5
 XX 11 11
 XX 1 INKK1 15
 XX
 XX RESUME
 XX AAW4552P Standard: peptide: 8 AA
 XX
 XX AAW4552P
 XX
 XX 15-JUN-1998 (first entry)
 XX
 XX Marker: protein C-terminal fragment
 XX
 XX Marker: protein: target protein, molecular weight, density: determination
 XX
 XX Synthesis
 XX
 XX E082694 A2.
 XX
 XX 04-MAR-1993. 97EP-0402023.
 XX
 XX 29-AUG-1997.
 XX
 XX 06-AUG-1996. 96JP-C245859.
 XX
 XX (ORLY) ORIENTAL YEAST CO. LTD.
 XX

PI Khira Y., Matsuo Y.
 XX
 XX W011998-161284/15.
 XX
 XX Determination of molecular weight and/or amount of target protein -
 FI by electrophoresis using marker consisting of proteins that have
 FI different molecular weights and are present in different amounts
 XX
 XX Disclosure: Page 5; Jipp; English.
 XX
 XX This peptide is used in a novel method for determining the molecular
 CC weight and/or amount of a target protein. The method involves
 CC subjecting the target protein to electrophoresis simultaneously
 CC with a marker consisting of proteins that have different molecular
 CC weights and are present in different amounts, staining the target
 CC protein and the marker proteins, and comparing the resulting bands by
 CC eye or with a densitometer. The molecular weight can be determined by
 CC comparing the position of the target protein band with the various
 CC positions of the marker protein bands, and the amount can be determined
 CC by comparing the density of the target protein band with the various
 CC densities of the marker protein bands.
 XX
 XX Sequence 8 AA:
 XX
 XX Query Match 36.4%; Score 4; DB 19; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 XX
 XX 6 TGR 4
 XX 11 11
 XX 1 TGR 4
 XX
 XX RESUME 7
 XX AAB26887
 XX
 XX ID AAB26887 Standard: peptide: 8 AA.
 XX
 XX AAB26887;
 XX
 XX 01-FEB-2002 (first entry)
 XX
 XX PR 39 derived analogues is regulatory peptide 3.
 XX
 XX Angiogenesis: stimulation; PR 49; anoxia; myocardial infarction;
 XX myocardial ischaemia; proteasome
 XX
 XX Synthesis
 XX
 XX W02005755-A1.
 XX
 XX 01-01-2000
 XX
 XX 15-MAR-2000. 2000MO-DS07050.
 XX
 XX 26-MAR-1999. 99US-C276568.
 XX
 XX (BEIH) BEIH ISRAEL HEAD-NESS MEDICAL CENT.
 XX
 XX Simons M., Gao Y.
 XX
 XX W0112000-028117/60.
 XX
 XX Stimulating angiogenesis in situ, useful e.g. for treating anoxia and
 FI infarction, by administering a PR-39 oligopeptide that regulates
 FI enzymatic activity of proteasomes -
 XX
 XX Claim 14, Page 41: 51pp; English.
 XX
 XX This invention relates to a method for the stimulation of angiogenesis in
 CC situ within a targeted collection of viable cells. The method comprises
 CC introducing into the cytoplasm, at least 1 member of the PR-39
 CC oligopeptide collective, which interacts with cytoplasmic proteasomes.
 CC Part of the proteolytic activity of the proteasomes is selectively


```

QY      9 RRRR 11
      111
DB      5 RRRR 8

RESULT 19
ID      AAY78498 standard; peptide: 9 AA
XX
AC      AAY78498
XX
DT      24 MAR-2000 (first entry)
XX
DE      Protein kinase A optimal peptide substrate sequence SEQ ID NO:17
XX
KW      Protein kinase; phosphorylation site; signal transduction
XX
OS      Synthetic
XX
PN      US6004767 A
XX
FJ      24 DEC 1994
XX
PF      06-JAN-1995; 95US-045964
XX
PR      07-JAN-1994; 94US-0178570
XX
PA      (HECH-) BECH ISRAEL HOSPITAL ASSOC.
XX
PI      Cantley LL, Schaffhausen BS
XX
DR      WPI: 2000-096 403/08
XX
XX      Peptide substrate for a kinase, useful for determining substrate
PI      specificity
XX
PS      Example 5: Column 28: 69pp; English
XX
CC      The present invention describes a substrate for lck comprising a 9 amino
CC      acid peptide (1). Also described is a method of inhibiting kinase
CC      activity of lck by contacting it with (1) in vitro. The peptide is
CC      useful for determining substrate specificity of a protein kinase.
CC      Information on the substrate specificity of protein kinases in signal
CC      transduction would provide an insight into signal transduction
CC      mechanisms and could allow for the design of therapeutic agents. The
CC      present sequence represents a peptide used in the exemplification of
CC      the present invention.
XX
SQ      Sequence 9 AA:

Query Match      36.4%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Prod. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 RRRR 11
DB      5 RRRR 8

RESULT 20
ID      AAY57964 standard; peptide: 9 AA
XX
AC      AAY57964
XX
DT      24 MAR-2000 (first entry)
XX
DE      Protein kinase A optimal peptide substrate sequence SEQ ID NO:17
XX
KW      Protein kinase; phosphorylation site; signal transduction
XX
OS      Synthetic
XX
PN      US6004767 A
XX
FJ      24 DEC 1994
XX
PF      06-JAN-1995; 95US-045964
XX
PR      07-JAN-1994; 94US-0178570
XX
PA      (HECH-) BECH ISRAEL HOSPITAL ASSOC.
XX
PI      Cantley LL, Schaffhausen BS
XX
DR      WPI: 2000-096 403/08
XX
XX      Peptide substrate for a kinase, useful for determining substrate
PI      specificity
XX
PS      Example 5: Column 28: 69pp; English
XX
CC      The present invention describes a substrate for lck comprising a 9 amino
CC      acid peptide (1). Also described is a method of inhibiting kinase
CC      activity of lck by contacting it with (1) in vitro. The peptide is
CC      useful for determining substrate specificity of a protein kinase.
CC      Information on the substrate specificity of protein kinases in signal
CC      transduction would provide an insight into signal transduction
CC      mechanisms and could allow for the design of therapeutic agents. The
CC      present sequence represents a peptide used in the exemplification of
CC      the present invention.
XX
SQ      Sequence 9 AA:

Query Match      36.4%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Prod. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 RRRR 11
DB      5 RRRR 8

RESULT 21
ID      AAY06375 standard; peptide: 9 AA
XX
AC      AAY06375
XX
DT      24 OCT-2001 (first entry)
XX
DE      Human Leukocyte Antigen-DR3b (HLA-DR3b) submotif peptide epitope #17.
XX
KW      Prostate cancer-associated antigen; supermotif; human leukocyte antigen;
KW      HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;
KW      immunoregulatory; immunosuppression; HTL
XX
OS      Homo sapiens
XX
PN      W020145728 A2

```

```

QY      9 RRRR 11
      111
DB      5 RRRR 8

RESULT 19
ID      AAY78498 standard; peptide: 9 AA
XX
AC      AAY78498
XX
DT      24 MAR-2000 (first entry)
XX
DE      Protein kinase A optimal peptide #5.
XX
KW      Cancer; SSX family; SSX 1; SSX 2; SSX 3; SSX 4; SSX 5; NY-ESO-1;
KW      HLA binding; human leukocyte antigen; cytotoxic T cell; CTL;
KW      cytotoxic; melanoma; synovial sarcoma
XX
OS      Homo sapiens
XX
PN      W02000024-A1
XX
FJ      06-JAN-2000
XX
PF      25 JUN-1999; 99WO-0514494
XX
PR      26 JUN 1998; 98US-0105649
XX
PA      CAUW 1 LEMING INST CANCER RES.
XX
PI      Tureci O, Sahin U, Pfundtser M, Rammensee H, Stevanovic S,
PI      Choe Y, Garre A, Old LJ
XX
DR      WPI: 2000 125933/15
XX
XX      Determining the possible presence of breast, endometrial, colorectal,
PT      lung, bladder or head-neck cancer
XX
PS      Example 13: Page 23; 40pp; English
XX
CC      A method has been developed for determining the possible presence of a
CC      cancer, which is not melanoma or synovial sarcoma. The method comprises
CC      assaying a sample taken from the subject to determine the expression of
CC      an SSX gene, and determining the expression as a determination of the
CC      possible presence of cancer. Expression of SSX1 gene indicates possible
CC      presence of breast, endometrial, colorectal, lung, bladder or head-neck
CC      cancer. These cancers are also detected by SSX2 and SSX4 gene
CC      expression. SSX2 gene expression and level of indicates possible presence
CC      of lymphoma, renal cell, colorectal, gallbladder and prostate cancer. Expression
CC      of SSX4 gene also indicates possible presence of bladder or stomach
CC      cancer. SSX5 gene expression indicates the same cancers as SSX1, except
CC      breast cancer. Determining expression of SSX gene can be used to monitor
CC      progress of melanoma or synovial sarcoma, which is not cancer. The
CC      SSX-derived peptide complex stimulates proliferation of cytolytic T
CC      cells. This is useful for treating cancer, especially melanoma. AAY78464
CC      to AAY78468 represent specifically HLA binding peptides for use
CC      in the method of the invention. AAY8432 to AAY8465 represent 39p
CC      primers used in the isolation of SSX genes in the exemplification of the
CC      present invention. AAY78469 to AAY78476, and AAY78486 to AAY78492
CC      represent peptides derived from SSX proteins of NY-ESO-1, which are used
CC      in the exemplification of the present invention
XX
SQ      Sequence 9 AA:

Query Match      36.4%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Prod. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 RRRR 11
      111
DB      5 RRRR 8

```


1F Ref: 2002-710510/77.
XX New composition comprising a substance that modulates the status of a
1F 125p528 gene or a molecule that is modulated by 125p528, useful for
1F treating or preventing cancer that expresses or over-expresses 125p528.
XX
1F Disclosure: Page 174: 274pp; English.
XX
XX The present invention relates to compositions comprising a substance that
XX modulates the status of 125p528 or a molecule that is modulated by
XX 125p528. The status of a cell that expresses 125p528 is modulated by
XX composition, is useful for treating cancer, particularly prostate
XX bladder, kidney, colon, ovary or breast cancer. The 125p528 protein
XX and/or a nucleotide sequence encoding the protein is useful for
XX identifying a mammal against cancer. The present sequence is a 125p528
XX peptide shown to the exemplification of the invention.
XX
XX Sequence: 9 AA:
XX Query Match: 36.4%; Score 4; DB 23; Length 9;
XX Best Local Similarity: 100.0%; Fred. No. 9.3e-05;
XX Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4 KKKG 7
XX 5 KKKG 8
XX
XX 29 NOV 2002 (first entry)
XX
XX PP2AA-binding peptide from human PAK-1.
XX
XX Cytotoxic T lymphocyte associated protein (CTLA4)
XX protein phosphatase 2; PP2AA; immune response; radiation; bone therapy;
XX autoimmune disorder; rheumatoid arthritis; myasthenia gravis;
XX autoimmune thyroiditis; systemic lupus erythematosus; Graves' disease;
XX type 1 diabetes mellitus; multiple sclerosis; transplant;
XX graft versus host disease; allergy; inflammatory disorder;
XX bacterial infection; viral infection; HIV; parasitic infection;
XX human immunodeficiency virus; hepatitis B; hepatitis C; PAK-1.
XX
XX Homo sapiens.
XX
XX W200206051 A2.
XX
XX 29 AUG 2002
XX
XX 15 FEB 2002: 2002W0-6S04459.
XX
XX 15 FEB 2001: 2001S-2697579.
XX
XX GENE: GENETICS INST LLC.
XX (340) RECENTS RES INST GEN INC.
XX (340) BRIGHAM 5 WOMENS HOSPITAL.
XX
XX COLLINS M, Madrenas J, Carron R, Kachar V.
XX WPI: 2002-674892/72.
XX
XX Modulating an immune response. The invention is a method having a
XX condition that would benefit from an immunomodulatory agent, an immune
XX response, e.g. autoimmune disorders, comprising: (a) identifying the
XX interaction between CTLA4 and PP2AA
XX
XX Example 5: Fig 1: 84pp; English

XX The invention relates to modulating an immune response comprising
XX contacting a cell expressing at least one first molecule having a
XX CTLA4 (cytotoxic T lymphocyte associated protein 4) lysine rich
XX motif, and at least one second molecule having a PP2AA (protein
XX phosphatase 2A regulatory subunit A) CTLA4-interacting domain with an
XX agent that modulates the interaction between the first molecule and the
XX second molecule. Also included are: (1) treating a subject having a
XX condition that would benefit from down-regulation of an immune response,
XX comprises administering an agent that inhibits the interaction between a
XX first molecule and a second molecule described above; (2) identifying a
XX compound that modulates the interaction of CTLA4 and PP2AA, and
XX (3) identifying a compound which modulates the interaction of a
XX molecule comprising at least one CTLA4 lysine rich motif and a PP2AA
XX molecule comprising a PP2AA CTLA4-interacting domain.
XX The methods are useful for modulating an immune response and
XX treating a subject having a condition that would benefit from
XX down-regulation of an immune response, such as autoimmune disorder
XX (e.g. rheumatoid arthritis, myasthenia gravis, autoimmune thyroiditis,
XX systemic lupus erythematosus, type 1 diabetes mellitus, Grave's
XX disease, or multiple sclerosis), a transplant (e.g. a bone marrow
XX transplant, a stem cell transplant, a heart transplant, a lung
XX transplant, a liver transplant, a kidney transplant, a cornea
XX transplant, or a skin transplant), graft versus host disease, an
XX allergy, or an inflammatory disorder. Enhancing an immune
XX response is useful in treating bacterial, viral (e.g. HIV-1 or 2,
XX human immunodeficiency virus, hepatitis B or C) or parasitic infections.
XX The present sequence is a PP2AA-binding peptide from human PAK-1.
XX
XX Sequence: 9 AA:
XX Query Match: 36.4%; Score 4; DB 23; Length 9;
XX Best Local Similarity: 100.0%; Fred. No. 9.3e-05;
XX Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4 KKKG 5
XX 5 KKKG 5
XX
XX 14 NOV 2002 (first entry)
XX
XX Bovine protein kinase A (PKA) peptide substrate.
XX
XX Kinase, cancer, tumor, vascularisation; angiopathy; antiosteoporosis;
XX chemotherapy induced alopecia; testosterone; chemotherapy; cytostatic;
XX protein kinase A; PKA; lovastatin; radiation therapy; vasodilator.
XX
XX Bos sp.
XX
XX Key: Location/Qualifiers
XX
XX Modified Site: /note: "Biotinylated"
XX
XX Modified Site: /note: "C terminal amide"
XX
XX W2002057240-A1.
XX
XX 25 JUL 2002
XX
XX 21 DEC 2001: 2001W-0550559.
XX
XX 22 DEC 2000: 2000US-257704P.
XX
XX (CRH-) ORTHO MC NEIL PHARM INC.
XX
XX Liu R, Campbell PJ, Weller S, Huang S, Emanuel S, Guringer R;
XX Modification S;

The present invention relates to novel human cancer related genes and proteins (ARZ78120-ARZ78168 and ARZ78169-ARZ78186). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of genes and/or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or the translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present invention is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

Query Match: 40.4%, Score 41, DB 24, Length 9;
 Best Local Similarity: 100.0%, Pred. No. 9, 3e-05;
 Matches: 4, Conservative 0, Mismatches 0, Gaps 0.

4 KKTG 7
 11
 6 KKTG 6

Query Match: 40.4%, Score 41, DB 24, Length 9;
 Best Local Similarity: 100.0%, Pred. No. 9, 3e-05;
 Matches: 4, Conservative 0, Mismatches 0, Gaps 0.

4 KKTG 7
 11
 6 KKTG 6

The present invention relates to novel human cancer related genes and proteins (ARZ78120-ARZ78168 and ARZ78169-ARZ78186). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of genes and/or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or the translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present invention is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

Query Match: 40.4%, Score 41, DB 24, Length 9;
 Best Local Similarity: 100.0%, Pred. No. 9, 3e-05;
 Matches: 4, Conservative 0, Mismatches 0, Gaps 0.

4 KKTG 7
 11
 6 KKTG 6

The present invention relates to novel human cancer related genes and proteins (ARZ78120-ARZ78168 and ARZ78169-ARZ78186). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of genes and/or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or the translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present invention is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

Query Match: 40.4%, Score 41, DB 24, Length 9;
 Best Local Similarity: 100.0%, Pred. No. 9, 3e-05;
 Matches: 4, Conservative 0, Mismatches 0, Gaps 0.

4 KKTG 7
 11
 6 KKTG 6

The present invention relates to novel human cancer related genes and proteins (ARZ78120-ARZ78168 and ARZ78169-ARZ78186). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of genes and/or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or the translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present invention is a human leukocyte antigen (HLA) peptide, used in an example from the invention.

Query Match: 40.4%, Score 41, DB 24, Length 9;
 Best Local Similarity: 100.0%, Pred. No. 9, 3e-05;
 Matches: 4, Conservative 0, Mismatches 0, Gaps 0.

4 KKTG 7
 11
 6 KKTG 6

```

DE      1111
        2 KKTG 5

RESULT 4:
ABR14465
ID      ABR14445 standard; Peptide: 9 AA.
XX
XX
XX      A:
XX
XX      19 MAY 2003 (first entry)
XX
XX      Human cancer related protein 156P5C12 HLA peptide #1470.
XX
XX      Human cytostatic vaccine; cancer; immune response; HLA
XX      human leukocyte antigen.
XX
XX      Homo sapiens.
XX
XX      W0200284921-A2.
XX
XX      24 OCT 2002.
XX
XX      19 APR 2002: 2002W0-0S11654.
XX
XX      19 APR 2001: 2001US-282749.
XX      19 APR 2001: 2001US-283112P.
XX      25 APR 2001: 2001US-286631P.
XX
XX      (AGEN-) AGENSYS INC.
XX
XX      Jaklovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS,
XX      Morrison K, Morrison KK, Raitano AB.
XX
XX      WPI: 2003-075555/07.
XX
XX      New composition comprising a substance that modulates the structure of
XX      proteins and polynucleotides, useful for therapeutic, prognostic and
XX      diagnostic reagents for eliciting cellular or humoral immune response
XX      in cancer patients.
XX
XX      Claim 19: Page 256; 1021pp; English.
XX
XX      The present invention relates to novel human cancer-related genes and
XX      proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
XX      proteins are useful for eliciting a humoral or cellular immune response.
XX      The genes are useful as probes and primers for the amplification and/or
XX      detection of genes, mRNAs or their fragments, as reagents for the
XX      diagnosis and/or prognosis of cancer, as coding sequences capable of
XX      directing the expression of the protein, as tools for modulating or
XX      inhibiting the expression of genes and/or translation of transcripts, and
XX      as therapeutic agents. The proteins and peptides are useful as
XX      therapeutic, prognostic and diagnostic reagents for cancer. The present
XX      sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX      from the invention.
XX
XX      Sequence 9 AA:
XX
XX      Query Match 36.4%; Score 4; DH 24; Length 9;
XX      Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX      0Y      4 KKTG 7
XX              1111
XX      0B      2 KKTG 5
XX
XX
XX
XX
XX      RESULT 4:
XX      ABR14446
XX      ID      ABR14436 standard; Peptide: 9 AA.
XX
XX      AC      ABR14446.
XX
XX      0Y      19 MAY 2003 (first entry)
XX
XX      Human cancer related protein 156P5C12 HLA peptide #1400.
XX
XX      Human cytostatic vaccine; cancer; immune response; HLA;
XX      human leukocyte antigen.
XX
XX      Homo sapiens.
XX
XX      W0200284921-A2
XX

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```

DT      19-MAY-2003 (first entry)
XX
XX      Human cancer related protein 156P5C12 HLA peptide #1371.
XX
XX      Human cytostatic vaccine; cancer; immune response; HLA;
XX      human leukocyte antigen.
XX
XX      Homo sapiens.
XX
XX      W0200284921-A2.
XX
XX      24 OCT 2002.
XX
XX      19 APR 2002: 2002W0-0S11654.
XX
XX      10-APR-2001: 2001US-282749.
XX      10-APR-2001: 2001US-283112P.
XX      25-APR-2001: 2001US-286631P.
XX
XX      (AGEN-) AGENSYS INC.
XX
XX      Jaklovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS,
XX      Morrison K, Morrison KK, Raitano AB.
XX
XX      WPI: 2003-075555/07.
XX
XX      New composition comprising a substance that modulates the structure of
XX      proteins and polynucleotides, useful for therapeutic, prognostic and
XX      diagnostic reagents for eliciting cellular or humoral immune response
XX      in cancer patients.
XX
XX      Claim 19: Page 256; 1021pp; English.
XX
XX      The present invention relates to novel human cancer-related genes and
XX      proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
XX      proteins are useful for eliciting a humoral or cellular immune response.
XX      The genes are useful as probes and primers for the amplification and/or
XX      detection of genes, mRNAs or their fragments, as reagents for the
XX      diagnosis and/or prognosis of cancer, as coding sequences capable of
XX      directing the expression of the protein, as tools for modulating or
XX      inhibiting the expression of genes and/or translation of transcripts, and
XX      as therapeutic agents. The proteins and peptides are useful as
XX      therapeutic, prognostic and diagnostic reagents for cancer. The present
XX      sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX      from the invention.
XX
XX      Sequence 9 AA:
XX
XX      Query Match 36.4%; Score 4; DH 24; Length 9;
XX      Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX
XX      0Y      4 KKTG 7
XX              1111
XX      0B      3 KKTG 6
XX
XX
XX
XX
XX      RESULT 44
XX      ABR14465
XX      ID      ABR14465 standard; Peptide: 9 AA.
XX
XX      AC      ABR14465.
XX
XX      0Y      19-MAY-2003 (first entry)
XX
XX      Human cancer related protein 156P5C12 HLA peptide #1400.
XX
XX      Human cytostatic vaccine; cancer; immune response; HLA;
XX      human leukocyte antigen.
XX
XX      Homo sapiens.
XX
XX      W0200284921-A2
XX

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XX WPI: 1993-134624/16.
XX Request for detecting antibodies to hepatitis C virus - comprises
PI peptide(s) with the same sequence as an epitope of an HCV
PT structural region
XX
XX Class 1: Page 43: 51pp; Japanese.
XX
XX The sequences given in AAR444/25 are peptides which can be used in a
XX test reagent for the detection of antibodies against hepatitis C.
XX The peptides represent epitopes of an HCV structural region and they
XX react specifically with antibodies against the HCV structural region.
XX Detection is sensitive and accurate and allows diagnosis of the
XX infection at a very early stage.
XX (Updated on 25 MAR-2003 to correct PN field.)
XX
XX Sequence: 10 AA:
XX
XX Query Match: 36.4%, Score 4; DB 14; Length 10;
XX Host Local Similarity: 100.0%, Pred. No. 8.5e+02;
XX Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX CY 7 GRGP 10
XX III
XX DB 7 GRGP 10
XX
XX
XX RESULT 47
XX AAR444/9
XX ID: AAR444/9 standard; peptide: 10 AA.
XX
XX AC AAR444/9:
XX
XX XX 25-MAR-2003 (updated)
XX DT 05-AUG-1993 (first entry)
XX
XX XX Hepatitis C Ab detection peptide #4.
XX
XX XX Test reagent: detection antibody; hepatitis C virus; HCV; epitope;
XX XX structural region; diagnosis; SS.
XX
XX XX Synthetic
XX
XX XX W09437486 A1.
XX
XX XX 15 APR-1993.
XX
XX XX 02-OCT-1992; 92WP JPO1276.
XX
XX XX 02-OCT-1992; 92JP 9259524.
XX
XX XX 26-MAR-1992; 92JP 9268695.
XX
XX XX (EIKEN) EIKEN KASAKO KK.
XX XX (TAKA) TAKARA SEIYAKU CO.
XX XX (OSAG) UNIV. OSAKA.
XX
XX XX Ishibashi K., Ito M., Shibutani I., Takamizawa A., Yoshida I.
XX
XX WPI: 1993-134624/16.
XX
XX Request for detecting antibodies to hepatitis C virus - comprises
PI peptide(s) with the same sequence as an epitope of an HCV
PT structural region
XX
XX Bioscience; Page 42: 51pp; Japanese.
XX
XX The sequences given in AAR444/25 are peptides which can be used in a
XX test reagent for the detection of antibodies against hepatitis C.
XX The peptides represent epitopes of an HCV structural region and they
XX react specifically with antibodies against the HCV structural region.
XX Detection is sensitive and accurate and allows diagnosis of the
XX infection at a very early stage.
XX (Updated on 25 MAR-2003 to correct PN field.)
XX
XX Sequence: 10 AA:
XX
XX Query Match: 36.4%, Score 4; DB 14; Length 10;
XX Host Local Similarity: 100.0%, Pred. No. 8.5e+02;
XX Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX CY 7 GRGP 10
XX III
XX DB 7 GRGP 10
XX
XX
XX RESULT 49
XX AAR444/9
XX ID: AAR444/9 standard; peptide: 10 AA.

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XX
XX Sequence: 10 AA:
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XX Query Match: 36.4%, Score 4; DB 14; Length 10;
XX Host Local Similarity: 100.0%, Pred. No. 8.5e+02;
XX Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX CY 7 GRGP 10
XX III
XX DB 7 GRGP 10
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XX RESULT 46
XX AAR444/20
XX ID: AAR444/20 standard; peptide: 10 AA.
XX
XX AC AAR444/20:
XX
XX XX 25-MAR-2003 (updated)
XX DT 05-AUG-1993 (first entry)
XX
XX XX Hepatitis C Ab detection peptide #4.
XX
XX XX Test reagent: detection antibody; hepatitis C virus; HCV; epitope;
XX XX structural region; diagnosis; SS.
XX
XX XX Synthetic
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XX XX W09437486 A1.
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XX XX 15 APR-1993.
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XX XX 02-OCT-1992; 92WP JPO1276.
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XX XX 02-OCT-1992; 92JP 9259524.
XX
XX XX 26-MAR-1992; 92JP 9268695.
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XX XX (EIKEN) EIKEN KASAKO KK.
XX XX (TAKA) TAKARA SEIYAKU CO.
XX XX (OSAG) UNIV. OSAKA.
XX
XX XX Ishibashi K., Ito M., Shibutani I., Takamizawa A., Yoshida I.
XX
XX WPI: 1993-134624/16.
XX
XX Request for detecting antibodies to hepatitis C virus - comprises
PI peptide(s) with the same sequence as an epitope of an HCV
PT structural region
XX
XX Bioscience; Page 43: 51pp; Japanese.
XX
XX The sequences given in AAR444/25 are peptides which can be used in a
XX test reagent for the detection of antibodies against hepatitis C.
XX The peptides represent epitopes of an HCV structural region and they
XX react specifically with antibodies against the HCV structural region.
XX Detection is sensitive and accurate and allows diagnosis of the
XX infection at a very early stage.
XX (Updated on 25 MAR-2003 to correct PN field.)
XX
XX Sequence: 10 AA:
XX
XX Query Match: 36.4%, Score 4; DB 14; Length 10;
XX Host Local Similarity: 100.0%, Pred. No. 8.5e+02;
XX Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX CY 7 GRGP 10
XX III
XX DB 7 GRGP 10
XX
XX
XX RESULT 49
XX AAR444/9
XX ID: AAR444/9 standard; peptide: 10 AA.

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configure version 1.1.6
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10M protein6 protein search, using SW-BLAST

Run on: September 09, 2003, 13:00:03 Search File: 2143_Seconds
(without alignment)
// 4.0 Release with updates/seq

Title: US-09-787-443-9

Protein search:

Sequence: 1 AINKKGRKRP 11

Search table:

Gap: 40.00 (default 60)

Searches: 566894 seqs, 15161094 residues

Word size:

0

Total number of hits satisfying chosen parameters: 6847

Minimum DB seq length: 6

Maximum DB seq length: 16

Post processing: Listing first 500 sequences

Database: Published Applications, AA*
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17: /cqn2_6/protein6/2143/seqs/US-09-787-443-9-oli.rapb
18: /cqn2_6/protein6/2143/seqs/US-09-787-443-9-oli.rapb

Pro 1: Note the number of sequences that are identical to the query sequence, and is derived by analysis. The number of sequences that are identical to the query sequence is derived by analysis.

Sequences

Result No.	Score	Query Match	Length	ID	Description
1	6	45.5	14	6	US-09-787-443-9-oli.rapb
2	5	45.5	14	12	US-09-787-443-9-oli.rapb
3	4	36.4	9	11	US-09-787-443-9-oli.rapb
4	4	36.4	9	11	US-09-787-443-9-oli.rapb
5	4	36.4	9	12	US-09-787-443-9-oli.rapb
6	4	36.4	9	12	US-09-787-443-9-oli.rapb
7	4	36.4	9	12	US-09-787-443-9-oli.rapb
8	4	36.4	9	12	US-09-787-443-9-oli.rapb
9	4	36.4	9	12	US-09-787-443-9-oli.rapb
10	4	36.4	9	15	US-09-787-443-9-oli.rapb
11	4	36.4	9	15	US-09-787-443-9-oli.rapb
12	4	36.4	10	11	US-09-787-443-9-oli.rapb
13	4	36.4	10	11	US-09-787-443-9-oli.rapb
14	4	36.4	10	11	US-09-787-443-9-oli.rapb
15	4	36.4	10	11	US-09-787-443-9-oli.rapb

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9	27.3	8	11	US-09-876-22-A-113	Sequence 120, Appl	163	3	27.3	8	15	US-10-006-869-2443	Sequence 2443, Appl
10	27.3	8	11	US-09-877-22-A-114	Sequence 120, Appl	164	3	27.3	8	15	US-10-006-869-2503	Sequence 2503, Appl
11	27.3	8	11	US-09-878-22-A-115	Sequence 120, Appl	165	3	27.3	8	15	US-10-006-869-2613	Sequence 2613, Appl
12	27.3	8	11	US-09-879-22-A-116	Sequence 120, Appl	166	3	27.3	8	15	US-10-006-869-2634	Sequence 2634, Appl
13	27.3	8	11	US-09-880-22-A-117	Sequence 120, Appl	167	3	27.3	8	15	US-10-006-869-2649	Sequence 2649, Appl
14	27.3	8	11	US-09-881-22-A-118	Sequence 120, Appl	168	3	27.3	8	15	US-10-006-869-2653	Sequence 2653, Appl
15	27.3	8	11	US-09-882-22-A-119	Sequence 120, Appl	169	3	27.3	8	15	US-10-006-869-2664	Sequence 2664, Appl
16	27.3	8	11	US-09-883-22-A-120	Sequence 120, Appl	170	3	27.3	8	15	US-10-006-869-2679	Sequence 2679, Appl
17	27.3	8	11	US-09-884-22-A-121	Sequence 120, Appl	171	3	27.3	8	15	US-10-006-869-2683	Sequence 2683, Appl
18	27.3	8	11	US-09-885-22-A-122	Sequence 120, Appl	172	3	27.3	8	15	US-10-006-869-2694	Sequence 2694, Appl
19	27.3	8	11	US-09-886-22-A-123	Sequence 120, Appl	173	3	27.3	8	15	US-10-006-869-2712	Sequence 2712, Appl
20	27.3	8	11	US-09-887-22-A-124	Sequence 120, Appl	174	3	27.3	8	15	US-10-006-869-2799	Sequence 2799, Appl
21	27.3	8	11	US-09-888-22-A-125	Sequence 120, Appl	175	3	27.3	8	15	US-10-006-869-2862	Sequence 2862, Appl
22	27.3	8	11	US-09-889-22-A-126	Sequence 120, Appl	176	3	27.3	8	15	US-10-006-869-2925	Sequence 2925, Appl
23	27.3	8	11	US-09-890-22-A-127	Sequence 120, Appl	177	3	27.3	8	15	US-10-006-869-2988	Sequence 2988, Appl
24	27.3	8	11	US-09-891-22-A-128	Sequence 120, Appl	178	3	27.3	8	15	US-10-006-869-3048	Sequence 3048, Appl
25	27.3	8	11	US-09-892-22-A-129	Sequence 120, Appl	179	3	27.3	8	15	US-10-006-869-3071	Sequence 3071, Appl
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29	27.3	8	11	US-09-896-22-A-133	Sequence 120, Appl	183	3	27.3	8	15	US-10-006-869-3251	Sequence 3251, Appl
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32	27.3	8	11	US-09-899-22-A-136	Sequence 120, Appl	186	3	27.3	8	15	US-10-006-869-3774	Sequence 3774, Appl
33	27.3	8	11	US-09-900-22-A-137	Sequence 120, Appl	187	3	27.3	8	15	US-10-006-869-3860	Sequence 3860, Appl
34	27.3	8	11	US-09-901-22-A-138	Sequence 120, Appl	188	3	27.3	8	15	US-10-006-869-4050	Sequence 4050, Appl
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38	27.3	8	11	US-09-905-22-A-142	Sequence 120, Appl	192	3	27.3	8	15	US-10-211-088-185	Sequence 185, Appl
39	27.3	8	11	US-09-906-22-A-143	Sequence 120, Appl	193	3	27.3	8	15	US-10-211-088-198	Sequence 198, Appl
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52	27.3	8	11	US-09-919-22-A-156	Sequence 120, Appl	206	3	27.3	8	15	US-09-344-824-165	Sequence 165, Appl
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58	27.3	8	11	US-09-925-22-A-162	Sequence 120, Appl	212	3	27.3	8	15	US-09-760-599-8	Sequence 8, Appl1
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60	27.3	8	11	US-09-927-22-A-164	Sequence 120, Appl	214	3	27.3	8	15	US-09-760-599-22	Sequence 22, Appl1
61	27.3	8	11	US-09-928-22-A-165	Sequence 120, Appl	215	3	27.3	8	15	US-09-760-599-23	Sequence 23, Appl1
62	27.3	8	11	US-09-929-22-A-166	Sequence 120, Appl	216	3	27.3	8	15	US-09-760-599-24	Sequence 24, Appl1
63	27.3	8	11	US-09-930-22-A-167	Sequence 120, Appl	217	3	27.3	8	15	US-09-765-086-114	Sequence 114, Appl
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79	27.3	8	11	US-09-946-22-A-183	Sequence 120, Appl	233	3	27.3	8	15		
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246	9	10	US-09-872-632-25	Sequence 26, App1	309	9	12	US-10-062-109A-562	Sequence 562, App
247	9	10	US-09-828-442-19	Sequence 18, App1	310	9	12	US-10-062-109A-564	Sequence 564, App
248	9	10	US-09-961-902-3	Sequence 4, App1	311	9	12	US-10-077-106-17	Sequence 12, App1
249	9	10	US-09-961-902-4	Sequence 6, App1	312	9	12	US-10-077-106-17	Sequence 17, App1
249	9	10	US-09-961-902-6	Sequence 6, App1	313	9	12	US-10-312-495-12	Sequence 12, App1
241	9	10	US-09-961-902-12	Sequence 12, App1	314	9	12	US-10-224-999A-702	Sequence 702, App
242	9	10	US-09-961-902-14	Sequence 14, App1	315	9	12	US-10-280-137-237	Sequence 237, App
243	9	10	US-09-961-902-17	Sequence 17, App1	316	9	12	US-09-833-039-76	Sequence 76, App1
244	9	10	US-09-961-902-18	Sequence 18, App1	317	9	12	US-09-833-039-77	Sequence 77, App1
245	9	11	US-09-961-902-18	Sequence 18, App1	318	9	12	US-09-833-039-99	Sequence 99, App1
246	9	11	US-09-961-902-18	Sequence 18, App1	319	9	12	US-10-020-269-109	Sequence 109, App
247	9	11	US-09-961-902-18	Sequence 18, App1	320	9	12	US-10-231-417-379	Sequence 379, App
248	9	11	US-09-961-902-18	Sequence 18, App1	321	9	12	US-10-239-313A-522	Sequence 522, App
249	9	11	US-09-961-902-18	Sequence 18, App1	322	9	12	US-10-012-756-26	Sequence 26, App1
250	9	11	US-09-961-902-18	Sequence 18, App1	323	9	12	US-10-211-207-12	Sequence 12, App1
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ALIGNMENTS

RESULT :
 US-09-859-699-7
 : Sequence 3, Application US/04859699A
 : Publication No. US20013007017A1
 : GENERAL INFORMATION:
 : APPLICANT: VELLKOVIC, Veljko
 : APPLICANT: MELLAS, Radmila
 : TITLE OF INVENTION: PEPTIDES WHICH REACT WITH ANTIBODY REPRESENTING THE
 : FILE REFERENCE: VELLKOVIC et al., 08/859,699
 : CURRENT FILING DATE: 1997-05-21
 : EARLIER APPLICATION NUMBER: GB 9610673.7
 : EARLIER FILING DATE: 1996-05-22
 : EARLIER APPLICATION NUMBER: GB 9623340.8
 : NUMBER OF SEQ ID NOS: 26
 : SOFTWARE: Patent in Ver. 2.0
 : SEQ ID NO 3
 : LENGTH: 14
 : TYPE: PRT

1 FEATURE:
2 OTHER INFORMATION: Optimized substrate peptide
3 US 10 294 686 141

Query Match 96.4%, Score 4, DB 12, Length 9,
Best Local Similarity 100.0%, Pred. No. 5, 1e+05,
Matches 4, Conservative 0, Mismatches 0, Gaps 0

QY 3 GRSP 9
111
14 4 GRSP 6

RESULT 6
US 10 294 686 141

1 Sequence 24, Application US/2002/000000
2 Publication No. US2002/0124000A1
3 GENERAL INFORMATION:
4 APPLICANT: BERNARDINI, ROBERT
5 APPLICANT: FRANKLIN, ROSELLA
6 APPLICANT: DESIDERIO, ANGELA
7 APPLICANT: FAVAIORAKI, PARASKEVI
8 TITLE OF INVENTION: STABILIZED PEPTIDES, POLYPEPTIDES AND ANALOGUES
9 TITLE OF INVENTION: WHICH INCLUDE THEM
10 FILE REFERENCE: 411 4
11 CURRENT APPLICATION NUMBER: US/10/09, 65
12 PRIOR FILING DATE: 2002 10 29
13 PRIOR APPLICATION NUMBER: 87/112/200034
14 PRIOR FILING DATE: 2000 12 29
15 PRIOR APPLICATION NUMBER: 11 899/460000
16 PRIOR FILING DATE: 1999 12 06
17 NUMBER OF SEQ ID NOS: 118
18 SOFTWARE: Patent In Ver. 2.1
19 SEQ ID NO 24
20 LENGTH: 9
21 TYPE: PPT
22 ORGANISM: Artificial Sequence
23 FEATURE:
24 OTHER INFORMATION: Description of Applicant's sequence: See Table 1
25 US 10 294 686 141

Query Match 96.4%, Score 4, DB 12, Length 9,
Best Local Similarity 100.0%, Pred. No. 5, 1e+05,
Matches 4, Conservative 0, Mismatches 0, Gaps 0

QY 3 GRSP 9
111
14 4 GRSP 6

RESULT 7
US 10 294 686 141

1 Sequence 16, Application US/01/000000
2 Publication No. US2002/0165000A1
3 GENERAL INFORMATION:
4 APPLICANT: Williams, Mary
5 APPLICANT: MACHENAS, JOAQUIN
6 APPLICANT: CURTIS, BEATRIZ
7 APPLICANT: KATHOL, VILLY
8 TITLE OF INVENTION: METHODS FOR PRODUCING PEPTIDES
9 TITLE OF INVENTION: RESPONSE BY MODULATING THE EXPRESSION OF PEPTIDE AN
10 TITLE OF INVENTION: EP2A
11 FILE REFERENCE: 899 027
12 CURRENT APPLICATION NUMBER: US/10/09, 65
13 PRIOR FILING DATE: 2002 12 29
14 PRIOR APPLICATION NUMBER: 96/20 730
15 PRIOR FILING DATE: 2001 02 16
16 NUMBER OF SEQ ID NOS: 25
17 SOFTWARE: FASTSEQ for Windows Ver. 3.1
18 SEQ ID NO 14
19 LENGTH: 9
20 TYPE: PPT
21 ORGANISM: Homo Sapiens

1 ORGANISM: Homo Sapiens
2 US 10 077 106 14
3
4
5 Query Match 96.4%, Score 4, DB 12, Length 9,
6 Best Local Similarity 100.0%, Pred. No. 5, 1e+05,
7 Matches 4, Conservative 0, Mismatches 0, Gaps 0

QY 2 GRSP 6
111
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RESULT 8
US 10 077 106 14

1 Sequence 24, Application US/2000/000000
2 Publication No. US2000/000000A1
3 GENERAL INFORMATION:
4 APPLICANT: DUGAN, JAMES
5 APPLICANT: SABLE, DAVID
6 APPLICANT: GRIFFIN, MICHAEL
7 TITLE OF INVENTION: Label Associated Peptide and Uses Thereof
8 FILE REFERENCE: US 5,223,111
9 CURRENT APPLICATION NUMBER: US/09/043,039
10 CURRENT FILING DATE: 2001 04 12
11 PRIOR APPLICATION NUMBER: US 09/409,455
12 PRIOR FILING DATE: 1999 09 30
13 PRIOR APPLICATION NUMBER: US 09/444,040
14 PRIOR FILING DATE: 1999 06 25
15 PRIOR APPLICATION NUMBER: US 09/105,839
16 PRIOR FILING DATE: 1998 06 26
17 PRIOR APPLICATION NUMBER: US 09/451,143
18 PRIOR FILING DATE: 1997 06 05
19 NUMBER OF SEQ ID NOS: 129
20 SEQ ID NO 24
21 LENGTH: 9
22 TYPE: PPT
23 ORGANISM: Homo Sapiens
24
25 US 09 433 039 24

Query Match 96.4%, Score 4, DB 12, Length 9,
Best Local Similarity 100.0%, Pred. No. 5, 1e+05,
Matches 4, Conservative 0, Mismatches 0, Gaps 0

QY 3 GRSP 11
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14 3 GRSP 7

RESULT 9
US 09 433 039 24

1 Sequence 46, Application US/2000/000000
2 Publication No. US2000/000000A1
3 GENERAL INFORMATION:
4 APPLICANT: LITTON, ROYCE
5 APPLICANT: SABLE, DAVID
6 APPLICANT: FRIEDMAN, MICHAEL
7 TITLE OF INVENTION: Label Associated Peptide and Uses Thereof
8 FILE REFERENCE: US 5,223,111
9 CURRENT APPLICATION NUMBER: US/09/043,039
10 CURRENT FILING DATE: 2001 04 12
11 PRIOR APPLICATION NUMBER: US 09/409,455
12 PRIOR FILING DATE: 1999 09 30
13 PRIOR APPLICATION NUMBER: US 09/444,040
14 PRIOR FILING DATE: 1999 06 25
15 PRIOR APPLICATION NUMBER: US 09/105,839
16 PRIOR FILING DATE: 1998 06 26
17 PRIOR APPLICATION NUMBER: US 09/451,143
18 PRIOR FILING DATE: 1997 06 05
19 NUMBER OF SEQ ID NOS: 129
20 SEQ ID NO 48
21 LENGTH: 7
22 TYPE: PPT
23 ORGANISM: Homo Sapiens
24
25

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US 09 787 443 9.48
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Best Local Similarity 100.0% Pred. No. 6 Gaps 0
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

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ID III
SD 3 RRRR 6

RESULT 13
US 10 211 207 15
Query Match 36.4% Score 41 DB 12 Length 10
Best Local Similarity 100.0% Pred. No. 6 Gaps 0
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

Publication No. US2003058411A1
GENERAL INFORMATION:
APPLICANT: Mary
APPLICANT: Madhusudhan, Mary
APPLICANT: Kuchroo, Vijay
TITLE OF INVENTION: METHODS FOR MODULATING AN IMPROVE
TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN PLEKHA1 AND
TITLE OF INVENTION: PD2A
FILE REFERENCE: GNN-027
CURRENT APPLICATION NUMBER: US/1-211-207
CURRENT FILING DATE: 2002-08-02
PRIORITY APPLICATION NUMBER: US/00-077-109
PRIORITY FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US 10 211 207 15

Query Match 36.4% Score 41 DB 12 Length 10
Best Local Similarity 100.0% Pred. No. 6 Gaps 0
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 RRRR 5
ID III
SD 4 RRRR 6

RESULT 11
US 10 211 207 45
Query Match 36.4% Score 41 DB 12 Length 10
Best Local Similarity 100.0% Pred. No. 6 Gaps 0
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

Publication No. US2003058411A1
GENERAL INFORMATION:
APPLICANT: SIMARD, David, Jr.
APPLICANT: DAMOND, David, Jr.
TITLE OF INVENTION: ANTICANCER COMPOSITIONS
TITLE OF INVENTION: CANCER
FILE REFERENCE: CTEMM-015A
CURRENT APPLICATION NUMBER: US/10/ 211-207
CURRENT FILING DATE: 2002-09-27
PRIORITY APPLICATION NUMBER: US 60/274 064
PRIORITY FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 109
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapien
US 10 211 207 45

Query Match 36.4% Score 41 DB 12 Length 10
Best Local Similarity 100.0% Pred. No. 6 Gaps 0
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 8 RRRR 12
ID III
SD 3 RRRR 6

RESULT 14
US 09 572 404B 477
Query Match 36.4% Score 41 DB 11 Length 10
Best Local Similarity 100.0% Pred. No. 6.1e+02
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 6 RRRR 9
ID III
SD 2 RRRR 5

RESULT 14
US 09 572 404B 461
Query Match 36.4% Score 41 DB 12 Length 10
Best Local Similarity 100.0% Pred. No. 6 Gaps 0
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

Publication No. US2003057837A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome

```


FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000 05 17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Protolent version 1.0
 SEQ ID NO: 481
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURES:
 OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 83-92 and may interact with
 OTHER INFORMATION: Sequence 481 in this patent

Query Match 36.4% Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 TGRK 9
 L I I
 LB 6 TGRK 9

RESULT 15
 US-09-572-404B-483
 Sequence 483, Application: US/09/572,404B
 Publication No. US2003007874A1

GENERAL INFORMATION:
 APPLICANT: Proteom Ltd
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000 05 17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Protolent version 1.0
 SEQ ID NO: 483
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURES:
 OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 83-92 and may interact with
 OTHER INFORMATION: Sequence 484 in this patent

Query Match 36.4% Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 TGRK 9
 L I I
 LB 6 TGRK 10

RESULT 16
 US-09-572-404B-484
 Sequence 484, Application: US/09/572,404B
 Publication No. US2003007874A1

GENERAL INFORMATION:
 APPLICANT: Proteom Ltd
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000 05 17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Protolent version 1.0
 SEQ ID NO: 484
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURES:
 OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 83-92 and may interact with
 OTHER INFORMATION: Sequence 484 in this patent

US-09-572-404B-489

Query Match 36.4% Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 TGRK 9
 L I I
 LB 7 TGRK 10

RESULT 17
 US-09-572-404B-405
 Sequence 405, Application: US/09/572,404B
 Publication No. US2003007874A1

GENERAL INFORMATION:
 APPLICANT: Proteom Ltd
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000 05 17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Protolent version 1.0
 SEQ ID NO: 405
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURES:
 OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 83-92 and may interact with
 OTHER INFORMATION: Sequence 406 in this patent

Query Match 36.4% Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 TGRK 9
 L I I
 LB 6 TGRK 9

RESULT 18
 US-09-572-404B-411
 Sequence 411, Application: US/09/572,404B
 Publication No. US2003007874A1

GENERAL INFORMATION:
 APPLICANT: Proteom Ltd
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000 05 17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Protolent version 1.0
 SEQ ID NO: 411
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURES:
 OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 87-96 and may interact with
 OTHER INFORMATION: Sequence 412 in this patent

Query Match 36.4% Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 6 TGRK 9
 L I I
 LB 6 TGRK 5

RESULT 19
 US-09-572-404B-588
 Sequence 588, Application: US/09/572,404B

```

: Publication No.: US2003078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide arrays from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572,404B
: PRIORITY FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 388
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: Sequence located in US/09/572,404B and may interact with Sequence
: US-09-572-404B-588
:
: Query Match: 36.4%; Score 4; DB 11; Length 10;
: Best Local Similarity: 100.0%; Pred. No. 6, 1e+02;
: Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 5 KRRR 8
: LE 1
: 1 KRRR 4
:
: RESULT 20
: US-09-572-404B-2156
: Sequence 2156; Application US/09/572,404B
: Publication No.: US2003078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide arrays from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572,404B
: PRIORITY FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 2156
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: Sequence located in US/09/572,404B and may interact with Sequence 2
: US-09-572-404B-2156
:
: Query Match: 36.4%; Score 4; DB 11; Length 10;
: Best Local Similarity: 100.0%; Pred. No. 6, 1e+02;
: Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 7 GRRP 10
: LE 1 GRRP 4
:
: RESULT 21
: US-09-572-404B-2904
: Sequence 2904; Application US/09/572,404B
: Publication No.: US2003078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide arrays from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572,404B
: PRIORITY FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 2904
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: Sequence located in US/09/572,404B and may interact with Sequence 2
: US-09-572-404B-2156
:
: Query Match: 36.4%; Score 4; DB 11; Length 10;
: Best Local Similarity: 100.0%; Pred. No. 6, 1e+02;
: Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 7 GRRP 10
: LE 1 GRRP 4
:
: RESULT 22
: US-09-572-270A-655
: Sequence 655; Application US/09/572,270A
: Publication No.: US2003078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Inter-complementary peptide listing
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/09/572,270A
: PRIORITY FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 1144
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 655
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Arabidopsis Thaliana
: FEATURE:
: OTHER INFORMATION: Sequence located in GSA1. at 47-56 and may interact with
: US-09-572-270A-655
:
: Query Match: 36.4%; Score 4; DB 12; Length 10;
: Best Local Similarity: 100.0%; Pred. No. 6, 1e+02;
: Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 8 RRRR 11
: LE 6 RRRR 9
:
: RESULT 23
: US-09-802-109-7
: Sequence 7; Application US/09/802109-7
: Patent No.: US2002005611A1
: GENERAL INFORMATION:
: APPLICANT: Steico, Steico
: TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
: FILE REFERENCE: 601,1983
: CURRENT APPLICATION NUMBER: US/09/802,109
: PRIORITY FILING DATE: 2002-04-08
: PRIORITY FILING DATE: 1998-03-19
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentL: Ver. 2.0
: SEQ ID NO 7
: LENGTH: 11
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus type 1
: FEATURE:
: OTHER INFORMATION: Same as Sequence ID 2, but with a substitution of
: OTHER INFORMATION: Gln to Pro.
: NAME/KEY: BINDING
: LOCATION: (10)
: OTHER INFORMATION: Cys(biotin)
: OTHER INFORMATION: Peptide has an N-terminal acetyl group.
: OTHER INFORMATION: Peptide has a C-terminal amide group.
: US-09-802-109-7
:
: Query Match: 36.4%; Score 4; DB 9; Length 11;
: Best Local Similarity: 100.0%; Pred. No. 6, 6e+02;
: Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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: FEATURE:
: OTHER INFORMATION: Sequence located in MK167 at 2835-2844 and may interact with
: US-09-572-404B-2904
:
: Query Match: 36.4%; Score 4; DB 11; Length 10;
: Best Local Similarity: 100.0%; Pred. No. 6, 1e+02;
: Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 6 RRRR 11
: LE 6 RRRR 9
:
: RESULT 24
: US-09-572-270A-655
: Sequence 655; Application US/09/572,270A
: Publication No.: US2003078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Inter-complementary peptide listing
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/09/572,270A
: PRIORITY FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 1144
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 655
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Arabidopsis Thaliana
: FEATURE:
: OTHER INFORMATION: Sequence located in GSA1. at 47-56 and may interact with
: US-09-572-270A-655
:
: Query Match: 36.4%; Score 4; DB 12; Length 10;
: Best Local Similarity: 100.0%; Pred. No. 6, 1e+02;
: Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY 8 RRRR 11
: LE 6 RRRR 9
:
: RESULT 25
: US-09-802-109-7
: Sequence 7; Application US/09/802109-7
: Patent No.: US2002005611A1
: GENERAL INFORMATION:
: APPLICANT: Steico, Steico
: TITLE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
: FILE REFERENCE: 601,1983
: CURRENT APPLICATION NUMBER: US/09/802,109
: PRIORITY FILING DATE: 2002-04-08
: PRIORITY FILING DATE: 1998-03-19
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentL: Ver. 2.0
: SEQ ID NO 7
: LENGTH: 11
: TYPE: PRT
: ORGANISM: Human immunodeficiency virus type 1
: FEATURE:
: OTHER INFORMATION: Same as Sequence ID 2, but with a substitution of
: OTHER INFORMATION: Gln to Pro.
: NAME/KEY: BINDING
: LOCATION: (10)
: OTHER INFORMATION: Cys(biotin)
: OTHER INFORMATION: Peptide has an N-terminal acetyl group.
: OTHER INFORMATION: Peptide has a C-terminal amide group.
: US-09-802-109-7
:
: Query Match: 36.4%; Score 4; DB 9; Length 11;
: Best Local Similarity: 100.0%; Pred. No. 6, 6e+02;
: Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 8 RRRR 11
1111
1B 4 RRRR 7

RESULT 24

US 09-775-052-55

Sequence 29, Application US/775-052

Publication No. US2004054003A1

GENERAL INFORMATION

APPLICANT: Dowdy, Steven F.

TITLE OF INVENTION: ANTI-CALCIUM SYSTEM AND METHOD OF USE THEREOF

FILE REFERENCE: 4388/1742

CURRENT APPLICATION NUMBER: US/29/775-052

PRIOR FILING DATE: 2001-02-01

PRIOR APPLICATION NUMBER: 09/235,966

PRIOR FILING DATE: 1998-12-10

PRIOR APPLICATION NUMBER: 62/082,462

PRIOR FILING DATE: 1998-04-25

PRIOR APPLICATION NUMBER: 63/059,012

PRIOR FILING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO: 55

LENGTH: 11

TYPE: PRI

ORGANISM: Human

US 09-775-052-55

Query Match 46.4% Score 4: 63.000; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RRRR 11
1111
1B 6 RRRR 9

RESULT 25

US 09-775-052-57

Sequence 57, Application US/775-052

Publication No. US2004054003A1

GENERAL INFORMATION

APPLICANT: Dowdy, Steven F.

TITLE OF INVENTION: ANTI-CALCIUM SYSTEM AND METHOD OF USE THEREOF

FILE REFERENCE: 4388/1742

CURRENT APPLICATION NUMBER: US/29/775-052

PRIOR FILING DATE: 2001-02-01

PRIOR APPLICATION NUMBER: 09/235,966

PRIOR FILING DATE: 1998-12-10

PRIOR APPLICATION NUMBER: 62/082,462

PRIOR FILING DATE: 1998-04-25

PRIOR APPLICATION NUMBER: 63/059,012

PRIOR FILING DATE: 1997-12-10

NUMBER OF SEQ ID NOS: 57

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO: 57

LENGTH: 11

TYPE: PRI

ORGANISM: Human

US 09-775-052-57

Query Match 46.4% Score 4: 63.000; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RRRR 11
1111
1B 6 RRRR 9

RESULT 26

US 10-116-212-29

Sequence 29, Application US/10116212

Publication No. US2004053844A1

GENERAL INFORMATION

APPLICANT: Hommonds, Brian A.

TITLE OF INVENTION: Calcium Regulated Kinase

FILE REFERENCE: 00113

CURRENT APPLICATION NUMBER: US/10/116,212

PRIOR FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: 09/09/116,062

PRIOR FILING DATE: 1998-09-12

PRIOR APPLICATION NUMBER: GB 97/1399,8

PRIOR FILING DATE: 1997-08-12

PRIOR APPLICATION NUMBER: GB 97/7497,9

PRIOR FILING DATE: 1998-08-19

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO: 29

LENGTH: 11

TYPE: PRI

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
OTHER INFORMATION: Internal peptide

US 10-116-212-29

Query Match 46.4% Score 4: 68.12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKKG 7
1111
1B 4 KKKG 7

RESULT 27

US 10-116-796-29

Sequence 29, Application US/10116795

Publication No. US2004053844A1

GENERAL INFORMATION

APPLICANT: Hommonds, Brian A.

TITLE OF INVENTION: Calcium Regulated Kinase

FILE REFERENCE: 00113

CURRENT APPLICATION NUMBER: US/10/106,795

PRIOR FILING DATE: 2002-11-28

PRIOR APPLICATION NUMBER: 09/733,062

PRIOR FILING DATE: 1998-08-14

PRIOR APPLICATION NUMBER: GB 97/749,8

PRIOR FILING DATE: 1997-06-12

PRIOR APPLICATION NUMBER: GB 97/749,9

PRIOR FILING DATE: 1998-08-19

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO: 29

LENGTH: 11

TYPE: PRI

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
OTHER INFORMATION: Internal peptide

US 10-116-796-29

Query Match 46.4% Score 4: 68.12; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKKG 7
1111
1B 4 KKKG 7

```

RESULT 29
US 10 172 425b 1
: Sequence 29, Application US/10/172 425b
: Publication No. US20020147906A1
: GENERAL INFORMATION:
: APPLICANT: Kacemter, Raymond
: TITLE OF INVENTION: Calcium Modulator Kinases
: PRIOR FILING DATE: 1998-09-10
: CURRENT APPLICATION NUMBER: US/10/172 425b
: PRIOR FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-08-12
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-08-14
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 29
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: Description of Applicant's Sequence
US 10 172 425b 1
Query Match: 36.4%, Score 41, DP 12, Length 12;
Best Local Similarity: 100.0%, Pred. No. 70-02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 INKK 1
DB 1 INKK 1

RESULT 30
US 10 172 425b 1
: Sequence 30, Application US/10/172 425b
: Publication No. US20020147906A1
: GENERAL INFORMATION:
: APPLICANT: Kacemter, Raymond
: TITLE OF INVENTION: Calcium Modulator Kinases
: PRIOR FILING DATE: 1998-09-10
: CURRENT APPLICATION NUMBER: US/10/172 425b
: PRIOR FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-08-12
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-08-14
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 30
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Homo Sapiens
US 10 172 425b 1
Query Match: 36.4%, Score 41, DP 12, Length 12;
Best Local Similarity: 100.0%, Pred. No. 70-02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 ATK 4
DB 2 ATK 5

RESULT 31
US 10 172 425b 1
: Sequence 31, Application US/10/172 425b
: Publication No. US20020147906A1
: GENERAL INFORMATION:
: APPLICANT: Kacemter, Raymond
: TITLE OF INVENTION: Calcium Modulator Kinases
: PRIOR FILING DATE: 1998-09-10
: CURRENT APPLICATION NUMBER: US/10/172 425b
: PRIOR FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-08-12
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-08-14
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 31
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Homo Sapiens
US 10 172 425b 1
Query Match: 36.4%, Score 41, DP 12, Length 12;
Best Local Similarity: 100.0%, Pred. No. 70-02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 ATK 4
DB 2 ATK 5

RESULT 32
US 10 172 425b 1
: Sequence 32, Application US/10/172 425b
: Publication No. US20020147906A1
: GENERAL INFORMATION:
: APPLICANT: Kacemter, Raymond
: TITLE OF INVENTION: Calcium Modulator Kinases
: PRIOR FILING DATE: 1998-09-10
: CURRENT APPLICATION NUMBER: US/10/172 425b
: PRIOR FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-08-12
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-08-14
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 32
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Homo Sapiens
US 10 172 425b 1
Query Match: 36.4%, Score 41, DP 12, Length 12;
Best Local Similarity: 100.0%, Pred. No. 70-02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 ATK 4
DB 2 ATK 5

RESULT 33
US 10 172 425b 1
: Sequence 33, Application US/10/172 425b
: Publication No. US20020147906A1
: GENERAL INFORMATION:
: APPLICANT: Kacemter, Raymond
: TITLE OF INVENTION: Calcium Modulator Kinases
: PRIOR FILING DATE: 1998-09-10
: CURRENT APPLICATION NUMBER: US/10/172 425b
: PRIOR FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-08-12
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-08-14
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 33
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Homo Sapiens
US 10 172 425b 1
Query Match: 36.4%, Score 41, DP 12, Length 12;
Best Local Similarity: 100.0%, Pred. No. 70-02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 ATK 4
DB 2 ATK 5

RESULT 34
US 10 172 425b 1
: Sequence 34, Application US/10/172 425b
: Publication No. US20020147906A1
: GENERAL INFORMATION:
: APPLICANT: Kacemter, Raymond
: TITLE OF INVENTION: Calcium Modulator Kinases
: PRIOR FILING DATE: 1998-09-10
: CURRENT APPLICATION NUMBER: US/10/172 425b
: PRIOR FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-08-12
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-08-14
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 34
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Homo Sapiens
US 10 172 425b 1
Query Match: 36.4%, Score 41, DP 12, Length 12;
Best Local Similarity: 100.0%, Pred. No. 70-02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 ATK 4
DB 2 ATK 5

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: APPLICANT: Acad. Gila
: TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
: FILE REFERENCE: A31967-PCT USA A A 066041 0164
: CURRENT APPLICATION NUMBER: US/10/172 425b
: CURRENT FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-09-10
: PRIOR APPLICATION NUMBER: PCT/IL97/00438
: PRIOR FILING DATE: 1997-12-30
: PRIOR APPLICATION NUMBER: ISRAEL 119938
: PRIOR FILING DATE: 1996-12-30
: NUMBER OF SEQ ID NOS: 57
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 1
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Streptococcus aureus
US 10 172 425b 1
Query Match: 36.4%, Score 41, DP 12, Length 12;
Best Local Similarity: 100.0%, Pred. No. 70-02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 2 INKK 5
DB 1 INKK 4

RESULT 41
US 10 172 425b 1
: Sequence 41, Application US/10/172 425b
: Publication No. US20020147906A1
: GENERAL INFORMATION:
: APPLICANT: Kacemter, Raymond
: TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
: FILE REFERENCE: A31967-PCT USA A A 066041 0164
: CURRENT APPLICATION NUMBER: US/10/172 425b
: CURRENT FILING DATE: 2002-06-14
: PRIOR APPLICATION NUMBER: US/09/12 458
: PRIOR FILING DATE: 1998-09-10
: PRIOR APPLICATION NUMBER: PCT/IL97/00438
: PRIOR FILING DATE: 1997-12-30
: PRIOR APPLICATION NUMBER: ISRAEL 119938
: PRIOR FILING DATE: 1996-12-30
: NUMBER OF SEQ ID NOS: 57
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO: 41
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Streptococcus aureus
US 10 172 425b 1
Query Match: 36.4%, Score 41, DP 12, Length 12;
Best Local Similarity: 100.0%, Pred. No. 70-02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 2 INKK 5
DB 1 INKK 4

RESULT 42
US 10 172 425b 1
: Sequence 42, Application US/10/172 425b
: Publication No. US20020147906A1
: GENERAL INFORMATION:
: APPLICANT: Kacemter, Raymond
: TITLE OF INVENTION: Constitutively Active, Hypersensitive,
: TITLE OF INVENTION: and No. US20020147906A1 Receptors as No. US200201

```

FILE REFERENCE: 00398/510002
 CURRENT APPLICATION NUMBER: US/10/011,645
 PRIOR FILING DATE: 2001-10-26
 PRIOR APPLICATION NUMBER: US 63/243,563
 PRIOR FILING DATE: 2000-10-26
 NUMBER OF SEQ ID NOS: 87
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 41
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-787-443-9

Query Match 66.4% Score 4 DB 14 Length 12
 Best Local Similarity 100.0% Prod. No. 787-443-9
 Matches 4 Conservative 0 Mismatches 0 Gaps 0

QY 1 AINX 4
 DB 2 AINX 5

RESULT 33
 US-09-787-443-9
 Sequence 1: Application US/10/011,645
 Patent No. US2002077574A
 GENERAL INFORMATION:
 APPLICANT: Masckel, Hans, E.
 TITLE OF INVENTION: EXOTOXIN
 FILE REFERENCE: MHP-011XX
 CURRENT APPLICATION NUMBER: US/10/011,645
 PRIOR FILING DATE: 2002-03-29
 PRIOR APPLICATION NUMBER: US 63/243,563
 PRIOR FILING DATE: 2001-10-26
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Bacterially Expressed Toxin

Query Match 66.4% Score 4 DB 14 Length 12
 Best Local Similarity 100.0% Prod. No. 787-443-9
 Matches 4 Conservative 0 Mismatches 0 Gaps 0

QY 2 AINX 5
 DB 3 AINX 4

RESULT 44
 US-10-114-809-2
 Sequence 2: Application US/10/011,645
 Patent No. US2002077574A
 GENERAL INFORMATION:
 APPLICANT: Masckel, Hans, E.
 TITLE OF INVENTION: EXOTOXIN
 FILE REFERENCE: MHP-011XX
 CURRENT APPLICATION NUMBER: US/10/011,645
 PRIOR FILING DATE: 2002-03-29
 PRIOR APPLICATION NUMBER: US 63/243,563
 PRIOR FILING DATE: 2001-10-26
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Bacterially Expressed Toxin

US-10-114-809-2

Query Match 66.4% Score 4 DB 14 Length 12
 Best Local Similarity 100.0% Prod. No. 787-443-9
 Matches 4 Conservative 0 Mismatches 0 Gaps 0

QY 2 AINX 5
 DB 3 AINX 4

RESULT 45
 US-10-114-809-2
 Sequence 4: Application US/10/011,645
 Patent No. US2002077574A
 GENERAL INFORMATION:
 APPLICANT: Masckel, Hans, E.
 TITLE OF INVENTION: Exotoxin
 FILE REFERENCE: MHP-011XX
 CURRENT APPLICATION NUMBER: US/10/011,645
 PRIOR FILING DATE: 2002-03-29
 PRIOR APPLICATION NUMBER: US 63/243,563
 PRIOR FILING DATE: 2001-10-26
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-114-809-2

Query Match 66.4% Score 4 DB 15 Length 12
 Best Local Similarity 100.0% Prod. No. 787-443-9
 Matches 4 Conservative 0 Mismatches 0 Gaps 0

QY 1 AINX 4
 DB 2 AINX 5

RESULT 46
 US-09-150-947R-5
 Sequence 5: Application US/09/050,947R
 Patent No. US200202211A1
 GENERAL INFORMATION:
 APPLICANT: Kacper, Raymond
 TITLE OF INVENTION: 199-AD SPECIFIC PYROGENIC EXOTOXINS
 FILE REFERENCE: A1997 PCT/US/94/047R
 CURRENT APPLICATION NUMBER: US/09/050,947R
 PRIOR FILING DATE: 1998-09-15
 PRIOR APPLICATION NUMBER: PCT/IL97/00438
 PRIOR FILING DATE: 1997-12-30
 PRIOR APPLICATION NUMBER: ISRAEL 119538
 PRIOR FILING DATE: 1996-12-30
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 5
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 FEATURE:
 NAME/KEY: LIP10
 LOCATION: (1)-(11)
 OTHER INFORMATION: N-larryl cysteine residue
 US-09-150-947R-5

Query Match 66.4% Score 4 DB 9 Length 13
 Best Local Similarity 100.0% Prod. No. 787-443-9
 Matches 4 Conservative 0 Mismatches 0 Gaps 0

QY 2 INKK 5
1-11
DB 2 INKK 5

RESULT 47
US-10-120-604-59
Sequence 59, Application US/10120604
Publication No. US2003096347A1
GENERAL INFORMATION:
APPLICANT: Bristol Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G PROTEIN COUPLED R
FILE REFERENCE: A31957-PCT/US/A 01/0154
CURRENT APPLICATION NUMBER: US/10-120-604
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: 09/750,947
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/IL/97/00146
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119948
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 13
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE
NAME/KEY: LTPID
LOCATION: (1)...(1)
OTHER INFORMATION: N lauryl cysteine desulfase
US-10-172-425B 5

Query Match 36.4% Score 4; BB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 INKK 5
1-11
DB 2 INKK 5

RESULT 48
US-10-159-224-25
Sequence 25, Application US/10159224
Publication No. US20030152946A1
GENERAL INFORMATION:
APPLICANT: SUMITOMO, Shigeomi
TITLE OF INVENTION: BR4-fused polypeptide
FILE REFERENCE: 1422-05170
CURRENT APPLICATION NUMBER: US/10-159-224
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: JP 11-471449
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: PCT/JP99/09254
PRIOR FILING DATE: 2000-12-26
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 4.1
SEQ ID NO 25
LENGTH: 13
TYPE: PRT
ORGANISM: Human T lymphocyte virus
US-10-159-224 25

Query Match 36.4% Score 4; BB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 INKK 9
1-11

DB 4 INKK 7
1-11

RESULT 49
US-10-120-604-59
Sequence 59, Application US/10120604
Publication No. US2003096347A1
GENERAL INFORMATION:
APPLICANT: Bristol Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G PROTEIN COUPLED R
FILE REFERENCE: A31957-PCT/US/A 01/0154
CURRENT APPLICATION NUMBER: US/10-120-604
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 60/283,145
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/283,161
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/288,468
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 60/300,619
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn version 4.0
SEQ ID NO 59
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-120-604 59

Query Match 36.4% Score 4; BB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 INKK 9
1-11
DB 6 INKK 9

RESULT 40
US-10-120-604-78
Sequence 78, Application US/10120604
Publication No. US2003096347A1
GENERAL INFORMATION:
APPLICANT: Bristol Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING TWO NOVEL HUMAN G PROTEIN COUPLED R
FILE REFERENCE: 7034387
CURRENT APPLICATION NUMBER: US/10-120-604
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US 60/283,145
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/283,161
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/288,468
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 60/300,619
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn version 4.0
SEQ ID NO 78
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-120-604-78

Query Match 36.4% Score 4; BB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 INKK 9
1-11

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DB:          6 10KK 5

RESULT 41
US-10-172-425B-22
Sequence 22: Application: US/0172425B
Publication No.: US2003014790A1
GENERAL INFORMATION:
APPLICANT: Kadner, Raymond
TITLE OF INVENTION: BROAD SPECTRUM ANTIAGENTS AND VACCINES
FILE REFERENCE: A1967-PCT-USA-A-066041.0164
CURRENT APPLICATION NUMBER: US/0172425B
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: PCT/1197/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119948
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 14
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-09-787-770A-22

Query Match
Best Local Similarity: 100.0% Score 41 DB 12 Length 14
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 10KK 5
DB 3 10KK 6

RESULT 42
US-10-172-425B-26
Sequence 26: Application: US/0172425B
Publication No.: US2003014790A1
GENERAL INFORMATION:
APPLICANT: Kadner, Raymond
TITLE OF INVENTION: BROAD SPECTRUM ANTIAGENTS AND VACCINES
FILE REFERENCE: A1967-PCT-USA-A-066041.0164
CURRENT APPLICATION NUMBER: US/0172425B
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: PCT/1197/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119948
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 14
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-10-172-425B-26

Query Match
Best Local Similarity: 100.0% Score 41 DB 12 Length 14
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 10KK 5
DB 3 10KK 6

RESULT 43
US-10-172-425B-27
Sequence 27: Application: US/0172425B
Publication No.: US2003014790A1
GENERAL INFORMATION:
APPLICANT: Kadner, Raymond
TITLE OF INVENTION: BROAD SPECTRUM ANTIAGENTS AND VACCINES
FILE REFERENCE: A1967-PCT-USA-A-066041.0164
CURRENT APPLICATION NUMBER: US/0172425B
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: PCT/1197/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119948
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 14
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-10-172-425B-27

Query Match
Best Local Similarity: 100.0% Score 41 DB 12 Length 14
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 10KK 5
DB 3 10KK 6

RESULT 44
US-10-172-425B-35
Sequence 35: Application: US/0172425B
Publication No.: US2003014790A1
GENERAL INFORMATION:
APPLICANT: Kadner, Raymond
TITLE OF INVENTION: BROAD SPECTRUM ANTIAGENTS AND VACCINES
FILE REFERENCE: A1967-PCT-USA-A-066041.0164
CURRENT APPLICATION NUMBER: US/0172425B
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: PCT/1197/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119948
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 14
TYPE: PRT
ORGANISM: Streptococcus aureus
US-10-172-425B-35

Query Match
Best Local Similarity: 100.0% Score 41 DB 12 Length 14
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 2 10KK 5
DB 3 10KK 6

RESULT 45
US-10-172-425B-36
Sequence 36: Application: US/0172425B
Publication No.: US2003014790A1
GENERAL INFORMATION:

```

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1 APPLICANT: Kaempfer, Raymond
2 APPLICANT: Arad, Gila
3 TITLE OF INVENTION: BROAD SPECTRUM ANTIAGONISTS AND VACCINES
4 TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
5 FILE REFERENCE: A31967-PCT-USA-A 066031.0164
6 CURRENT APPLICATION NUMBER: US/10/172.425B
7 CURRENT FILING DATE: 2002-06-13
8 PRIOR APPLICATION NUMBER: PCT/1597/00438
9 PRIOR FILING DATE: 1997-09-10
10 PRIOR FILING DATE: 1997-09-10
11 PRIOR FILING DATE: 1997-12-30
12 PRIOR FILING DATE: 1997-12-30
13 PRIOR FILING DATE: 1997-12-30
14 NUMBER OF SEQ ID NOS: 57
15 SOFTWARE: FASTSEQ for Windows Version 4.0
16 SEQ ID NO: 4
17 LENGTH: 14
18 TYPE: PRT
19 ORGANISM: Staphylococcus aureus
20 US 10-172-425B-45

Query Match 36.4% Score 41 DB 12: Length 14:
Best Local Similarity 100.0% Pred. No. 7.9e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

SY 2 INKK 5
ID 3 INKK 6

RESULT 46
US-10-172-425B-45
1 Sequence 45: Application US/10172425B
2 Publication No. US20030147908A1
3 GENERAL INFORMATION:
4 APPLICANT: Kaempfer, Raymond
5 APPLICANT: Arad, Gila
6 TITLE OF INVENTION: BROAD SPECTRUM ANTIAGONISTS AND VACCINES
7 TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
8 FILE REFERENCE: A31967-PCT-USA-A 066031.0164
9 CURRENT APPLICATION NUMBER: US/10/172.425B
10 CURRENT FILING DATE: 2002-06-13
11 PRIOR APPLICATION NUMBER: PCT/1597/00438
12 PRIOR FILING DATE: 1997-09-10
13 PRIOR FILING DATE: 1997-12-30
14 PRIOR FILING DATE: 1997-12-30
15 NUMBER OF SEQ ID NOS: 57
16 SOFTWARE: FASTSEQ for Windows Version 4.0
17 SEQ ID NO: 4
18 LENGTH: 14
19 TYPE: PRT
20 ORGANISM: Staphylococcus aureus
21 US 10-172-425B-41

Query Match 36.4% Score 41 DB 12: Length 14:
Best Local Similarity 100.0% Pred. No. 7.9e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

SY 2 INKK 5
ID 3 INKK 6

RESULT 47
US-10-172-425B-41
1 Sequence 44: Application US/10172425B
2 Publication No. US20030147908A1
3 GENERAL INFORMATION:
4 APPLICANT: Kaempfer, Raymond
5 APPLICANT: Arad, Gila
6 TITLE OF INVENTION: BROAD SPECTRUM ANTIAGONISTS AND VACCINES

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1 TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
2 FILE REFERENCE: A31967-PCT-USA-A 066031.0164
3 CURRENT APPLICATION NUMBER: US/10/172.425B
4 CURRENT FILING DATE: 2002-06-13
5 PRIOR APPLICATION NUMBER: PCT/1597/00438
6 PRIOR FILING DATE: 1997-09-10
7 PRIOR APPLICATION NUMBER: PCT/1597/00438
8 PRIOR FILING DATE: 1997-12-30
9 PRIOR APPLICATION NUMBER: ISRAEL 114938
10 PRIOR FILING DATE: 1996-12-30
11 NUMBER OF SEQ ID NOS: 57
12 SOFTWARE: FASTSEQ for Windows Version 4.0
13 SEQ ID NO: 4
14 LENGTH: 14
15 TYPE: PRT
16 ORGANISM: Staphylococcus aureus
17 US-10-172-425B-43

Query Match 36.4% Score 41 DB 12: Length 14:
Best Local Similarity 100.0% Pred. No. 7.9e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

SY 2 INKK 5
ID 3 INKK 6

RESULT 48
US-10-172-425B-43
1 Sequence 45: Application US/10172425B
2 Publication No. US20030147908A1
3 GENERAL INFORMATION:
4 APPLICANT: Kaempfer, Raymond
5 APPLICANT: Arad, Gila
6 TITLE OF INVENTION: BROAD SPECTRUM ANTIAGONISTS AND VACCINES
7 TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
8 FILE REFERENCE: A31967-PCT-USA-A 066031.0164
9 CURRENT APPLICATION NUMBER: US/10/172.425B
10 CURRENT FILING DATE: 2002-06-13
11 PRIOR APPLICATION NUMBER: PCT/1597/00438
12 PRIOR FILING DATE: 1997-09-10
13 PRIOR APPLICATION NUMBER: PCT/1597/00438
14 PRIOR FILING DATE: 1997-12-30
15 PRIOR APPLICATION NUMBER: ISRAEL 114938
16 PRIOR FILING DATE: 1996-12-30
17 NUMBER OF SEQ ID NOS: 57
18 SOFTWARE: FASTSEQ for Windows Version 4.0
19 SEQ ID NO: 4
20 LENGTH: 14
21 TYPE: PRT
22 ORGANISM: Staphylococcus aureus
23 US 10-172-425B-45

Query Match 36.4% Score 41 DB 12: Length 14:
Best Local Similarity 100.0% Pred. No. 7.9e-02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

SY 2 INKK 5
ID 3 INKK 6

RESULT 49
US-10-172-425B-48
1 Sequence 45: Application US/10172425B
2 Publication No. US20030147908A1
3 GENERAL INFORMATION:
4 APPLICANT: Kaempfer, Raymond
5 APPLICANT: Arad, Gila
6 TITLE OF INVENTION: BROAD SPECTRUM ANTIAGONISTS AND VACCINES
7 TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
8 FILE REFERENCE: A31967-PCT-USA-A 066031.0164
9 CURRENT APPLICATION NUMBER: US/10/172.425B

```



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1 CURRENT FILING DATE: 2002-09-12
2 PRIOR APPLICATION NUMBER: 09/150,047
3 PRIOR FILING DATE: 1998-09-16
4 PRIOR APPLICATION NUMBER: 07/117,004
5 PRIOR FILING DATE: 1997-12-30
6 PRIOR APPLICATION NUMBER: ISRAEL 1,998,000
7 PRIOR FILING DATE: 1996-12-30
8 NUMBER OF SEQ ID NOS: 07
9 SOFTWARE: FASTSEQ for Windows Version 1.4
10 SEQ ID NO: 49
11 LENGTH: 14
12 TYPE: CDS
13 ORGANISM: Staphylococcus aureus
14 US 10,172,425B 48

Query Match
Best Local Similarity: 100.00% Positives: 100.00%
Matches: 43 Conservative: 43 Divergent: 00

      2 18KK 5
      1
      3 18KK 5

Result: 1
US 10,172,425B 50
1 Sequence No: Application: US/117,004
2 Publication No: US2003/147,064A1
3 GENERAL INFORMATION:
4 APPLICANT: Kometec, Rayco Ltd
5 APPLICANT: Avram, Gila
6 TITLE OF INVENTION: BROAD SPECTRUM ANTIMICROBIAL COMPOSITION
7 TITLE OF INVENTION: DIRECTED AGAINST PNEUMONIA FOR PREVENTION
8 DATE REFERENCE: A1967-01-25A & 01-25B
9 CURRENT APPLICATION NUMBER: US/07/117,004
10 PRIOR FILING DATE: 2002-09-13
11 PRIOR APPLICATION NUMBER: 09/150,047
12 PRIOR FILING DATE: 1996-09-16
13 PRIOR APPLICATION NUMBER: 07/117,004
14 PRIOR FILING DATE: 1997-12-30
15 PRIOR APPLICATION NUMBER: ISRAEL 1,998,000
16 PRIOR FILING DATE: 1996-12-30
17 NUMBER OF SEQ ID NOS: 07
18 SOFTWARE: FASTSEQ for Windows Version 1.4
19 SEQ ID NO: 49
20 LENGTH: 14
21 TYPE: CDS
22 ORGANISM: Staphylococcus aureus
23 US 10,172,425B 50

Query Match
Best Local Similarity: 100.00% Positives: 100.00%
Matches: 43 Conservative: 43 Divergent: 00

      2 18KK 5
      1
      3 18KK 5

Search Completed: September 30, 2003 11:07:18
Job File: 2003-09-30
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493	3	27.3	3	27.3	466	3	27.3	9	4	US 09-319-417-6	Sequence 6, Appli
494	3	27.3	3	27.3	467	3	27.3	9	4	US 09-319-417-7	Sequence 7, Appli
495	3	27.3	3	27.3	468	3	27.3	9	4	US 09-025-596-109	Sequence 109, App
496	3	27.3	3	27.3	469	3	27.3	9	4	US 09-227-157-660	Sequence 160, App
497	3	27.3	3	27.3	470	3	27.3	9	4	US 08-637-654-132	Sequence 132, App
498	3	27.3	3	27.3	471	3	27.3	9	4	US 09-187-859-210	Sequence 210, App
499	3	27.3	3	27.3	472	3	27.3	9	4	US 09-187-859-280	Sequence 280, App
500	3	27.3	3	27.3	473	3	27.3	9	4	US 09-187-859-308	Sequence 308, App
401	3	27.3	3	27.3	474	3	27.3	9	4	US 09-187-859-403	Sequence 403, App
402	3	27.3	3	27.3	475	3	27.3	9	4	US 09-187-859-431	Sequence 431, App
403	3	27.3	3	27.3	476	3	27.3	9	4	US 09-187-859-473	Sequence 473, App
404	3	27.3	3	27.3	477	3	27.3	9	4	US 09-187-859-503	Sequence 503, App
405	3	27.3	3	27.3	478	3	27.3	9	4	US 09-187-859-1381	Sequence 1381, App
406	3	27.3	3	27.3	479	3	27.3	9	4	US 09-187-859-1411	Sequence 1411, App
407	3	27.3	3	27.3	480	3	27.3	9	4	US 09-187-859-1456	Sequence 1456, App
408	3	27.3	3	27.3	481	3	27.3	9	4	US 09-187-859-1486	Sequence 1486, App
409	3	27.3	3	27.3	482	3	27.3	9	4	US 09-187-859-1531	Sequence 1531, App
410	3	27.3	3	27.3	483	3	27.3	9	4	US 09-187-859-1576	Sequence 1576, App
411	3	27.3	3	27.3	484	3	27.3	9	4	US 09-187-859-1805	Sequence 1805, App
412	3	27.3	3	27.3	485	3	27.3	9	4	US 09-187-859-1820	Sequence 1820, App
413	3	27.3	3	27.3	486	3	27.3	9	4	US 09-187-859-1835	Sequence 1835, App
414	3	27.3	3	27.3	487	3	27.3	9	4	US 09-187-859-1850	Sequence 1850, App
415	3	27.3	3	27.3	488	3	27.3	9	4	US 09-187-859-1865	Sequence 1865, App
416	3	27.3	3	27.3	489	3	27.3	9	4	US 09-187-859-1883	Sequence 1883, App
417	3	27.3	3	27.3	490	3	27.3	9	4	US 09-187-859-1951	Sequence 1951, App
418	3	27.3	3	27.3	491	3	27.3	9	4	US 09-187-859-1978	Sequence 1978, App
419	3	27.3	3	27.3	492	3	27.3	9	4	US 09-187-859-2002	Sequence 2002, App
420	3	27.3	3	27.3	493	3	27.3	9	4	US 09-187-859-2028	Sequence 2028, App
421	3	27.3	3	27.3	494	3	27.3	9	4	US 09-187-859-2052	Sequence 2052, App
422	3	27.3	3	27.3	495	3	27.3	9	4	US 09-187-859-2081	Sequence 2081, App
423	3	27.3	3	27.3	496	3	27.3	9	4	US 09-187-859-2326	Sequence 2326, App
424	3	27.3	3	27.3	497	3	27.3	9	4	US 09-187-859-2386	Sequence 2386, App
425	3	27.3	3	27.3	498	3	27.3	9	4	US 09-187-859-2446	Sequence 2446, App
426	3	27.3	3	27.3	499	3	27.3	9	4	US 09-187-859-2506	Sequence 2506, App
427	3	27.3	3	27.3	500	3	27.3	9	5	PCT-US95/00147-40	Sequence 40, Appli
428	3	27.3	3	27.3							
429	3	27.3	3	27.3							
430	3	27.3	3	27.3							
431	3	27.3	3	27.3							
432	3	27.3	3	27.3							
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ALIGNMENTS

RESULT 1
US-09-406-809-1
Sequence 1, Application US/084,6809
Patent No. 5580789
GENERAL INFORMATION:
APPLICANT: KIHARA, YASUOHI
TITLE OF INVENTION: IMMUNOGENIC HINDING ARTIFICIAL
NUMBER OF SEQUENCES: 1
CORRESPONDENT ADDRESS:
ADDRESS: Broadway and Newark
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPILED RELEASABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: PatentLig Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08406,809
FILING DATE:
CLASSIFICATION: 547
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08409,477
FILING DATE: 24 MARCH 1993
ATTORNEY/AGENT INFORMATION:
NAME: Tarzica, John E.
REGISTRATION NUMBER: 35,138
REFERENCE/ID# KEY NUMBER: K01174 1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-747-9528
 TELEX: 248614
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 SOURCE: Synthetic single
 FEATURE: Linear
 Molecule type: Peptide
 US 58 439 809-1

Query Match 36.4% Score 4: DB 1: Length 9:
 Best Local Similarity 100.0%: Pred. No. 2.5e+05:
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 CORR 9
 11
 1 CORR 4

RESULT 4
 US 09-007 288E 149
 Sequence 149: Application US/09-007 288E
 Patent No. 6495457

GENERAL INFORMATION:

APPLICANT: Enkels, Claus
 APPLICANT: Enkels, Jens
 APPLICANT: Petersen, Dorte
 APPLICANT: Parkar, Shankar
 APPLICANT: Thelersen, Marianne
 APPLICANT: Swenden, Allan
 APPLICANT: Smith, Kim
 APPLICANT: Kretzelmar, Lutz
 APPLICANT: Backer, Torben
 APPLICANT: Vind, Jesper
 APPLICANT: Jendensen, Sten

TITLE OF INVENTION: NO. 6495457: Lipolytic Enzymes

FILE REFERENCE: 4455,434 US

CURRENT APPLICATION NUMBER: 09/007 288E

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patent version 4.1

SEQ ID NO: 149

LENGTH: 8

TYPE: 14

FEATURES: Artificial Sequence

OTHER INFORMATION: Peptide (amino acid)

US-09-007 288E 149

Query Match 36.4% Score 4: DB 1: Length 8:
 Best Local Similarity 100.0%: Pred. No. 2.5e+05:
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 GRAP 10
 10
 5 GRAP 8

RESULT 4
 US 58 439-970 17
 Sequence 17: Application US/08/78574
 Patent No. 550247

GENERAL INFORMATION:

APPLICANT: Lewis C. Cantley
 APPLICANT: Zhou Song Yang
 TITLE OF INVENTION: Substrate Specificity of Protein Kinases
 NUMBER OF SEQUENCES: 77
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD

STREET: 40 STATE STREET, Suite 510
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02109-1874
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/08/178,570
 FILING DATE: JANUARY 7, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: GONCALVES, GLOBO A., JR.
 REGISTRATION NUMBER: 41,503
 REFERENCE/DOCKET NUMBER: B01-004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 FEATURE: Linear
 Molecule type: Peptide
 Fragment type: Informal
 US 08 178-570-17

Query Match 36.4% Score 4: DB 1: Length 9:
 Best Local Similarity 100.0%: Pred. No. 2.5e+05:
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 CORR 9
 11
 4 CORR 4

RESULT 4

US 08 594 447 38

Sequence 38: Application US/08594447

Patent No. 5776716

GENERAL INFORMATION:

APPLICANT: Rod, David
 APPLICANT: Napolitano, Eugene W.
 APPLICANT: Vorobova, Anna P.
 TITLE OF INVENTION: MECHANISMS FOR IDENTIFYING AGENTS WHICH
 TITLE OF INVENTION: BLOCK THE INTERACTION OF FYN WITH PKC-THETA, AND USES
 TITLE OF INVENTION: THEREOF
 NUMBER OF SEQUENCES: 75

SOFTWARE: Patent Release #1.0, Version #1.30

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & MORRISON

STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20036 1828

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/594,447

FILING DATE: 31-JAN 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22550-20025.24

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 822-0168
 TELETYPE: 90-4030 MRSNFORWSH
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..9
 OTHER INFORMATION: /label=delta-V63
 US-08-594-447-38

Query Match 36.4%, Score 4: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4: Conservative 0: Mismatches 0: Gaps 0;

QY 4 KKG 7
 DB 5 KKG 8

RESULT 5
 US-08-541-964-47
 Sequence 37, Application US/08541964
 Patent No. 5763425

GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Dorit
 APPLICANT: Ron, Dorit
 APPLICANT: Kavar, Lawrence M
 APPLICANT: Napolitano, Eugene W
 TITLE OF INVENTION: A RAPID SCREENING METHOD FOR SELECTING
 TITLE OF INVENTION: OF SIGNAL TRANSDUCTION
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FIERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW STE. 550
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1888

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 10-02-1995
 APPLICATION NUMBER: US/08/541-964
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mulishlag, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 2250-2003-25
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-1500

TELEFAX: (202) 822-0168
 TELETYPE: 90-4030 MRSNFORWSH
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..9
 OTHER INFORMATION: /label=delta-V63
 US-08-541-964-47

Query Match 36.4%, Score 4: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4: Conservative 0: Mismatches 0: Gaps 0;
 QY 4 KKG 7
 DB 5 KKG 8
 RESULT 6
 US-08-465-647-52
 Sequence 52, Application US/08465647
 Patent No. 5935803
 GENERAL INFORMATION:
 APPLICANT: Desque2, Nicki J.
 APPLICANT: Ron, Dorit
 APPLICANT: Vozniak, Anna F
 APPLICANT: Napolitano, Eugene W
 TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS
 TITLE OF INVENTION: USING ORNATE INTERACTION OF PKC-THETA
 NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FIERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW STE. 5500
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1888

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 18 JUN 1996
 APPLICATION NUMBER: US/08/565,647
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mulishlag, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 2250-2002-25
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 822-0168
 TELETYPE: 90-4030 MRSNFORWSH
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1..9
 OTHER INFORMATION: /label=delta-V63
 US-08-465-647-52

Query Match 36.4%, Score 4: DB 2: Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4: Conservative 0: Mismatches 0: Gaps 0;
 QY 4 KKG 7
 DB 5 KKG 8
 RESULT 7
 US-08-469-643-77
 Sequence 17, Application US/08469643A
 Patent No. 6504967
 GENERAL INFORMATION:
 APPLICANT: Paulley, Lewis C.

```

APPLICANT: Sunnydial, Zhou
TITLE OF INVENTION: Substrate Specificity of Protein Kinases
FILE REFERENCE: US-0013P
CURRENT APPLICATION NUMBER: US/09/443434
CURRENT FILING DATE: 1999-06-26
PAST APPLICANT NUMBER: US 06/126,524
LATEST FILING DATE: 1994-01-17
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 17
LENGTH: 9
TYPE: 187
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: See above.
OTHER INFORMATION: Substrate based on information within the field
US 08 459-654-17

Query Match          96.4%   Score 47   DB 5: Length 9:
Best Local Similarity 100.0%   Prod. No. 2.5e+05:
Matches 4: conservative 0: Mismatches 0: Gaps 0:

Q# 4 187P 9
L# 1 187P 5

RESULT 7
US 09 443 6400 23
Sequence 23: Application US/09/443434
Patent No. 654664
APPLICANT: Sunnydial, Zhou
APPLICANT: Sunnydial, Zhou
APPLICANT: Sunnydial, Zhou
APPLICANT: Sunnydial, Zhou
APPLICANT: Sunnydial, Zhou
TITLE OF INVENTION: Method for determining Presence of Cancer in a Sample By Det
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX C
FILE REFERENCE: US-0013P
CURRENT APPLICATION NUMBER: US/09/443434
CURRENT FILING DATE: 1999-06-26
PAST APPLICANT NUMBER: US 06/126,524
LATEST FILING DATE: 1994-01-17
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 17
LENGTH: 9
TYPE: 187
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: See above.
OTHER INFORMATION: Substrate based on information within the field
US 08 459-654-17

Query Match          96.4%   Score 47   DB 4: Length 9:
Best Local Similarity 100.0%   Prod. No. 2.5e+05:
Matches 4: conservative 0: Mismatches 0: Gaps 0:

Q# 8 187P 11
L# 1 187P 5

RESULT 17
PCT US95 00147 17
Sequence 17: App. No. 09/00147
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Substrate Specificity of Protein Kinases
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COMPANY
STREET: 40 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109-1875
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00147
FILING DATE:
PST OR APPLICATION DATA:
APPLICATION NUMBER: US 87/47,570
FILING DATE: JANUARY 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: DOUGELL, GLENN A., JR.
REGISTRATION NUMBER: 31,503
REFERENCE/BACKET NUMBER: PRI 0047PPO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
Topology: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT US95 00147-17

Query Match          96.4%   Score 47   DB 5: Length 9:
Best Local Similarity 100.0%   Prod. No. 2.5e+05:
Matches 4: conservative 0: Mismatches 0: Gaps 0:

Q# 6 187P 9
L# 1 187P 5

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APPLICANT: Sunnydial, Zhou
TITLE OF INVENTION: Substrate Specificity of Protein Kinases
FILE REFERENCE: US-0013P
CURRENT APPLICATION NUMBER: US/09/443434
CURRENT FILING DATE: 1999-06-26
PAST APPLICANT NUMBER: US 06/126,524
LATEST FILING DATE: 1994-01-17
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 17
LENGTH: 9
TYPE: 187
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: See above.
OTHER INFORMATION: Substrate based on information within the field
US 08 459-654-17

Query Match          96.4%   Score 47   DB 5: Length 9:
Best Local Similarity 100.0%   Prod. No. 2.5e+05:
Matches 4: conservative 0: Mismatches 0: Gaps 0:

Q# 4 187P 9
L# 1 187P 5

RESULT 7
US 09 443 6400 23
Sequence 23: Application US/09/443434
Patent No. 654664
APPLICANT: Sunnydial, Zhou
APPLICANT: Sunnydial, Zhou
APPLICANT: Sunnydial, Zhou
APPLICANT: Sunnydial, Zhou
APPLICANT: Sunnydial, Zhou
TITLE OF INVENTION: Method for determining Presence of Cancer in a Sample By Det
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
FILE REFERENCE: US-0013P
CURRENT APPLICATION NUMBER: US/09/443434
CURRENT FILING DATE: 1999-06-26
PAST APPLICANT NUMBER: US 06/126,524
LATEST FILING DATE: 1994-01-17
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 17
LENGTH: 9
TYPE: 187
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: See above.
OTHER INFORMATION: Substrate based on information within the field
US 08 459-654-17

Query Match          96.4%   Score 47   DB 4: Length 9:
Best Local Similarity 100.0%   Prod. No. 2.5e+05:
Matches 4: conservative 0: Mismatches 0: Gaps 0:

Q# 8 187P 11
L# 1 187P 5

RESULT 17
PCT US95 00147 17
Sequence 17: App. No. 09/00147
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Substrate Specificity of Protein Kinases
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COMPANY
STREET: 40 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109-1875
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00147
FILING DATE:
PST OR APPLICATION DATA:
APPLICATION NUMBER: US 87/47,570
FILING DATE: JANUARY 7, 1994
ATTORNEY/AGENT INFORMATION:
NAME: DOUGELL, GLENN A., JR.
REGISTRATION NUMBER: 31,503
REFERENCE/BACKET NUMBER: PRI 0047PPO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
Topology: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
PCT US95 00147-17

Query Match          96.4%   Score 47   DB 5: Length 9:
Best Local Similarity 100.0%   Prod. No. 2.5e+05:
Matches 4: conservative 0: Mismatches 0: Gaps 0:

Q# 6 187P 9
L# 1 187P 5

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11. CURK 63

[illegible]

	Mean	Stdev	Min	Max
Quality Match	96.4%	8.0%	79.0%	100.0%
Best Local Similarity	100.0%	0.0%	99.0%	100.0%
Matrices - 4 - Conservative	99.8%	0.0%	99.0%	100.0%

[illegible][illegible]

Country	Market	Good	Service	Country	Good	Service
Belgium	Post	100%	100%	France	100%	100%
Denmark	Post	100%	100%	Germany	100%	100%
Finland	Post	100%	100%	Italy	100%	100%
France	Post	100%	100%	Japan	100%	100%
Germany	Post	100%	100%	Spain	100%	100%
Italy	Post	100%	100%	Sweden	100%	100%
Japan	Post	100%	100%	Switzerland	100%	100%
Spain	Post	100%	100%	United Kingdom	100%	100%
Sweden	Post	100%	100%	United States	100%	100%
Switzerland	Post	100%	100%			
United Kingdom	Post	100%	100%			
United States	Post	100%	100%			

[illegible]

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1 CURRENT APPLICATION NUMBER: US-04/644,411A
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3 CURRENT FILING DATE: 1998-04-19
4
5 NUMBER OF SEQ ID NOS: 10
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7 SOFTWARE: Patent In Vols. 2.0
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9 SEQ ID NO: 1
10     1: 1
11     2: 1
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Best Local Similarity: 1.06; Prod. No. 2.4e-92;
Matches: 4; Conservative: 0; Mismatches: 0; Indels:

[illegible]

1 585111 14
 2 US 5913562A 23
 3 September 29, Application US 09/130623
 4 Patent No. 6254796
 5
 6 GENERAL INFORMATION:
 7
 8 APPLICANT: ROBERTS PETER A
 9 APPLICANT: MILLARD, Thomas A
 10 TITLE OF INVENTION: Calculus Required Knowledge
 11 FILE REFERENCE: 0111
 12
 13 CURRENT APPLICATION NUMBER: US 09/130623
 14 PENDING DATE: 09/08/12
 15 FIRST APPLICATION NUMBER: 09/130623
 16 FIRST FILING DATE: 1997-09-12
 17 FIRST APPLICATION NUMBER: 09/130623
 18 FIRST FILING DATE: 1997-09-12
 19
 20 NUMBER OF SEQ. LISTS: 1
 21
 22 SOFTWARE: Calculus Version 2.0
 23 SEQ. ID NO. 29
 24 LENGTH: 11
 25 TYPE: TPI
 26
 27 FEATURES: Artificial Sequence
 28
 29 OTHER INFORMATION: Description of Artificial
 30 OTHER INFORMATION: Intellectual Property
 31 US 5913562A 29

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Best Local	3	Locality	100.0%	Prod. No. 2.4e+02
Min. Slen	4	Conservative	0	Mismatches 0
		Conservative	0	Indices 0
				Gaps 0

[illegible]

RECEIVED 15
JANUARY 1964
Epidemiol. Infect. 52: 557
ACCEPTED 17 FEBRUARY 1964
FROM THE DEPARTMENT OF MICROBIOLOGY, KANSAS
STATE COLLEGE OF VETERINARY MEDICINE
MANASSAS, VIRGINIA
K 99532-1137

1 CURRENT APPLICATION DATA:
 2 APPLICATION NUMBER: US/07/247,617
 3 FILING DATE: 20-SEP-1986
 4 PRIOR APPLICATION DATA:
 5 APPLICATION NUMBER: 102,180
 6 FILING DATE: 29-SEP-1987
 7 SEQ ID NO:12
 8 LENGTH: 11
 9 6224254 12

Query Match 36.4% Score 4 DB 2 Length 12
 Best Local Similarity 100.0% Pred. No. 2.5e-02
 Matches 4: Conservative 0: Mismatches 0: Indels

QY 6 TGR 9
 DB 4 TGR 7

RESULT 16
 US-08-752-852A-7

1 Sequence 7, Application US/08/96984
 2 Patent No. 585476
 3 GENERAL INFORMATION:
 4 APPLICANT: MacLennan, A. John
 5 TITLE OF INVENTION: Molecular Cloning and Expression of
 6 G-Protein Coupled Receptors
 7 NUMBER OF SEQUENCES: 14
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 10 STREET: 2421 N.W. 41st Street, Suite A-1
 11 CITY: Gainesville
 12 STATE: FL
 13 COUNTRY: US
 14 ZIP: 32606

1 COMPUTER READABLE FORM:
 2 COMPUTER: IBM PC compatible
 3 OPERATING SYSTEM: PC DOS/MS-DOS
 4 SOFTWARE: Patent In Release #1.0, Version #1.25
 5 CURRENT APPLICATION DATA:
 6 APPLICATION NUMBER: US/98/796,936
 7 FILING DATE: 15-FEB-1994
 8 CLASSIFICATION: 546

1 ATTORNEY/AGENT INFORMATION:
 2 NAME: Lloyd, Jeff
 3 REGISTRATION NUMBER: 45,589
 4 REFERENCE/DOCKET NUMBER: MAC 100C1
 5 TELECOMMUNICATION INFORMATION:
 6 TELEPHONE: 352-375-8100
 7 TELEFAX: 352-372-5800
 8 INFORMATION FOR SEQ ID NO: 7:
 9 SEQUENCE CHARACTERISTICS:
 10 LENGTH: 12 amino acids
 11 TYPE: amino acid
 12 TOPOLOGY: linear
 13 MOLECULE TYPE: peptide
 14 US-08-752-852A-7

Query Match 36.4% Score 4 DB 2 Length 12
 Best Local Similarity 100.0% Pred. No. 2.5e-02
 Matches 4: Conservative 0: Mismatches 0: Indels

QY 6 TGR 9
 DB 7 TGR 10

RESULT 17

1 US-08-760-936-7
 2 Sequence 7, Application US/08/760943
 3 Patent No. 5856443
 4 GENERAL INFORMATION:

1 APPLICANT: MacLennan, A. John
 2 TITLE OF INVENTION: Molecular Cloning and Expression of
 3 G-Protein Coupled Receptors
 4 NUMBER OF SEQUENCES: 14
 5 CORRESPONDENCE ADDRESS:
 6 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 7 STREET: 2421 N.W. 41st Street, Suite A-1
 8 CITY: Gainesville
 9 STATE: FL
 10 COUNTRY: US
 11 ZIP: 32606

1 COMPUTER READABLE FORM:
 2 COMPUTER: IBM PC compatible
 3 OPERATING SYSTEM: PC-DOS/MS-DOS
 4 SOFTWARE: Patent In Release #1.0, Version #1.25
 5 CURRENT APPLICATION DATA:
 6 APPLICATION NUMBER: US/08/796,936
 7 FILING DATE: December 6, 1996
 8 CLASSIFICATION: 546

1 ATTORNEY/AGENT INFORMATION:
 2 NAME: PACC, DOUG R.
 3 REGISTRATION NUMBER: 48,261
 4 REFERENCE/DOCKET NUMBER: MAC 100C1
 5 TELECOMMUNICATION INFORMATION:
 6 TELEPHONE: 352-375-8100
 7 TELEFAX: 352-372-5800
 8 INFORMATION FOR SEQ ID NO: 7:
 9 SEQUENCE CHARACTERISTICS:
 10 LENGTH: 12 amino acids
 11 TYPE: amino acid
 12 TOPOLOGY: linear
 13 MOLECULE TYPE: peptide
 14 US-08-752-852A-7

Query Match 46.4% Score 4 DB 2 Length 12
 Best Local Similarity 100.0% Pred. No. 2.5e-02
 Matches 4: Conservative 0: Mismatches 0: Indels

QY 6 TGR 9
 DB 7 TGR 10

RESULT 18

1 US-08-752-852A-221
 2 Sequence 221, Application US/08/52852A
 3 Patent No. 5944306

1 GENERAL INFORMATION:
 2 APPLICANT: Grand, Conway
 3 APPLICANT: Su, Chao-Liang
 4 APPLICANT: Giam, Jie
 5 APPLICANT: Stelberger, Deborah
 6 APPLICANT: Lebert, Robert
 7 APPLICANT: Barlow, Sylvia
 8 TITLE OF INVENTION: FINE TUNED PROTEOLINS
 9 NUMBER OF SEQUENCES: 242

1 CORRESPONDENCE ADDRESS:
 2 ADDRESSEE: PENNIE & EDWARDS LLP
 3 STREET: 1155 Avenue of the Americas
 4 CITY: New York
 5 STATE: NY

1 COUNTRY: USA
 2 ZIP: 10036-2711

1 COMPUTER READABLE FORM:

1 MEDIC TYPE: Cassette
 2 COMPUTER: IBM compatible
 3 OPERATING SYSTEM: DOS
 4 SOFTWARE: FASTSEQ Version 2.0
 5 CURRENT APPLICATION DATA:
 6 APPLICATION NUMBER: US/08/752,852A
 7 FILING DATE: 21-NOV-1996
 8 CLASSIFICATION: 435


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1 TITLE OF INVENTION: METHODS FOR DETECTING CARRIERS OF THE VHL
2 TITLE OF INVENTION: DISEASE GENE
3 NUMBER OF SEQUENCES: 20
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: MORGAN & FINNEGAN
6 CITY: NEW YORK
7 STATE: NEW YORK
8 COUNTRY: USA
9 ZIP: 10154
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: FLOPPY DISK
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: WORDPERFECT 5.1
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/442,611
16 FILING DATE: 05-JUNE 1995
17 CLASSIFICATION: 435
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: 08/041,489
20 FILING DATE: 14 MAY 1993
21 CLASSIFICATION: 435
22 ATTORNEY/AGENT INFORMATION:
23 NAME: RICHARD W. BORK
24 REGISTRATION NUMBER: 36,457
25 REFERENCE/DOCKET NUMBER: 2026-407803
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (212) 758-4800
28 TELEFAX: (212) 751-6849
29 INDEX: 422792
30 INFORMATION FOR SEQ ID NO: 10:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 13 amino acid residues
33 TYPE: amino acid
34 SPANADDRESS: unknown
35 LENGTH: unknown
36 US 08-442-611-10
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38 Query Match 36.48% Score 41 DB 11 Length 13
39 Best Local Similarity 100.0% Pred. No. 2 787-443
40 Matches 4: Conservative 0: Mismatches 0: Indels 0:
41
42 CY 6 TORR 9
43 DB 2 TORR 5
44
45 RESULT 22
46 US 08-751-767A-64
47 Sequence 64, Application US/08/751767A
48 Patent No. 594104
49 GENERAL INFORMATION:
50 APPLICANT: ANDERSON, ROBERT G.
51 APPLICANT: GRANT, HUGH
52 APPLICANT: MACDONALD, IAN D.
53 TITLE OF INVENTION: INTERLEUKIN-12 SUBUNIT PROTEIN
54 NUMBER OF SEQUENCES: 80
55 CORRESPONDENCE ADDRESS:
56 ADDRESSEE: NIXON & VANDERKIEF P.C.
57 STREET: 1103 NORTH GLEBE ROAD
58 CITY: ARLINGTON
59 STATE: VA
60 COUNTRY: USA
61 ZIP: 22201
62 COMPUTER READABLE FORM:
63 MEDIUM TYPE: Floppy disk
64 OPERATING SYSTEM: IBM PC compatible
65 SOFTWARE: Patent In Release #1.0, Version #1.0.0
66 CURRENT APPLICATION DATA:
67 APPLICATION NUMBER: US/08/751,767A
68 FILING DATE: 08-NOV-1995

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1 CLASSIFICATION: 536
2 ATTORNEY/AGENT INFORMATION:
3 NAME: SADOFF, R.J.
4 REGISTRATION NUMBER: 36,563
5 REFERENCE/DOCKET NUMBER: 117-221
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: 7038164091
8 TELEFAX: 7038164100
9 INFORMATION FOR SEQ ID NO: 64:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 13 amino acids
12 TYPE: amino acid
13 TOPOLOGY: linear
14 MOLECULE TYPE: protein
15 US-08-751-767A-64
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17 Query Match 36.48% Score 41 DB 2 Length 13
18 Best Local Similarity 100.0% Pred. No. 2 787-02
19 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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21 CY 6 TORR 9
22 DB 6 TORR 9
23
24 RESULT 23
25 US-08-623-428D-36
26 Sequence 36, Application US/08/623428D
27 Patent No. 6312890
28 GENERAL INFORMATION:
29 APPLICANT: W. MARSTON LINEHAN, MICHAEL
30 LERNAN, FARIDA LATIF AND BERTON
31 ZHAK
32 TITLE OF INVENTION: PARTIAL INTRON SEQUENCE
33 OF VHL DISEASE GENE AND ITS USE IN DIAGNOSIS
34 OF DISEASE CARRIERS
35 NUMBER OF SEQUENCES: 63
36 CORRESPONDENCE ADDRESS:
37 ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
38 STREET: 345 PARK AVENUE
39 CITY: NEW YORK
40 STATE: NEW YORK
41 COUNTRY: USA
42 ZIP: 10154
43 COMPUTER READABLE FORM:
44 MEDIUM TYPE: FLOPPY DISK
45 OPERATING SYSTEM: IBM PC compatible
46 SOFTWARE: MICROSOFT WORD 97
47 CURRENT APPLICATION DATA:
48 APPLICATION NUMBER: US/08/623,428D
49 FILING DATE: 05-Sep-2000
50 PRIOR APPLICATION DATA:
51 APPLICATION NUMBER: 08/623,428
52 FILING DATE: MARCH 28, 1996
53 APPLICATION NUMBER: 08/061,889
54 FILING DATE: May 14, 1993
55 ATTORNEY/AGENT INFORMATION:
56 NAME: KATHLYN M. BROWN
57 REGISTRATION NUMBER: 34,556
58 REFERENCE/DOCKET NUMBER: 2026-407803
59 TELECOMMUNICATION INFORMATION:
60 TELEPHONE: (212) 758-4800
61 TELEFAX: (212) 751-6849
62 INDEX: 422792
63 INFORMATION FOR SEQ ID NO: 46:
64 SEQUENCE CHARACTERISTICS:
65 LENGTH: 13 amino acids
66 TYPE: amino acid
67 TOPOLOGY: linear
68 SEQUENCE DESCRIPTION: SEQ ID NO: 36:
69 US-08-623-428D-36

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Query Match: 46.4%, Score 4: 1b 4b, Length 14:
Best Local Similarity: 100.0%, Prod. No. 2.8e+02
Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 6 GRRP 9
ID 11
1b 1b GRRP 13

RESULT 27
US 06/03/99-03/17
Sequence 17: Application US/09-0906077
Patent No. 6,543,949
GENERAL INFORMATION:
1 APPLICANT: Per Antonsson, Per Bjork, Michael J. Westro,
2 APPLICANT: David Hansson, Torje Karlsson, Lars
3 APPLICANT: Abrahamson and Goran Forsberg
4 TITLE OF INVENTION: MODIFIED/IMMERSED SUBSTRATES
5 TITLE OF INVENTION: AND THEIR USE
6 NUMBER OF SEQUENCES: 24
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Traveler, Hewlett, Kimberly & McLeod
9 STREET: 1177 West Loop South, Fort Worth
10 CITY: Houston
11 STATE: TX
12 COUNTRY: USA
13 ZIP: 75207-9095
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 OPERATING SYSTEM: IBM PC compatible
17 SOFTWARE: Patent Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US 09/0906077
20 FILING DATE: 23-MAY-1994
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Bok, Mary E.
23 REGISTRATION NUMBER: 41,215
24 REFERENCE/EXCERPT NUMBER: 18244907
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 214-540-9209
27 TELEFAX: 214-540-5818
28 INFORMATION FOR SEQ ID NO: 1:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 14 amino acids
31 TYPE: amino acid
32 TOPOLOGY: unknown
33 MOLECULE TYPE: peptide
34 PCT: US95-06077 7

Query Match: 46.4%, Score 4: 1b 4b, Length 14:
Best Local Similarity: 100.0%, Prod. No. 2.8e+02
Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 8 GRRP 11
ID 11
1b 7 GRRP 13

RESULT 28
US 06/03/99-03/17
Sequence 17: Application US/09-0906077
Patent No. 6,543,949
GENERAL INFORMATION:
1 APPLICANT: Immunobiology Resources, Inc. et al.
2 APPLICANT: Vaccine Institute of Canada et al.
3 TITLE OF INVENTION: Transfection of cells with nucleic acids
4 TITLE OF INVENTION: and other methods for producing viral
5 TITLE OF INVENTION: and other methods for producing viral
6 NUMBER OF SEQUENCES: 38

```

```

CORRESPONDENCE ADDRESS:
1 ADDRESSEE: Jensen and Howson
2 STREET: Spring House Corporate Cntr., PO Box 457
3 CITY: Spring House
4 STATE: Pennsylvania
5 COUNTRY: USA
6 ZIP: 19477
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 OPERATING SYSTEM: IBM PC compatible
10 SOFTWARE: Patent Release #1.0, Version #1.25
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: PCT/US95/06077
13 FILING DATE:
14 CLASSIFICATION:
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 08/247,991
17 FILING DATE: 23-MAY-1994
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Bok, Mary E.
20 REGISTRATION NUMBER: 41,215
21 REFERENCE/EXCERPT NUMBER: 18244907
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: 214-540-9209
24 TELEFAX: 214-540-5818
25 INFORMATION FOR SEQ ID NO: 1:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 14 amino acids
28 TYPE: amino acid
29 TOPOLOGY: unknown
30 MOLECULE TYPE: peptide
31 PCT: US95-06077 7

Query Match: 46.4%, Score 4: 1b 5b, Length 14:
Best Local Similarity: 100.0%, Prod. No. 2.8e+02
Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 8 GRRP 11
ID 11
1b 7 GRRP 13

RESULT 29
US 06/03/99-03/17
Sequence 17: Application US/09-0906077
Patent No. 6,543,949
GENERAL INFORMATION:
1 APPLICANT: Feller, Jeffrey S. et al.
2 APPLICANT: Feller, Jeffrey S. et al.
3 TITLE OF INVENTION: HNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
4 TITLE OF INVENTION:
5 NUMBER OF SEQUENCES: 17
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/07/277,943
8 FILING DATE: 23-MAY-1988
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 34,203
11 FILING DATE: 02-APR-1987
12 SEQ ID NO: 14
13 LENGTH: 14
14 5224425-14

Query Match: 46.4%, Score 4: 1b 6b, Length 14:
Best Local Similarity: 100.0%, Prod. No. 2.8e+02
Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 7 GRRP 10
ID 11
1b 6 GRRP 9

RESULT 30
US 06/03/99-03/17
Sequence 17: Application US/09-0906077

```

1 PATENT NO. 5408547
 2 GENERAL INFORMATION:
 3 APPLICANT: LAFITA, SYDNEY K
 4 APPLICANT: KALIVAREMAL, ARUNAS
 5 TITLE OF INVENTION: LOCALIZATION OF RNA IN PROTEIN AND POLYPEPTIDES FOR NUCLEOSIDE ANALYSIS
 6 FILE OF INVENTION: 10 JUL 99
 7 FILE REFERENCE: 200 100 75002 5003
 8 CURRENT APPLICATION NUMBER: US/09/044303
 9 CURRENT FILING DATE: 2000 04 28
 10 PRIOR APPLICATION NUMBER: US 60/101,147
 11 PRIOR FILING DATE: 1999 04 24
 12 NUMBER OF SEQ ID NOS: 41
 13 SOFTWARE: PATENT IN VERSION 5.1
 14 SEQ ID NO: 10
 15 LENGTH: 15
 16 TYPE: DS
 17 ORGANISM: Artificial Sequence
 18 FEATURE:
 19 OTHER INFORMATION: Histone H1 domain
 20 US 09 04 4303 10
 21 Query Match 36.4%, Score 4, DB 1, Length 15,
 22 Best Local Similarity 100.0%, Prod No. 5408547
 23 Matches 4, Conservative 0, Mismatches 0, Indels 0
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1 US 08 947 486 2
 2 Query Match 27.4%, Score 4, DB 1, Length 8;
 3 Best Local Similarity 100.0%, Prod No. 2.5e+05;
 4 Matches 0, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
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1 APPLICANT: Ausich, Rodney L.
 2 APPLICANT: Brinkhaus, Friedrich
 3 APPLICANT: Mukharji, Indran
 4 APPLICANT: Proffitt, John H
 5 APPLICANT: Varger, James G
 6 APPLICANT: Yen, Huei-Chue B
 7 TITLE OF INVENTION: Beta Carotene Biosynthesis in
 8 TITLE OF INVENTION: Genetically Engineered Hosts
 9 NUMBER OF SEQUENCES: 79
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESSEE: Amoco Corp., Patents and Intellectual Prop
 12 STREET: 200 E Randolph St
 13 CITY: Chicago
 14 STATE: IL
 15 COUNTRY: USA
 16 ZIP: 60606-0703
 17 COMPUTER READABLE FORM:
 18 MEDIUM TYPE: Floppy disk
 19 COMPUTER: IBM PC compatible
 20 OPERATING SYSTEM: PC-DOS/MS-DOS
 21 SOFTWARE: Patent in Release #1.24
 22 CURRENT APPLICATION DATA:
 23 APPLICATION NUMBER: US/09/787-443
 24 FILING DATE: 27-JUL-1993
 25 CLASSIFICATION: 445
 26 PRIOR APPLICATION DATA:
 27 APPLICATION NUMBER: US 07/786,116
 28 FILING DATE: 30-OCT-1991
 29 ATTORNEY/AGENT INFORMATION:
 30 NAME: Gallegos, No. 5530194941 B
 31 TELECOMMUNICATION INFORMATION:
 32 TELEPHONE: 3128567180
 33 TELEFAX: 3128564972
 34 INFORMATION FOR SEQ ID NO: 54
 35 SEQUENCE CHARACTERISTICS:
 36 LENGTH: 8 amino acids
 37 TYPE: amino acid
 38 TOPOLOGY: linear
 39 MOLECULE TYPE: peptide
 40 US-09-787-443-9
 41 Query Match: 27.9% Score 31 Indels 0
 42 Best Local Similarity: 100.0% Prod. No. 2.5e-05
 43 Matches: 4 Conservative 0 Mismatches 0 Indels 0
 44 SY 4 KKT 1
 45 1
 46 2 KKT 4
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 48 RESULT 4
 49 US-09-787-443-9
 50 Sequence 51, Application US/09/787-443-9
 51 Patent No. 5530189
 52 GENERAL INFORMATION:
 53 APPLICANT: Ausich, Rodney L.
 54 APPLICANT: Brinkhaus, Friedrich
 55 APPLICANT: Mukharji, Indran
 56 APPLICANT: Proffitt, John H
 57 APPLICANT: Varger, James G
 58 APPLICANT: Yen, Huei-Chue B
 59 TITLE OF INVENTION: Lycopene Biosynthesis in
 60 TITLE OF INVENTION: Genetically Engineered Hosts
 61 NUMBER OF SEQUENCES: 79
 62 CORRESPONDENCE ADDRESS:
 63 ADDRESSEE: Amoco Corp., Patents and Intellectual Prop
 64 STREET: 200 E Randolph St
 65 CITY: Chicago
 66 STATE: IL
 67 COUNTRY: USA
 68 ZIP: 60606-0703
 69 COMPUTER READABLE FORM:
 70 MEDIUM TYPE: Floppy disk

1 COMPUTER: IBM PC compatible
 2 OPERATING SYSTEM: PC-DOS/MS-DOS
 3 SOFTWARE: Patent in Release #1.24
 4 CURRENT APPLICATION DATA:
 5 APPLICATION NUMBER: US/09/787-443
 6 FILING DATE: 27-JUL-1993
 7 CLASSIFICATION: 445
 8 PRIOR APPLICATION DATA:
 9 APPLICATION NUMBER: US 07/786,116
 10 FILING DATE: 30-OCT-1991
 11 ATTORNEY/AGENT INFORMATION:
 12 NAME: Gallegos, No. 5530194941 B
 13 TELECOMMUNICATION INFORMATION:
 14 TELEPHONE: 3128567180
 15 TELEFAX: 3128564972
 16 INFORMATION FOR SEQ ID NO: 51
 17 SEQUENCE CHARACTERISTICS:
 18 LENGTH: 8 amino acids
 19 TYPE: amino acid
 20 TOPOLOGY: linear
 21 MOLECULE TYPE: peptide
 22 US-09-787-443-9
 23 Query Match: 27.9% Score 31 Indels 0
 24 Best Local Similarity: 100.0% Prod. No. 2.5e-05
 25 Matches: 4 Conservative 0 Mismatches 0 Indels 0
 26 SY 4 KKT 6
 27 111
 28 2 KKT 4
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 30 RESULT 55
 31 US-09-787-443-9
 32 Sequence 15, Application US/09/787-443-9
 33 Patent No. 5530189
 34 GENERAL INFORMATION:
 35 APPLICANT: COMBELLIO, PAOLO
 36 APPLICANT: PENZETTO, CAROLA
 37 TITLE OF INVENTION: PEPTIDE INHIBITORS OF MITOGENESIS AND
 38 TITLE OF INVENTION: MITOGENESIS
 39 NUMBER OF SEQUENCES: 31
 40 CORRESPONDENCE ADDRESS:
 41 ADDRESSEE: OBIOL, SPIVAK, McCLELLAND, MAIER & NEUSTAEDT,
 42 ADDRESSEE: P.O.
 43 STREET: 1765 S. Jefferson Davis Highway, Suite 400
 44 CITY: Arlington
 45 STATE: Virginia
 46 COUNTRY: U.S.A.
 47 ZIP: 22202
 48 COMPUTER READABLE FORM:
 49 MEDIUM TYPE: Floppy disk
 50 COMPUTER: IBM PC compatible
 51 OPERATING SYSTEM: PC-DOS/MS-DOS
 52 SOFTWARE: Patent in Release #1.0, Version #1.25
 53 CURRENT APPLICATION DATA:
 54 APPLICATION NUMBER: US/09/266,514
 55 FILING DATE: 27-JUN-1994
 56 CLASSIFICATION: 530
 57 PRIOR APPLICATION DATA:
 58 APPLICATION NUMBER: GB 9415928
 59 FILING DATE: 30-JUN-1993
 60 PRIOR APPLICATION DATA:
 61 APPLICATION NUMBER: GB 9407673.4
 62 FILING DATE: 18-APR-1994
 63 ATTORNEY/AGENT INFORMATION:
 64 NAME: OBIOL, No. 5594105man F.
 65 REGISTRATION NUMBER: 24.618
 66 REFERENCE/DRAWING NUMBER: 769-323-0
 67 TELECOMMUNICATION INFORMATION:
 68 TELEPHONE: (703) 413-6000
 69 TELEFAX: (703) 413-2220
 70 TELEX: 248655 OPAI DE


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1  INFORMATION FOR SEQ ID NO: 1:
2  SEQUENCE CHARACTERISTICS:
3     LENGTH: 8 amino acids
4     TYPE: amino acid
5     TOPOLOGY: unknown
6  MOLECULE TYPE: peptide
7  FEATURES:
8     NAME/KEY: Modified site
9     LOCATION: 1
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11  OTHER INFORMATION: /note "The 1st residue at position 1 is
12  OTHER INFORMATION: be phosphorylated."
13  US-09-787-443-9
14
15  Query Match: 27.4% Score 3: DB 1: Length 8:
16  Best Local Similarity: 100.0% Pred. No. 2.5e+05:
17  Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
18
19  27 7 KKK 7
20  30 7 KKK 7
21
22  RESULT 37
23  US-09-787-443-9
24  Sequence ID: Application US/09-787-443-9
25  Patent No. 5594145
26  GENERAL INFORMATION:
27  APPLICANT: BOWEN, WILLIAM J.
28  APPLICANT: BOWEN, WILLIAM J.
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74  APPLICANT: BOWEN, WILLIAM J.
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98  APPLICANT: BOWEN, WILLIAM J.
99  APPLICANT: BOWEN, WILLIAM J.
100 APPLICANT: BOWEN, WILLIAM J.

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1  INFORMATION FOR SEQ ID NO: 1:
2  SEQUENCE CHARACTERISTICS:
3     LENGTH: 8 amino acids
4     TYPE: amino acid
5     TOPOLOGY: unknown
6  MOLECULE TYPE: peptide
7  FEATURES:
8     NAME/KEY: Modified site
9     LOCATION: 1
10
11  OTHER INFORMATION: /note "The 1st residue at position 1 is
12  OTHER INFORMATION: be phosphorylated."
13  US-09-787-443-9
14
15  Query Match: 27.4% Score 3: DB 1: Length 8:
16  Best Local Similarity: 100.0% Pred. No. 2.5e+05:
17  Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
18
19  27 7 KKK 7
20  30 7 KKK 7
21
22  RESULT 37
23  US-09-787-443-9
24  Sequence ID: Application US/09-787-443-9
25  Patent No. 5594145
26  GENERAL INFORMATION:
27  APPLICANT: BOWEN, WILLIAM J.
28  APPLICANT: BOWEN, WILLIAM J.
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99  APPLICANT: BOWEN, WILLIAM J.
100 APPLICANT: BOWEN, WILLIAM J.

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Sequence 4: Application: US/0837048
Patent No. 5648225
GENERAL INFORMATION:
APPLICANT: Van den Eynde, Bartlett, Leback, et al.
TITLE OF INVENTION: Isolated, Translated Nucleic Acid
TITLE OF INVENTION: Methods and Compositions for the Treatment of Cancer
TITLE OF INVENTION: The Family Rejection Antigen and Uses Thereof
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felto & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 100 Kbit per byte
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0837048
FILING DATE: 10 JANUARY 1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/270,192
FILING DATE: 27 MAY 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/06,000
FILING DATE: 22 JULY 1994
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5648225, 0.
REGISTRATION NUMBER: 40,448
REFERENCE/BOOK NUMBER: 110-32-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9400
TELEFAX: (212) 638-3883
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
MOL. WEIGHT: 1000
US-08 426,644
Query Match: 27.00, Score 3, DB 1, Length 8,
Best Local Similarity: 100.00, Pred. No. 2, 5e-05
Matches: 0, Mismatches 0, Indels 0
13 4849 11
14 4849 4
RES: 11 11
US-08-065,624-A-59
Sequence 59: Application: US/0496064
Patent No. 5648218
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedrich
APPLICANT: Mukharji, Indira
APPLICANT: Proffitt, John B.
APPLICANT: Varner, James G.
APPLICANT: Yen, Hui-Che R.
TITLE OF INVENTION: Biosynthesis of a novel lipid and
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Walsh & Katz, Ltd.
STREET: 120 S. Riverside Plaza
CITY: Chicago
STATE: IL

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COUNTRY: USA
ZIP: 60605
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,624A
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/605,061
FILING DATE: 09-07-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/602,927
FILING DATE: 26 FEB 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/592,674
FILING DATE: 03 AUG 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/525,551
FILING DATE: 18 MAY 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,633
FILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,481
REFERENCE/BOOK NUMBER: AMO-006.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 655-1500
TELEFAX: (312) 655-1500
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
Topology: Linear
MOLECULE TYPE: Peptide
US 08-096-624A-59
Query Match: 27.00, Score 3, DB 1, Length 8,
Best Local Similarity: 100.00, Pred. No. 2, 5e-05
Matches: 0, Mismatches 0, Indels 0
59 4 881 4
10 4 881 4
RES: 4 4
US-08 291,065-7
Sequence 9: Application: US/0629106
Patent No. 5646069
GENERAL INFORMATION:
APPLICANT: Payson, Lowell M.
APPLICANT: Sick, August M.
TITLE OF INVENTION: No. 5646069: Bacillus thuringiensis isolates
TITLE OF INVENTION: Active Against Lepidopteran Pests
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Softwaretek & Softwaretek
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32609
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

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FILING DATE: 16-JUN-1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Mitchell, Leonard J.
 REGISTRATION NUMBER: 29,609
 REFERENCE/PACKET NUMBER: 604,285
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4005
 TELEFAX: (703) 816-4100
 TELEX: 200757 NIXN UR
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 PEPTIDE TYPE: peptide
 US 08 244 855 3
 Query Match: 27.38% Score 41 DB 13 Length 8
 Best Local Similarity 100.00% Prod. No. 2.5e+05
 Matches 0 Conservative 0 Mismatches 0 Indels 0 Gaps 0

27 8 RRP 10
 111
 4 RRP 5

RESULT 44
 US 08-244-855 3
 : Sequence 3, Application US/08244855
 : Patent No. 5762966
 : GENERAL INFORMATION:
 : APPLICANT: Mitchell, Leonard J.
 : TITLE OF INVENTION: FURTHER IMPROVEMENTS RELATING TO
 : TITLE OF INVENTION: RADIO-LABELLING OF PROTEINS
 : NUMBER OF SEQUENCES: 15
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: NIXON & VANDERHYE
 : STREET: 818 FLOOR, 1100 NORTH GLEBE ROAD
 : CITY: ARLINGTON
 : STATE: VIRGINIA
 : COUNTRY: U.S.A.
 : ZIP: 22201-4714
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/244,855
 : FILING DATE: 16-JUN-1994
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Mitchell, Leonard J.
 : REGISTRATION NUMBER: 29,609
 : REFERENCE/PACKET NUMBER: 604,285
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (703) 816-4005
 : TELEFAX: (703) 816-4100
 : TELEX: 200757 NIXN UR
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 8 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : PEPTIDE TYPE: peptide
 : US 08-244-855 3

Query Match: 27.38% Score 41 DB 13 Length 8
 Best Local Similarity 100.00% Prod. No. 2.5e+05
 Matches 0 Conservative 0 Mismatches 0 Indels 0 Gaps 0

0: Gaps

27 8 RRP 10
 111
 4 RRP 5

RESULT 45
 US 08 244 855 3
 : Sequence 3, Application US/08244855
 : Patent No. 5762966
 : GENERAL INFORMATION:
 : APPLICANT: Mitchell, Leonard J.
 : TITLE OF INVENTION: FURTHER IMPROVEMENTS RELATING TO
 : TITLE OF INVENTION: RADIO-LABELLING OF PROTEINS
 : NUMBER OF SEQUENCES: 15
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: NIXON & VANDERHYE
 : STREET: 818 FLOOR, 1100 NORTH GLEBE ROAD
 : CITY: ARLINGTON
 : STATE: VIRGINIA
 : COUNTRY: U.S.A.
 : ZIP: 22201-4714
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/244,855
 : FILING DATE: 16-JUN-1994
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Mitchell, Leonard J.
 : REGISTRATION NUMBER: 29,609
 : REFERENCE/PACKET NUMBER: 604,285
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (703) 816-4005
 : TELEFAX: (703) 816-4100
 : TELEX: 200757 NIXN UR
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 8 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : PEPTIDE TYPE: peptide
 : US 08-244-855 3

Query Match: 27.38% Score 41 DB 13 Length 8
 Best Local Similarity 100.00% Prod. No. 2.5e+05
 Matches 0 Conservative 0 Mismatches 0 Indels 0 Gaps 0

27 8 RRP 10
 111
 4 RRP 5

RESULT 46
 US 08-191-3884 3
 : Sequence 3, Application US/081913884
 : Patent No. 5753164
 : GENERAL INFORMATION:
 : APPLICANT: Genentech, Inc.
 : TITLE OF INVENTION: Immunogenic Cancer Proteins and Peptides
 : TITLE OF INVENTION: and Method of Use
 : NUMBER OF SEQUENCES: 38
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Arnold, White & Barker
 : STREET: 321 No. 576316401, Clark Street, Suite 800
 : CITY: Chicago
 : STATE: IL
 : COUNTRY: USA
 : ZIP: 60610

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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: Patent In Release #1.0, Version #1.25
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/191,438A
8  FILING DATE: 12-JAN-1994
9  CLASSIFICATION: 436
10 ATTORNEY/AGENT INFORMATION:
11 NAME: No. 5763164thrup, Thomas E.
12 REGISTRATION NUMBER: 33,268
13 REFERENCE/DCKET NUMBER: 0000002
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 312-744-0090
16 TELEFAX: 312-755-4489
17 INFORMATION FOR SEQ ID NO: 3:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 8 amino acids
20 TYPE: amino acid
21 STRANDEDNESS: single
22 TOPOLOGY: linear
23 MOLECULE TYPE: peptide
24 FEATURE:
25 NAME/KEY: Xaa
26 LOCATION: 2
27 IDENTIFICATION METHOD: Phosphorylated Serine
28 US-08-191-438A 3
29
30 Query Match 27.38; Score 3; DB 1; Length 8;
31 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
32 Matches 3; Conservative 0; Mismatches 0; Indels 0; Caps 0;
33
34 QY 7 GRR 9
35
36 GB 4 GRR 6
37
38 RESULT 48
39 US-08-191-438A-20
40 Sequence 20; Application US/08/191438A
41 Patent No. 5763164
42 GENERAL INFORMATION:
43 APPLICANT: Caresoft, Emanuel
44 TITLE OF INVENTION: Immunogenic Cancer Proteins and Peptides
45 TITLE OF INVENTION: and Method of Use
46 NUMBER OF SEQUENCES: 38
47 CORRESPONDENCE ADDRESS:
48 ADDRESSEE: Arnold, White & Burke
49 STREET: 321 No. 5763164th Clark Street, Suite 800
50 CITY: Chicago
51 STATE: IL
52 COUNTRY: USA
53 ZIP: 60610
54 COMPUTER READABLE FORM:
55 MEDIUM TYPE: Floppy disk
56 COMPUTER: IBM PC compatible
57 OPERATING SYSTEM: PC-DOS/MS-DOS
58 SOFTWARE: Patent In Release #1.0, Version #1.25
59 CURRENT APPLICATION DATA:
60 APPLICATION NUMBER: US/08/191,438A
61 FILING DATE: 12-JAN-1994
62 CLASSIFICATION: 436
63 ATTORNEY/AGENT INFORMATION:
64 NAME: No. 5763164thrup, Thomas E.
65 REGISTRATION NUMBER: 33,268
66 REFERENCE/DCKET NUMBER: 0000002
67 TELECOMMUNICATION INFORMATION:
68 TELEPHONE: 312-744-0090
69 TELEFAX: 312-755-4489
70 INFORMATION FOR SEQ ID NO: 20:
71 SEQUENCE CHARACTERISTICS:
72 LENGTH: 9 amino acids
73 TYPE: amino acid
74 STRANDEDNESS: single
75 TOPOLOGY: linear
76 MOLECULE TYPE: peptide
77 FEATURE:
78 NAME/KEY: Xaa
79 LOCATION: 2,13
80 IDENTIFICATION METHOD: Phosphorylated Serine
81 US-08-191-438A-20
82
83 Query Match 27.38; Score 3; DB 1; Length 8;
84 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
85 Matches 3; Conservative 0; Mismatches 0; Indels 0; Caps 0;
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87 QY 7 GRR 9
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89 GB 4 GRR 6
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91 RESULT 47
92 US-08-191-438A-19
93 Sequence 19; Application US/08/191438A
94 Patent No. 5763164
95 GENERAL INFORMATION:
96 APPLICANT: Caresoft, Emanuel
97 TITLE OF INVENTION: Immunogenic Cancer Proteins and Peptides
98 TITLE OF INVENTION: and Method of Use
99 NUMBER OF SEQUENCES: 38
100 CORRESPONDENCE ADDRESS:
101 ADDRESSEE: Arnold, White & Burke
102 STREET: 321 No. 5763164th Clark Street, Suite 800
103 CITY: Chicago
104 STATE: IL
105 COUNTRY: USA
106 ZIP: 60610
107 COMPUTER READABLE FORM:
108 MEDIUM TYPE: Floppy disk
109 COMPUTER: IBM PC compatible
110 OPERATING SYSTEM: PC-DOS/MS-DOS
111 SOFTWARE: Patent In Release #1.0, Version #1.25
112 CURRENT APPLICATION DATA:
113 APPLICATION NUMBER: US/08/191,438A
114 FILING DATE: 12-JAN-1994
115 CLASSIFICATION: 436
116 ATTORNEY/AGENT INFORMATION:
117 NAME: No. 5763164thrup, Thomas E.
118 REGISTRATION NUMBER: 33,268
119 REFERENCE/DCKET NUMBER: 0000002
120 TELECOMMUNICATION INFORMATION:
121 TELEPHONE: 312-744-0090

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Query Match: 27.4% Score 3; DB 1; Length 8;
Best Local Similarity: 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

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97 7 GRK 9
98 1
99 4 GRK 6

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RESULT 50
US-09-787-443-9
Sequence 22, Application: US/09/787-443-9
Patent No. 5763164
GENERAL INFORMATION:
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: Immunogenic Peptide Products and Peptides
TITLE OF INVENTION: and Method of Use
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: 421 No. 5763164th Clark Street, Suite 800
CITY: Chicago
STATE: IL
COUNTRY: USA

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ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/787-443-9
FILING DATE: 12 JAN 1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: No. 5763164th Clark Street, Suite 800
REGISTRATION NUMBER: 5763164
REFERENCE/KEY NUMBER: 09/000002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 412-744-0090
TELEFAX: 412-744-4489
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Xaa
LOCATION: 1
IDENTIFICATION METHOD: Phosphorylated Serine
FEATURE:
NAME/KEY: Xaa
LOCATION: 8
IDENTIFICATION METHOD: Phosphorylated Serine
US-09-787-443-9

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Query Match: 27.4% Score 3; DB 1; Length 8;
Best Local Similarity: 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

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97 7 GRK 9
98 1
99 4 GRK 6

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Search completed: September 30, 2003, 10:28:41
Job time: 14,946.67 secs

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[illegible]

DR EMBL: U28818; AAA57151.1;
 DR MED: M019737; Nf2;
 FT N-TER 1
 SQ SEQUENCE 11 AA: 1238 MW: 251240.977414085; KR94;

Query Match 36.4% Score 4; DB 11; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5; 2002;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GRP 10
 1 1
 5 GRP 8

RESULT 2

QY QKSE1 PRELIMINARY: PFI: 12 AA:
 AC QKSE1:
 DI 01-OCT-2000 (TRENBLER: 15; Created)
 DI 01-OCT-2000 (TRENBLER: 15; Last sequence update)
 DI 01-MAR-2002 (TRENBLER: 20; Last annotation update)
 DI 01-OCT-2002 (TRENBLER: 22; Last sequence update)
 DI 01-OCT-2002 (TRENBLER: 22; Last annotation update)
 DI Truncated protein kinase.
 DI VANS.
 DI Enterococcus faecium (Streptococcus faecium).
 DI P. asmid p0W796.
 DI Bacteria; Firmicutes; Lactobacterales; Enterococcaceae; Enterococcus.
 DI NCBI_TaxID=1352;
 DI [1]
 DI SEQUENCE FROM N.A.
 DI STRAIN-UW789;
 DI Werlet G., Klare J., Wittl W.
 DI "Multi-resistance gene cluster on a plasmid in a clinical isolate of
 DI Enterococcus faecium".
 DI Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DI EMBL: AF52435; AAM77883.1;
 DI K. nase; Plasmid.
 DI SEQUENCE 14 AA: 1628 MW: 2444480.6720434 CRC64;

Query Match 36.4% Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 6.4e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NKX 6
 1 1
 7 NKX 10

Query Match 36.4% Score 4; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.0e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RGR 11
 1 1
 9 RGR 12

RESULT 3

QY QKSE1 PRELIMINARY: PFI: 12 AA:
 AC QKSE1:
 DI 01-MAY-2000 (TRENBLER: 15; Created)
 DI 01-MAY-2000 (TRENBLER: 15; Last sequence update)
 DI 01-JUN-2002 (TRENBLER: 21; Last annotation update)
 DI GP-083 (GP-083) STATIC peptide (Fragment).
 DI Gasta (orange phase).
 DI Eukaryota; Metazoa; Chordata; Crustacea; Vertebrata; Euteleostomi.
 DI Mammalia; Eutheria; Rodentia; Muridae; Mus musculus.
 DI NCBI_TaxID=10140;
 DI [1]
 DI SEQUENCE.
 DI MEDLINE 94062075; PubMed-165940.
 DI B. J. Bennett H.P., Lazare G., Soudan S.
 DI "Isolation and characterization of synthetic static peptides from quinea
 DI pig bone marrow".
 DI Biochem. Biophys. Res. Commun. 1994; 204:119-23.
 DI N-TER 1
 DI N-TER 13
 DI SEQUENCE 13 AA: 1706 MW: 226701.646685; KR94.

Query Match 36.4% Score 4; DB 11; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKT 6
 1 1
 4 KKT 6

RESULT 6

QY QKSE1 PRELIMINARY: PFI: 8 AA:
 AC QKSE1:
 DI 01-MAY-2000 (TRENBLER: 15; Created)
 DI 01-MAY-2000 (TRENBLER: 15; Last sequence update)
 DI 01-MAY-2000 (TRENBLER: 15; Last annotation update)
 DI Stage V speculation protein E (Fragment).
 DI SPAGE.
 DI Bacillus subtilis.
 DI Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 DI NCBI_TaxID=1424;
 DI [1]
 DI SEQUENCE FROM N.A.
 DI STRAIN-158;
 DI MEDLINE 94004529; PubMed-1391053;
 DI Henriques A.G., de Lencastre H., Paquot P.J.
 DI "A Bacillus subtilis morphane cluster that includes spage is
 DI homologous to the mra region of Escherichia coli".
 DI Biochimie 74:745-748 (1992).
 DI EMBL: X64258; CAA45556.1;
 DI N-TER 8
 DI SEQUENCE 8 AA: 893 MW: 97551.631218166 CRC64;

Query Match 27.0% Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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KW Chloroplast. 11
SQ SEQUENCE 11 AA: 1260 MW: 937605944086181 Length 11:
 27.48, Score 3: DB 8: Length 11:
 100.0%, Pred. No. 6.6e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match: 27.48, Score 3: DB 8: Length 11:
Best Local Similarity 100.0%, Pred. No. 6.6e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 TOR 8
LD 5 TOR 7

RESULT 24
QMB58 PRELIMINARY: PRI: 11 AA:
AC QMB58
LT 01-OCT-2002 (EMBLrel: 22, Last sequence update)
DT 01-OCT-2002 (EMBLrel: 22, Last sequence update)
DE PSBJ (Fragment)
GN PSBJ
OS Chloroplast
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Asteridae; Lamiales; Solanales; Convolvulaceae; Ipomoea
  NCBI TaxID: 89614;
PN 1;
PP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
  lineages based on DNA sequences of multiple chloroplast loci."
  Am. J. Bot. 0:0-0(2002)
DR EMBL: AY100936; AAM55865.1;
KW Chloroplast. 11
ET NON_TER 11
SQ SEQUENCE 11 AA: 1260 MW: 937605944086181 Length 11:
 27.48, Score 3: DB 8: Length 11:
 100.0%, Pred. No. 6.6e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 TOR 8
LD 5 TOR 7

RESULT 24
QMB58 PRELIMINARY: PRI: 11 AA:
AC QMB58
LT 01-OCT-2002 (EMBLrel: 22, Last sequence update)
DT 01-OCT-2002 (EMBLrel: 22, Last sequence update)
DE PSBJ (Fragment)
GN PSBJ
OS Chloroplast
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Asteridae; Lamiales; Solanales; Convolvulaceae; Ipomoea
  NCBI TaxID: 197444;
PN 1;
PP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
  lineages based on DNA sequences of multiple chloroplast loci."
  Am. J. Bot. 0:0-0(2002)
DR EMBL: AY100936; AAM55865.1;
KW Chloroplast. 11
ET NON_TER 11
SQ SEQUENCE 11 AA: 1260 MW: 937605944086181 Length 11:
 27.48, Score 3: DB 8: Length 11:
 100.0%, Pred. No. 6.6e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 TOR 8
LD 5 TOR 7

RESULT 24
QMB58 PRELIMINARY: PRI: 11 AA:
AC QMB58
LT 01-OCT-2002 (EMBLrel: 22, Last sequence update)
DT 01-OCT-2002 (EMBLrel: 22, Last sequence update)
DE PSBJ (Fragment)
GN PSBJ
OS Chloroplast
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Asteridae; Lamiales; Solanales; Convolvulaceae; Mariposa
  NCBI TaxID: 197412;
PN 1;
PP SEQUENCE FROM N.A.
RA Stefanovic S., Krueger L., Olmstead R.G.;
RT "Monophyly of the Convolvulaceae and circumscription of their major
  lineages based on DNA sequences of multiple chloroplast loci."
  Am. J. Bot. 0:0-0(2002)
DR EMBL: AY100936; AAM55865.1;
KW Chloroplast. 11
ET NON_TER 11
SQ SEQUENCE 11 AA: 1260 MW: 937605944086181 Length 11:
 27.48, Score 3: DB 8: Length 11:
 100.0%, Pred. No. 6.6e+03;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 TOR 8
LD 5 TOR 7

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[illegible]


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Q7      8 KRP 19
LD      15 KRP 15

PES-12 47
AC Q15444 PRELIMINARY: 18 AA
DE 01 NOV 1996 (TrEMBLrel. 12, Created)
DI 01 NOV 1999 (TrEMBLrel. 12, Last sequence update)
DI 01 NOV 1999 (TrEMBLrel. 12, Last annotation update)
DE Anti Protein (Fragment).
GN AM11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homin;
OX NCBI_TaxID:9606
RN [1]
RP SEQUENCE FROM N.A.
RX MIM-106224.97; PubMed:864347.
SA Levanon D., Bernstein Y., Neigam V., Omer M., Bar-Adi I.,
FA Aloya K., Goldenberg D., Lotan J., Groer Y.,
RT "A large variety of alternatively spliced and differentially expressed
RN mRNAs are encoded by the human acute myeloid leukemia gene AM11."
RL DNA Cell Biol. 15:175-185(1996).
RK EMBL: X69807; AA62467.2;
FT NON-TER 1
FT NON-TER 15
SQ SEQUENCE 15 AA: 193; MW: 226540.00; pI:4.0; CRC64:

Query Match 27.4% Score 21 DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 8,30+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7      4 KRI 6
LD      11
LD      4 KRI 6

PES-12 46
AC Q15444 PRELIMINARY: 18 AA
DE 01 MAY 2000 (TrEMBLrel. 12, Created)
DI 01 MAY 2000 (TrEMBLrel. 12, Last sequence update)
DI 01 MAR 2002 (TrEMBLrel. 12, Last annotation update)
DE Glycogen debranching enzyme (Fragment).
GN AG1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Suidae;
OC Monotremata; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus;
OX NCBI_TaxID:9623
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-prod. Landrace, and crossbred.
SA Stolt J. A., Hlaskova P., Kopecky M., Matyska J., Van Papeko M.,
FA Pechlan L.J., Fontanesi L., Lovell P., Sestini G., Russo V.,
RA Gellemann H.,
RT "Characterization of a SINE linked polymorphism in the porcine AG1 gene
RT and assignment of the gene to chromosome 2q31."
RL Submitted (04P-2002) to the EMBL/GenBank/DDBJ databases.
RK EMBL: AJ511347; CA954081.1;
RK EMBL: AF511347; CA954081.1;
KW Glycosidase; Hydrolase.
FT NON-TER 1
FT NON-TER 15
SQ SEQUENCE 15 AA: 1659; MW: 185961.06; pI:4.0; CRC64:

Query Match 27.4% Score 21 DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 8,30+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Q7      6 TER 8
LD      1
LD      9 TER 11

PES-12 49
AC Q95055 PRELIMINARY: 8 AA
DE 01 MAY 2000 (TrEMBLrel. 12, Created)
DI 01 MAY 2000 (TrEMBLrel. 12, Last sequence update)
DI 01 MAY 2000 (TrEMBLrel. 12, Last annotation update)
DE Putative IS60 transposase (Fragment).
GN EScherichia coli.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID:562
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-A2950;
RX MEDLINE:99194747; PubMed:10094716;
RA Rahn A., Brummel-Smith J., Whitfield C.,
RT "Conserved organization in the cps gene clusters for expression of
RI Escherichia coli group 1 K antigens: relationship to the colanic acid
RI biosynthesis locus and the cps genes from Klebsiella pneumoniae."
RL J. Bacteriol. 181:2307-2313(1999).
RK EMBL: AF182511; AA509641.1;
FT NON-TER 8
FT NON-TER 8
SQ SEQUENCE 8 AA: 103; MW: 12107.47; pI:4.14; CRC64:

Query Match 18.2% Score 21 DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8,30+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7      6 KRP 9
LD      1
LD      2 KRP 3

PES-12 5
AC Q9A314 PRELIMINARY: 8 AA
DE 01 JUN 2002 (TrEMBLrel. 12, Created)
DI 01 JUN 2002 (TrEMBLrel. 12, Last sequence update)
DI 01 MAR 2002 (TrEMBLrel. 20, Last annotation update)
DE Serine hydroxymethyltransferase (Fragment).
GN G1YA.
OS Archaea; Archaeobacteria; Actinobacteridae; Actinomycetales;
OC Bacterota; Actinobacteria; Micrococcales; Actinobacter.
OX NCBI_TaxID:153021
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN 111.
RA Nesky K., Harris K. L., Casalta V., Hasran J., Scrutton N.S.,
RT "Genetic organization of the genes involved in dimethylglycine and
RT sarcosine degradation in Actinobacter spp.: implications for glycine
RT betaine catabolism."
RL Submitted (DEC 2000) to the EMBL/GenBank/DDBJ databases.
RK EMBL: AF224781; AA16446.1;
RK KX Methyyltransferase; Transferase.
FT NON-TER 1
FT NON-TER 1
SQ SEQUENCE 8 AA: 648; MW: 681670.53; pI:7.2457; CRC64:

Query Match 18.2% Score 21 DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8,30+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7      4 KRP 7
LD      1
LD      4 KRP 3

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Search completed: September 30, 2003, 10:13:19
Total time: 40.5597 secs

GenePro version 1.0.6
Copyright (c) 1993 - 2003 GenePro Ltd

ORF protein protein search, using s-se model

Run on: September 30, 2003, 10:23:04 Search time 6:27 Seconds

(with 1000 iterations)
82,967 Matches, 60,144 hits/s/sec

Title: US-09-787-443-9

Perfect score: 11

Sequence: 1 AAKKKGSKPK 11

Scoring table: 01133

Gapop: 60.0, Gapext: 1.0

Searched: 123863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 707

Maximum DB seq length: 6

Maximum DB seq length: 15

Post Processing: Listing first 500 summaries

Database: 1 SwissProt_41.*

Note: No. is the number of residues predicted to change to have a
score greater than or equal to the score of the result being viewed,
and is derived by analysis of the total set of descriptions.

SUMMARYS

Res ID	Seq	Score	Match	Length	DB	ID	Description
1	1	27.3	6	1	PKK1_PPRAM	1	60212 periplaneta
2	2	27.3	9	1	NEUT_PAVPO	1	15496 cavia porco
3	3	27.3	10	1	COXK_PAT	1	80041 rattus norv
4	4	27.3	10	1	XYSP_P1394	1	18012 dictyostell
5	5	27.3	11	1	AS22_PAS-S	1	18117 bacteroides
6	6	27.3	12	1	PKK1_PPRAM	1	15496 cavia porco
7	7	27.3	12	1	NEUT_PAVPO	1	15496 cavia porco
8	8	27.3	12	1	PKK1_PPRAM	1	15496 cavia porco
9	9	27.3	12	1	NEUT_PAVPO	1	15496 cavia porco
10	10	27.3	13	1	PKK1_PPRAM	1	15496 cavia porco
11	11	27.3	13	1	NEUT_PAVPO	1	15496 cavia porco
12	12	27.3	13	1	NEUT_PAVPO	1	15496 cavia porco
13	13	27.3	13	1	NEUT_PAVPO	1	15496 cavia porco
14	14	27.3	13	1	NEUT_PAVPO	1	15496 cavia porco
15	15	27.3	13	1	NEUT_PAVPO	1	15496 cavia porco
16	16	27.3	13	1	NEUT_PAVPO	1	15496 cavia porco
17	17	27.3	15	1	PKK1_PPRAM	1	15496 cavia porco
18	18	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
19	19	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
20	20	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
21	21	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
22	22	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
23	23	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
24	24	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
25	25	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
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27	27	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
28	28	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
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32	32	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
33	33	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
34	34	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco
35	35	27.3	15	1	NEUT_PAVPO	1	15496 cavia porco

P80632 zea mays (m
P55575 rattus norv
P30087 homo sapien
P81814 carcinus ma
P82678 chlamydomon
P38556 carcinus ma
P05487 corus stria
P16339 locusta miq
P81279 macrobachi
P41172 ascaris suu
P19346 erythrocebu
P19345 macaca fusc
P19344 papio anubi
P19343 papio hanad
P19342 theopitheci
P83058 bombina var
P08946 phyllomedu
P41489 locusta miq
P36884 staphylococ
P04277 homo sapien
P23879 cyprinus ca
P42998 eisenia toe
P81179 diatrepe a
P82691 periplaneta
P31929 homo sapien
P25825 azotobacter
P51022 bothriops ja
O59121 oncorhynch
P20866 litorea cit
P56264 litorea xan
P83382 oncorhynch
P80337 ovis aries
P41468 locusta miq
P81135 mycobacteri
P11180 bos taurus
P83382 locusta miq
P83325 bacillus th
P81545 dictyostell
Q20947 halocynthia
P19851 gallus gall
P42634 aedes aegypt
P42635 aedes aegypt
P19118 nicotiana gl
P30091 homo sapien
P32118 homo sapien
P38007 chlamydia t
P80699 bacillus su
P30423 bothriops in
P30424 bothriops in
P01021 adkistredon
P04562 adkistredon
P12797 megalocolla
P82087 litorea cit
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P22790 archetina tu
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P83321 ponacus mon
P82684 carausius m
P80464 comanonas t
P08951 rana pipien
P42341 conopholis
P82651 hoplobatrach
P88616 urolophora r
P28498 gadus morhu
P01290 equus caball
P28499 oncorhynch
P41333 scyllorhinu
P08615 physalaemus
P50983 corus imper


```

OK PROSITE: PS00423; PEROXISOMAL SURF. PARTIAL
KW Peroxisomal protein: IRRA-binding
FI N-TER 1
SQ SEQUENCE 12 AA: 437-486E90855AA440044

Query Match
Best Local Similarity 27.4% Score 31 DB 1; Length 13;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : AIN 5
DB 10 AIN 12

RESULT 11
LIGASE_TRAVE STANDARD PRI: 13 AA
AC P20312
DT 01-FEB-1991 (Ref. 17, Created)
DT 01-FEB-1991 (Ref. 17, Last sequence update)
DT 28-FEB-2003 (Ref. 40, Last annotation update)
DE Ligninase B (EC 1.11.1.14) (Diarylpropane peroxidase) (Lignin
peroxidase) (Fragment)
OS Trametes versicolor (White-rot fungus)
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphelophorales; Trametes
CX NCBI_TaxID:5125;
KN [1]
RP SEQUENCE
KX MEDLINE:89211442; PubMed:2767445;
KA Jonsson L., Karlsson O., Lundquist K., Nyman P.G.
K1 "Trametes versicolor ligninase: isozyme sequence homology and
substrate specificity."
RG FEBS Lett. 247:143-146(1989).
CC 1- FUNCTION: Depolymerization of lignin. Catalyzes the C(alpha)-
C(beta) cleavage of the propyl side chains of lignin.
CC 1- CATALYTIC ACTIVITY: 1,2-bis(3,4-dimethoxyphenyl)propane-1,1-diol +
H(2)O(2) -> veratraldehyde + 1-(3,4-dimethylphenyl)ethane-1,2-diol
+ 4 H(2)O.
CC 1- PATHWAY: Lignin degradation; First step.
CC 1- SIMILARITY: BELONGS TO THE PEROXIDASE FAMILY. LIGNINASE SUBFAMILY.
DB PROSITE: PS00424; S04014
DB UniProt: P5040201; Peroxidase.
OR PROSITE: PS00435; PEROXIDASE_1; PARTIAL.
OR PROSITE: PS00436; PEROXIDASE_2; PARTIAL.
KW Oxidoreductase; Peroxidase; Iron; Heme; Glycoprotein;
KW Multigene family: Lignin degradation.
FT N-TER 13
SQ SEQUENCE 13 AA: 1269 MW; 22050ED5872A52C8 CRC64;

Query Match
Best Local Similarity 27.4% Score 31 DB 1; Length 13;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : AIN 5
DB 10 AIN 12

RESULT 12
NEUT_BOEVA STANDARD PRI: 13 AA
AC P41796
DT 16-SEP-2001 (Ref. 40, Created)
DT 16-SEP-2001 (Ref. 40, Last sequence update)
DT 28-FEB-2004 (Ref. 41, Last annotation update)
DE Neutrotenin (Nt)
OS Euteleostomi; Chordata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

```

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AC Amphibia: Batrachia: Anura: Neobatrachia: and suborder: Anuroidea
AC Info:
CX NCBI TaxID: 680;
LN 111
SEQUENCE: ANS SYNTHESIS
KW MEDLINE: 9706115; PubMed: 9724176;
KA Watanabe, F., Inohara, K., Goto, M.,
KI "purification, characterization, and sequencing of cDNA of
PL Peptide from the Toad Bufo marinus."
C2 C1 FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE.
C2 C1 FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE.
C2 C1 FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE.
C2 C1 FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE.
C2 C1 SUBCELLULAR LOCATION: Secreted.
C2 C1 SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
KW VASOACTIVE PYROLIDONE CARBOXYLIC ACID.
FT MOLRES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA: 1515 MW: 560066454 Da; CRC64:
Query Match 27.4% Score 3; DB 1; Length 13;
Best local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 RRP 10
LB 8 RRP 10
RESULT 15
MEDLINE:
AC NEUT. RANIE STANDARD; PRT: 13 AA
AC P41536;
C1 01-NOV-1995 (Rel. 42; Created)
C1 01-NOV-1995 (Rel. 42; Last sequence update)
C1 28-FEB-2003 (Rel. 41; Last annotation update)
C2 C1 FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE.
C2 C1 SUBCELLULAR LOCATION: Secreted.
C2 C1 TISSUE SPECIFICITY: IDENTIFIED IN BRAIN, INTESTINE, AND RECTUM.
C2 C1 BUT NOT IN STOMACH OR SKIN.
C2 C1 SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
DR PIP: A61067; A61067.
KW VASOACTIVE PYROLIDONE CARBOXYLIC ACID.
FT MOLRES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA: 1569 MW: 56A54D69EF4100D3 CRC64:
Query Match 27.4% Score 3; DB 1; Length 13;
Best local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 RRP 10
LB 8 RRP 10
RESULT 16
MEDLINE:
AC RANIE STANDARD; PRT: 13 AA
AC P47724;
C1 01-FEB-1999 (Rel. 35; Created)
C1 28-FEB-2003 (Rel. 41; Last sequence update)

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DE Neotensin (NP).
CS Gallus gallus (chicken).
CC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
CC Archosauria: Aves: Neognathae: Galliformes: Phasianidae: Phasianinae:
CC Gallus
CX NCBI TaxID: 9011;
LN 111
SEQUENCE:
KW MEDLINE: 8806192; PubMed: 8824091;
KA Tsubuchi, H., Koseki, S., Ohashi, H., Kimura, S.,
KI "The amino acid sequence of a smooth muscle-contracting peptide from
KI chicken rectum: identity to chicken neotensin."
RL Jpn. J. Pharmacol. 44:455-459(1987).
C2 C1 FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE.
C2 C1 SUBCELLULAR LOCATION: Secreted.
C2 C1 SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
DR PIR: A28505; A28505.
KW VASOACTIVE PYROLIDONE CARBOXYLIC ACID.
FT MOLRES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA: 1608 MW: 4C949E714C4100D3 CRC64:
Query Match 27.4% Score 3; DB 1; Length 13;
Best local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 RRP 10
LB 8 RRP 10
RESULT 17
MEDLINE:
AC NEUT. RANIE STANDARD; PRT: 13 AA
AC P41536;
C1 01-NOV-1995 (Rel. 42; Created)
C1 01-NOV-1995 (Rel. 42; Last sequence update)
C1 28-FEB-2003 (Rel. 41; Last annotation update)
C2 C1 FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE.
C2 C1 SUBCELLULAR LOCATION: Secreted.
C2 C1 TISSUE SPECIFICITY: IDENTIFIED IN BRAIN, INTESTINE, AND RECTUM.
C2 C1 BUT NOT IN STOMACH OR SKIN.
C2 C1 SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
DR PIP: A61067; A61067.
KW VASOACTIVE PYROLIDONE CARBOXYLIC ACID.
FT MOLRES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 13 AA: 1569 MW: 56A54D69EF4100D3 CRC64:
Query Match 27.4% Score 3; DB 1; Length 13;
Best local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 RRP 10
LB 8 RRP 10
RESULT 18
MEDLINE:
AC RANIE STANDARD; PRT: 13 AA
AC P47724;
C1 01-FEB-1999 (Rel. 35; Created)
C1 28-FEB-2003 (Rel. 41; Last sequence update)

```


Best Local Similarity 100.0%, Score 2, DH 1, Length 8;
Matches 2: Conservative 0; Mismatches 0; Indels 0;

27 0 AIN 3
14 0 AIN 3

RESULT 24
AKH3.GSYM
AC AKH3.GSYM STANDARD: PPI: 8 AA
PL4067

QY 01 JAN 1999 (Rel. 13, Created)
16 28, Score 2, DH 1, Length 8;
17 01 FEB 1994 (Rel. 28, Last sequence update)
18 01 FEB 2003 (Rel. 41, Last annotation update)
19 01 FEB 2003 (Rel. 41, Last annotation update)
20 01 FEB 2003 (Rel. 41, Last annotation update)
21 01 FEB 2003 (Rel. 41, Last annotation update)
22 01 FEB 2003 (Rel. 41, Last annotation update)
23 01 FEB 2003 (Rel. 41, Last annotation update)
24 01 FEB 2003 (Rel. 41, Last annotation update)
25 01 FEB 2003 (Rel. 41, Last annotation update)
26 01 FEB 2003 (Rel. 41, Last annotation update)
27 01 FEB 2003 (Rel. 41, Last annotation update)
28 01 FEB 2003 (Rel. 41, Last annotation update)
29 01 FEB 2003 (Rel. 41, Last annotation update)
30 01 FEB 2003 (Rel. 41, Last annotation update)
31 01 FEB 2003 (Rel. 41, Last annotation update)
32 01 FEB 2003 (Rel. 41, Last annotation update)
33 01 FEB 2003 (Rel. 41, Last annotation update)
34 01 FEB 2003 (Rel. 41, Last annotation update)
35 01 FEB 2003 (Rel. 41, Last annotation update)
36 01 FEB 2003 (Rel. 41, Last annotation update)
37 01 FEB 2003 (Rel. 41, Last annotation update)
38 01 FEB 2003 (Rel. 41, Last annotation update)
39 01 FEB 2003 (Rel. 41, Last annotation update)
40 01 FEB 2003 (Rel. 41, Last annotation update)
41 01 FEB 2003 (Rel. 41, Last annotation update)
42 01 FEB 2003 (Rel. 41, Last annotation update)
43 01 FEB 2003 (Rel. 41, Last annotation update)
44 01 FEB 2003 (Rel. 41, Last annotation update)
45 01 FEB 2003 (Rel. 41, Last annotation update)
46 01 FEB 2003 (Rel. 41, Last annotation update)
47 01 FEB 2003 (Rel. 41, Last annotation update)
48 01 FEB 2003 (Rel. 41, Last annotation update)
49 01 FEB 2003 (Rel. 41, Last annotation update)
50 01 FEB 2003 (Rel. 41, Last annotation update)

Best Local Similarity 100.0%, Score 2, DH 1, Length 8;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 BP 10
14 2 BP 3

RESULT 25
ALL4.CALVO
TD ALL4.CALVO STANDARD: PPI: 8 AA
AC F41840
16 01 NOV 1995 (Rel. 42, Created)
17 01 NOV 1995 (Rel. 42, Last sequence update)
18 01 NOV 1995 (Rel. 42, Last sequence update)
19 01 NOV 1995 (Rel. 42, Last sequence update)
20 01 NOV 1995 (Rel. 42, Last sequence update)
21 01 NOV 1995 (Rel. 42, Last sequence update)
22 01 NOV 1995 (Rel. 42, Last sequence update)
23 01 NOV 1995 (Rel. 42, Last sequence update)
24 01 NOV 1995 (Rel. 42, Last sequence update)
25 01 NOV 1995 (Rel. 42, Last sequence update)
26 01 NOV 1995 (Rel. 42, Last sequence update)
27 01 NOV 1995 (Rel. 42, Last sequence update)
28 01 NOV 1995 (Rel. 42, Last sequence update)
29 01 NOV 1995 (Rel. 42, Last sequence update)
30 01 NOV 1995 (Rel. 42, Last sequence update)
31 01 NOV 1995 (Rel. 42, Last sequence update)
32 01 NOV 1995 (Rel. 42, Last sequence update)
33 01 NOV 1995 (Rel. 42, Last sequence update)
34 01 NOV 1995 (Rel. 42, Last sequence update)
35 01 NOV 1995 (Rel. 42, Last sequence update)
36 01 NOV 1995 (Rel. 42, Last sequence update)
37 01 NOV 1995 (Rel. 42, Last sequence update)
38 01 NOV 1995 (Rel. 42, Last sequence update)
39 01 NOV 1995 (Rel. 42, Last sequence update)
40 01 NOV 1995 (Rel. 42, Last sequence update)
41 01 NOV 1995 (Rel. 42, Last sequence update)
42 01 NOV 1995 (Rel. 42, Last sequence update)
43 01 NOV 1995 (Rel. 42, Last sequence update)
44 01 NOV 1995 (Rel. 42, Last sequence update)
45 01 NOV 1995 (Rel. 42, Last sequence update)
46 01 NOV 1995 (Rel. 42, Last sequence update)
47 01 NOV 1995 (Rel. 42, Last sequence update)
48 01 NOV 1995 (Rel. 42, Last sequence update)
49 01 NOV 1995 (Rel. 42, Last sequence update)
50 01 NOV 1995 (Rel. 42, Last sequence update)


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RS2_PXCL1
ID RS2_PXCL1 STANDARD: 191 8 AA
AC P45564.1
DE 01-APR-1994 (Rel. 26, Created)
DE 01-APR-1994 (Rel. 26, Last sequence update)
DE 28-FEB-2003 (Rel. 43, Last annotation update)
DE 08-Ribosomal protein S7 (Fragment)
GN RS2CL
OS Mycobacterium intracellulare
OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Mycobacteriaceae
OC NCBI_TaxID:1767;
PN 1
PE SEQUENCE FROM N.A.
FX MEDLINE 93397130; PubMed 24521270
KA Smith C., Kease D.A., Morris S.L.
KI "Nucleotide sequence analysis of the ribosomal S12 gene 1
KI Mycobacterium intracellulare".
KL Nucleic Acids Res. 21:1049-1053(1993).
CO 1. EMBL/GENE/CCDS of the primary RNA coding proteins, 1. Bands
CO delivery to 28S rRNA where it facilitates assembly of the head
CO domain of the 60S subunit. It is located at the subunit interface
CO close to the decoding center, probably, blocks exit of the E site
CO tRNA (by similarity).
CO 2. Similarity: part of the 30S ribosomal subunit. Contact's proteins S9
CO and S11 (by similarity)
CO 3. SIMILARITY: BELONGS TO THE S10 FAMILY 1. 19P SMALL PROTEINS.
CO 4. THIS SWISS-PROT entry is copyrighted by the Swiss Institute of Bioinformatics
CO between the Swiss Institute of Bioinformatics and the EMBL European
CO Bioinformatics Institute. There are no restrictions on its
CO use by non-profit institutions as long as the copyright is acknowledged
CO and this statement is not removed. Usage by and for commercial
CO carriers requires a license agreement. See http://www.sdb.scripps.edu/
CO or send an email to: license@sdb.scripps.edu.
IR EMBL: U0177; AAA25376.1;
IR EMBL: S35548; S45548.
IR HAMM: ME 001402.1;
IR GenInfo: 19930245; Ribosomal_S7.
IR EMBL: F50352; RIBOSOMAL_S7; N.A.
KW RIBOSOMAL PROTEIN; RNA binding; RNA binding
FT CDS JOINED 1..6 BY STOP TAGS
FT NON_CODING 8..85
FT SEQUENCE 8 AA, 850 MW, 662 a.a. (by similarity)
Quality Match: 18.2%, Score 2, 109 1, Length 8;
Post-annot. Similarity: 100.0%, Pred. N: 1.4e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 1 1 1 1
CU 1 1 1 1 1
RESULT 14
ID 01A1 HUMAN STANDARD: 191 8 AA
AC P45687.1
DE 01-APR-1994 (Rel. 26, Created)
DE 01-APR-1994 (Rel. 26, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
GN NCBI_TaxID 9606;
PN 11
PE SEQUENCE
FX MEDLINE 94052447; PubMed 1459597;
KA Hughes G., Frutiger S., Paquet N., Ravier F., Pasquali C.,
KA Sanchez J.C., Jones R., Lissol M.D., Bjellqvist B.,
KA Hochstrasser D.F.
KA "Plasma protein map: mapping data by microsequencing."
KO Electrophoresis 13:207-214(1992)

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FA Bernellier J., Chazotte M., de Vienne D.
FI "Le maizé two dimensional gel proteome database: towards an integrated
FI genome analysis platform".
FI Theor. Appl. Genet. 93:997-1005(1996).
FI 1. MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED P1 OF THIS UNKNOWN
FI PROTEIN IS: 7.7, PIS MW IS: 57.2 KDa.
DE Marker2DPAGE: PAGE 42; COLLEOPTILE.
DE NON_TER 1
DE NON_TER 8
DE SEQUENCE 8 AA, 990 MW, 96 904.63AA(17561D CR664;
Quality Match: 18.2%, Score 2, 109 1, Length 8;
Post-annot. Similarity: 100.0%, Pred. N: 1.4e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 1 1 1 1
CU 1 1 1 1 1
RESULT 35
ID 01C9_RAT STANDARD: 191 8 AA
AC P56575.1
DE 15-DEC-1998 (Rel. 47, Created)
DE 15-DEC-1998 (Rel. 47, Last sequence update)
DE 15-DEC-1998 (Rel. 47, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
GN NCBI_TaxID:10116;
PN 11
PE SEQUENCE
FX STRAIN-WISLUT, TISSUE: Heart;
KA Li X., P., Pleissner K., P., Scheller C., Reitz-Zagrosek V., Salikov A.,
KA Jungblut P.R.
KA Submitted (SEP-1998) to the SWISS-PROT data bank.
FI 1. MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED P1 OF THIS UNKNOWN
FI PROTEIN IS: 8.9, PIS MW IS: 4.2 KDa.
FT NON_TER 8
FT SEQUENCE 8 AA, 1629 MW, 95 779.63AA(1408/6 CR664;
Quality Match: 18.2%, Score 2, 109 1, Length 8;
Post-annot. Similarity: 100.0%, Pred. N: 1.4e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 1 1 1 1
CU 1 1 1 1 1
RESULT 44
ID 01A1 HUMAN STANDARD: 191 8 AA
AC P45687.1
DE 01-APR-1994 (Rel. 26, Created)
DE 01-APR-1994 (Rel. 26, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D page of plasma (Spot 2) (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
GN NCBI_TaxID 9606;
PN 11
PE SEQUENCE
FX MEDLINE 94052447; PubMed 1459597;
KA Hughes G., Frutiger S., Paquet N., Ravier F., Pasquali C.,
KA Sanchez J.C., Jones R., Lissol M.D., Bjellqvist B.,
KA Hochstrasser D.F.
KA "Plasma protein map: mapping data by microsequencing."
KO Electrophoresis 13:207-214(1992)

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10 1 MUSCULAREUS: ON THE CELL, THE DETERMINED 10 + 1015 UNK UNK
11 09 GENES 4 2 150 MW 18 24 30 Kbp
12 SWISS-PROT: P4087: HUMAN
13 N-TER 1 1
14 UNTER 8 8
15 N-TER 8 8
16 N-TER 8 8
17 SEQUENCE 9 AA: 944 MW: 201223.73 g/mol: 6.96010
18
19 Query Name: 18 24 Score: 100.00, 100.00, 100.00
20 Best Local Similarity: 100.00, 100.00, 100.00
21 Matches 2: Conservative 0; Mismatches 0; Gaps 0
22
23 10 10 1
24 1 1 1
25 1 1 1
26
27 PEST: 47
28 ALL-ARMA STANDARD: PEST: 9 AA
29 10 10 1
30 10 10 1
31 10 10 1
32 10 10 1
33 10 10 1
34 10 10 1
35 10 10 1
36 10 10 1
37 10 10 1
38 10 10 1
39 10 10 1
40 10 10 1
41 10 10 1
42 10 10 1
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87 10 10 1
88 10 10 1
89 10 10 1
90 10 10 1
91 10 10 1
92 10 10 1
93 10 10 1
94 10 10 1
95 10 10 1
96 10 10 1
97 10 10 1
98 10 10 1
99 10 10 1
100 10 10 1

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10 1 MUSCULAREUS: ON THE CELL, THE DETERMINED 10 + 1015 UNK UNK
11 09 GENES 4 2 150 MW 18 24 30 Kbp
12 SWISS-PROT: P4087: HUMAN
13 N-TER 1 1
14 UNTER 8 8
15 N-TER 8 8
16 N-TER 8 8
17 SEQUENCE 9 AA: 944 MW: 201223.73 g/mol: 6.96010
18
19 Query Name: 18 24 Score: 100.00, 100.00, 100.00
20 Best Local Similarity: 100.00, 100.00, 100.00
21 Matches 2: Conservative 0; Mismatches 0; Gaps 0
22
23 10 10 1
24 1 1 1
25 1 1 1
26
27 PEST: 47
28 ALL-ARMA STANDARD: PEST: 9 AA
29 10 10 1
30 10 10 1
31 10 10 1
32 10 10 1
33 10 10 1
34 10 10 1
35 10 10 1
36 10 10 1
37 10 10 1
38 10 10 1
39 10 10 1
40 10 10 1
41 10 10 1
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67 10 10 1
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80 10 10 1
81 10 10 1
82 10 10 1
83 10 10 1
84 10 10 1
85 10 10 1
86 10 10 1
87 10 10 1
88 10 10 1
89 10 10 1
90 10 10 1
91 10 10 1
92 10 10 1
93 10 10 1
94 10 10 1
95 10 10 1
96 10 10 1
97 10 10 1
98 10 10 1
99 10 10 1
100 10 10 1

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```

FX SEQUENCE 9 AA: 959 MW: 656861A-610644L-579-4.
SQ SEQUENCE 9 AA: 959 MW: 656861A-610644L-579-4.

Query Match
Best Local Similarity 18.2% Score 2: DB 1: Length 9;
Matches 2: Conservative 0: Mismatches 0: Gaps 0:

QY 6 10 7
ID 7 13 8

RESULT 46
FASTA_HEADERS STANDARD: PK1: 9 AA
AC 15 AUG 1998 (Rel. 15, Created)
UT 01 AUG 1998 (Rel. 15, Last sequence update)
FT 15 AUG 1998 (Rel. 15, Last sequence update)
PE 15 AUG 1998 (Rel. 15, Last sequence update)
CS 15 AUG 1998 (Rel. 15, Last sequence update)
CC 15 AUG 1998 (Rel. 15, Last sequence update)
CQ 15 AUG 1998 (Rel. 15, Last sequence update)
KW 15 AUG 1998 (Rel. 15, Last sequence update)
SQ SEQUENCE 9 AA: 959 MW: 656861A-610644L-579-4.

Query Match
Best Local Similarity 18.2% Score 2: DB 1: Length 9;
Matches 2: Conservative 0: Mismatches 0: Gaps 0:

QY 6 10 7
ID 7 13 8

RESULT 47
FASTA_HEADERS STANDARD: PK1: 9 AA
AC 15 AUG 1998 (Rel. 15, Created)
UT 01 AUG 1998 (Rel. 15, Last sequence update)
FT 15 AUG 1998 (Rel. 15, Last sequence update)
PE 15 AUG 1998 (Rel. 15, Last sequence update)
CS 15 AUG 1998 (Rel. 15, Last sequence update)
CC 15 AUG 1998 (Rel. 15, Last sequence update)
CQ 15 AUG 1998 (Rel. 15, Last sequence update)
KW 15 AUG 1998 (Rel. 15, Last sequence update)
SQ SEQUENCE 9 AA: 959 MW: 656861A-610644L-579-4.

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FX SEQUENCE 9 AA: 959 MW: 656861A-610644L-579-4.
SQ SEQUENCE 9 AA: 959 MW: 656861A-610644L-579-4.

Query Match
Best Local Similarity 18.2% Score 2: DB 1: Length 9;
Matches 2: Conservative 0: Mismatches 0: Gaps 0:

QY 6 10 7
ID 7 13 8

RESULT 48
FASTA_HEADERS STANDARD: PK1: 9 AA
AC 15 AUG 1998 (Rel. 15, Created)
UT 01 AUG 1998 (Rel. 15, Last sequence update)
FT 15 AUG 1998 (Rel. 15, Last sequence update)
PE 15 AUG 1998 (Rel. 15, Last sequence update)
CS 15 AUG 1998 (Rel. 15, Last sequence update)
CC 15 AUG 1998 (Rel. 15, Last sequence update)
CQ 15 AUG 1998 (Rel. 15, Last sequence update)
KW 15 AUG 1998 (Rel. 15, Last sequence update)
SQ SEQUENCE 9 AA: 959 MW: 656861A-610644L-579-4.

Query Match
Best Local Similarity 18.2% Score 2: DB 1: Length 9;
Matches 2: Conservative 0: Mismatches 0: Gaps 0:

QY 6 10 7
ID 7 13 8

RESULT 49
FASTA_HEADERS STANDARD: PK1: 9 AA
AC 15 AUG 1998 (Rel. 15, Created)
UT 01 AUG 1998 (Rel. 15, Last sequence update)
FT 15 AUG 1998 (Rel. 15, Last sequence update)
PE 15 AUG 1998 (Rel. 15, Last sequence update)
CS 15 AUG 1998 (Rel. 15, Last sequence update)
CC 15 AUG 1998 (Rel. 15, Last sequence update)
CQ 15 AUG 1998 (Rel. 15, Last sequence update)
KW 15 AUG 1998 (Rel. 15, Last sequence update)
SQ SEQUENCE 9 AA: 959 MW: 656861A-610644L-579-4.

```

Result 49

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FASTA_ASCII
ID: FAK9_ASCII          STANDARD:      9 AA
AC: 143172
DT: 01-NOV-1995 (rel. 32, Last sequence update)
DI: 01-NOV-1995 (rel. 32, Last sequence update)
DE: 01-FEB-1996 (rel. 33, Last annotation update)
DE: FMRFamide-like neuropeptide APV
OS: Ascaris suum (pig roundworm) (Ascaris suum roundworm)
OC: Eukaryota; Metazoa; Nematoda; Chromida; Ascaridida; Ascarididae
OX: NCBI_TaxID:6253
RN: 1
RP: SEQ ID# 1
PX: MEDLINE: 95463462; PubMed 7651964;
KA: Gowen C, Striffler A O W;
*EctH novel FMRFamide-like neuropeptides isolated from the nematode
PI: Ascaris suum*;
RL: peptides 161492-500 (1995);
CC: 1. SIMILARITY: BELONGS TO THE FAMP (FMRFAMILE RELATED PEPTIDE)
    FAMILY;
KW: Neuropeptide; Amidation;
FT: M52_RUS 9 9 AMJAL18
SQ: SEQ ID# 9 AA: 1012 MW: 524307274; 16477 CRC64;

Query Match      14.2%, Score 2, DB 1, Length 9;
Best Local Similarity 100.0%, Pred. No. 1.3e-05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CR 11
   1
   4 CR 5

RESULT 44
FAMR_FYDA
ID: FIBB_FYDA          STANDARD:      9 AA
AC: 19436
DT: 01-NOV-1995 (rel. 16, Created)
DI: 01-NOV-1995 (rel. 16, Last sequence update)
DE: 28-FEB-2004 (rel. 41, Last annotation update)
DE: Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
OS: Erythrocytes patas (Red monkey) (Erythrocytes)
OC: Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
    Cercopitheciinae; Macaca;
OX: NCBI_TaxID:95543
RN: 1
RP: SEQ ID# 1
PX: MEDLINE: 85289140; PubMed-928610;
KA: Nakamura S, Takemaka O, Takahashi K;
*Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
PI: patas monkey (Erythrocytes patas); their amino acid sequences,
    restricted mutations, and a molecular phylogeny for macaques,
    quonous, and baboons*;
RL: J. Biochem. 97:1487-1492 (1985);
CC: 1. FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
    POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
    AGGREGATION;
    2. SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
    (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS;
    3. MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
    THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
    CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
    RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT;
DR: EIK: 024180; 024180
LR: InterPro: IPR002181; Fibrinogen_C
DR: PROSITE: PS00514; FIBRINAG_GLYCOPOLYMERIN; PARTIAL
KW: Blood coagulation; Plasma;
FT: PEPTIDE 1 9 FIBRINOPEPTIDE B;
FT: NON_TER 9 9
SQ: SEQ ID# 9 AA: 1008 MW: 63645960735BB1B CRC64;

Query Match      14.2%, Score 2, DB 1, Length 9;
Best Local Similarity 100.0%, Pred. No. 1.3e-05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CR 8
   1
   8 CR 9

RESULT 45
FIBB_PALAN
ID: FIBB_PALAN          STANDARD:      9 AA
AC: 193447
DT: 01-NOV-1995 (rel. 16, Created)
DI: 01-NOV-1995 (rel. 16, Last sequence update)
DE: 28-FEB-2003 (rel. 41, Last annotation update)
DE: Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
OS: Papio anubis (olive baboon)
OC: Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
    Cercopitheciinae; Papio;
OX: NCBI_TaxID:9555
RN: 1
RP: SEQ ID# 1
PX: MEDLINE: 95463462; PubMed 7651964;
KA: Gowen C, Striffler A O W;
*EctH novel FMRFamide-like neuropeptides isolated from the nematode
PI: Ascaris suum*;
RL: peptides 161492-500 (1995);
CC: 1. SIMILARITY: BELONGS TO THE FAMP (FMRFAMILE RELATED PEPTIDE)
    FAMILY;
KW: Neuropeptide; Amidation;
FT: M52_RUS 9 9 AMJAL18
SQ: SEQ ID# 9 AA: 1012 MW: 524307274; 16477 CRC64;

Query Match      14.2%, Score 2, DB 1, Length 9;
Best Local Similarity 100.0%, Pred. No. 1.3e-05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CR 8
   1
   8 CR 9

RESULT 46
FIBB_PALAN
ID: FIBB_PALAN          STANDARD:      9 AA
AC: 193447
DT: 01-NOV-1995 (rel. 16, Created)
DI: 01-NOV-1995 (rel. 16, Last sequence update)
DE: 28-FEB-2003 (rel. 41, Last annotation update)
DE: Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
OS: Papio anubis (olive baboon)
OC: Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
    Cercopitheciinae; Papio;
OX: NCBI_TaxID:9555
RN: 1
RP: SEQ ID# 1
PX: MEDLINE: 95463462; PubMed 7651964;
KA: Gowen C, Striffler A O W;
*EctH novel FMRFamide-like neuropeptides isolated from the nematode
PI: Ascaris suum*;
RL: peptides 161492-500 (1995);
CC: 1. SIMILARITY: BELONGS TO THE FAMP (FMRFAMILE RELATED PEPTIDE)
    FAMILY;
KW: Neuropeptide; Amidation;
FT: M52_RUS 9 9 AMJAL18
SQ: SEQ ID# 9 AA: 1012 MW: 524307274; 16477 CRC64;

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SEQUENCE
RX MEDLINE #416,b22; PubMed-642422;
RA Nakamura S., Takenaka O., Takahashi K.,
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas
and Theropithecus gelada): their amino acid sequences and
evolutionary rates and a molecular phylogeny for the baboons."
RJ J. Biochem. 94:1973-1978(1983)
CS 1- FUNCTION: FIBRINOGEN HAS A MOLECULAR FUNCTION: POLYMERIZING INTO
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
AGGREGATION.
CC 1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC 1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES.
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
PR F28854; F28854.
LR INFORMATION: PR002181; Fibrinogen.
DS PROSITE: PS00514; FIBRIN_A2_C-TERMINAL_FRAGMENT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRIN-PEPTIDE B
FT NON-TER 3 9
SQ SEQUENCE 9 AA: 1576 MW: 105649.28 kDa; Charge 1;
Quality Match 15.28; Score 2; ID 1; Length 9;
Best Local Similarity 100.00; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GR 8
L 8 GR 9
RESULT 4;
FIBR FIBRIN STANDARD; PPT: 9 AA.
A* F28854;
DI 01-NOV-1990 (Rel. 16; Created)
DI 01-NOV-1990 (Rel. 16; Last sequence update)
DI 26-FEB-2003 (Rel. 41; Last annotation update)
DE Fibrinogen beta chain. Contains: Fibrinopeptide B; (Fragment).
EN FGS.
CS Theropithecus gelada (Gelada baboon).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
CC Cercopithecoidea; Theropithecus.
CX NCBI_TaxID:9553;
RN [1]
PP SEQUENCE.
RX MEDLINE #416,b22; PubMed-642422;
RA Nakamura S., Takenaka O., Takahashi K.,
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
and Theropithecus gelada): their amino acid sequences and
evolutionary rates and a molecular phylogeny for the baboons."
RJ J. Biochem. 94:1973-1978(1983)
CS 1- FUNCTION: FIBRINOGEN HAS A MOLECULAR FUNCTION: POLYMERIZING INTO
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
AGGREGATION.
CC 1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC 1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES.
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
PR F28854; F28854.
LR INFORMATION: PR002181; Fibrinogen.
DS PROSITE: PS00514; FIBRIN_A2_C-TERMINAL_FRAGMENT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRIN-PEPTIDE B
FT NON-TER 3 9
SQ SEQUENCE 9 AA: 1576 MW: 105649.28 kDa; Charge 1;
Quality Match 15.28; Score 2; ID 1; Length 9;
Best Local Similarity 100.00; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GR 8
L 8 GR 9

```

```

SEQUENCE
RX MEDLINE #416,b22; PubMed-642422;
RA Nakamura S., Takenaka O., Takahashi K.,
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas
and Theropithecus gelada): their amino acid sequences and
evolutionary rates and a molecular phylogeny for the baboons."
RJ J. Biochem. 94:1973-1978(1983)
CS 1- FUNCTION: FIBRINOGEN HAS A MOLECULAR FUNCTION: POLYMERIZING INTO
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
AGGREGATION.
CC 1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC 1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES.
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
PR F28854; F28854.
LR INFORMATION: PR002181; Fibrinogen.
DS PROSITE: PS00514; FIBRIN_A2_C-TERMINAL_FRAGMENT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRIN-PEPTIDE B
FT NON-TER 3 9
SQ SEQUENCE 9 AA: 1576 MW: 105649.28 kDa; Charge 1;
Quality Match 15.28; Score 2; ID 1; Length 9;
Best Local Similarity 100.00; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GR 8
L 8 GR 9
RESULT 4;
FIBR FIBRIN STANDARD; PPT: 9 AA.
A* F28854;
DI 01-NOV-1990 (Rel. 16; Created)
DI 01-NOV-1990 (Rel. 16; Last sequence update)
DI 26-FEB-2003 (Rel. 41; Last annotation update)
DE Fibrinogen beta chain. Contains: Fibrinopeptide B; (Fragment).
EN FGS.
CS Theropithecus gelada (Gelada baboon).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
CC Cercopithecoidea; Theropithecus.
CX NCBI_TaxID:9553;
RN [1]
PP SEQUENCE.
RX MEDLINE #416,b22; PubMed-642422;
RA Nakamura S., Takenaka O., Takahashi K.,
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
and Theropithecus gelada): their amino acid sequences and
evolutionary rates and a molecular phylogeny for the baboons."
RJ J. Biochem. 94:1973-1978(1983)
CS 1- FUNCTION: FIBRINOGEN HAS A MOLECULAR FUNCTION: POLYMERIZING INTO
POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
AGGREGATION.
CC 1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
(ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC 1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
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CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES.
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
PR F28854; F28854.
LR INFORMATION: PR002181; Fibrinogen.
DS PROSITE: PS00514; FIBRIN_A2_C-TERMINAL_FRAGMENT.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRIN-PEPTIDE B
FT NON-TER 3 9
SQ SEQUENCE 9 AA: 1576 MW: 105649.28 kDa; Charge 1;
Quality Match 15.28; Score 2; ID 1; Length 9;
Best Local Similarity 100.00; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GR 8
L 8 GR 9

```


Genome version 3.1.0
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EM Protein - protein search, using S. mod.

Run on: September 03, 2003, 10:01:00 (with an additional 90,040,941 hits, 0.00044176/Sec)

Title: us-09-787-443-9

Protein source: 11

Sequence: 1: AINRRIGSEPR 11

Scoring table: 1130
Gapop: 60.0 / Gapext: 6.0

Searched: 253308 seqs, 9516866 hits found

Word size: 6

Total number of hits satisfying chosen parameters: 263

William: 18 seq length: 8
Maximum: 36 seq length: 15

Test processing: testing first 500 sequences

Database: 1: p1r76:*

2: p1r1:*

3: p1r2:*

4: p1r3:*

5: p1r4:*

Note: hit is the number of results found that are equal to, better, or worse than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SDMMATCH

Seq. ID	Score	Match	Length	DB	ID	Description
1	3	36.4	13	2	p1r76:1	cardiac troponin I
2	3	27.3	13	2	p1r76:2	ribosomal protein
3	3	27.3	13	2	p1r76:3	14.6 heavy chain
4	3	27.3	13	2	p1r76:4	14.6 heavy chain
5	3	27.3	11	2	p1r76:5	14.6 heavy chain
6	3	27.3	11	2	p1r76:6	14.6 heavy chain
7	3	27.3	11	2	p1r76:7	14.6 heavy chain
8	3	27.3	11	2	p1r76:8	14.6 heavy chain
9	3	27.3	12	2	p1r76:9	14.6 heavy chain
10	3	27.3	12	2	p1r76:10	14.6 heavy chain
11	3	27.3	13	1	UNR01	14.6 heavy chain
12	3	27.3	13	2	p1r76:11	14.6 heavy chain
13	3	27.3	13	2	p1r76:12	14.6 heavy chain
14	3	27.3	13	2	p1r76:13	14.6 heavy chain
15	3	27.3	13	2	p1r76:14	14.6 heavy chain
16	3	27.3	13	2	p1r76:15	14.6 heavy chain
17	3	27.3	13	2	p1r76:16	14.6 heavy chain
18	3	27.3	14	2	p1r76:17	14.6 heavy chain
19	3	27.3	14	2	p1r76:18	14.6 heavy chain
20	3	27.3	14	2	p1r76:19	14.6 heavy chain
21	3	27.3	14	2	p1r76:20	14.6 heavy chain
22	3	27.3	14	2	p1r76:21	14.6 heavy chain
23	3	27.3	14	2	p1r76:22	14.6 heavy chain
24	3	27.3	14	2	p1r76:23	14.6 heavy chain
25	3	27.3	15	2	p1r76:24	14.6 heavy chain
26	3	27.3	15	2	p1r76:25	14.6 heavy chain
27	3	27.3	15	2	p1r76:26	14.6 heavy chain
28	3	27.3	15	2	p1r76:27	14.6 heavy chain
29	3	27.3	15	2	p1r76:28	14.6 heavy chain
30	3	27.3	15	2	p1r76:29	14.6 heavy chain

31	3	27.3	15	2	p1r76:30	phenotypic variant
32	3	27.3	15	2	p1r76:31	protein QF200302
33	3	27.3	15	2	p1r76:32	heparin-binding le
34	3	27.3	15	2	p1r76:33	hypothetical prote
35	3	27.3	15	2	p1r76:34	hypothetical prote
36	3	27.3	15	2	p1r76:35	hypothetical prote
37	3	27.3	15	2	p1r76:36	hypothetical prote
38	3	27.3	15	2	p1r76:37	hypothetical prote
39	3	27.3	15	2	p1r76:38	hypothetical prote
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43	3	27.3	15	2	p1r76:42	hypothetical prote
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45	3	27.3	15	2	p1r76:44	hypothetical prote
46	3	27.3	15	2	p1r76:45	hypothetical prote
47	3	27.3	15	2	p1r76:46	hypothetical prote
48	3	27.3	15	2	p1r76:47	hypothetical prote
49	3	27.3	15	2	p1r76:48	hypothetical prote
50	3	27.3	15	2	p1r76:49	hypothetical prote
51	3	27.3	15	2	p1r76:50	hypothetical prote
52	3	27.3	15	2	p1r76:51	hypothetical prote
53	3	27.3	15	2	p1r76:52	hypothetical prote
54	3	27.3	15	2	p1r76:53	hypothetical prote
55	3	27.3	15	2	p1r76:54	hypothetical prote
56	3	27.3	15	2	p1r76:55	hypothetical prote
57	3	27.3	15	2	p1r76:56	hypothetical prote
58	3	27.3	15	2	p1r76:57	hypothetical prote
59	3	27.3	15	2	p1r76:58	hypothetical prote
60	3	27.3	15	2	p1r76:59	hypothetical prote
61	3	27.3	15	2	p1r76:60	hypothetical prote
62	3	27.3	15	2	p1r76:61	hypothetical prote
63	3	27.3	15	2	p1r76:62	hypothetical prote
64	3	27.3	15	2	p1r76:63	hypothetical prote
65	3	27.3	15	2	p1r76:64	hypothetical prote
66	3	27.3	15	2	p1r76:65	hypothetical prote
67	3	27.3	15	2	p1r76:66	hypothetical prote
68	3	27.3	15	2	p1r76:67	hypothetical prote
69	3	27.3	15	2	p1r76:68	hypothetical prote
70	3	27.3	15	2	p1r76:69	hypothetical prote
71	3	27.3	15	2	p1r76:70	hypothetical prote
72	3	27.3	15	2	p1r76:71	hypothetical prote
73	3	27.3	15	2	p1r76:72	hypothetical prote
74	3	27.3	15	2	p1r76:73	hypothetical prote
75	3	27.3	15	2	p1r76:74	hypothetical prote
76	3	27.3	15	2	p1r76:75	hypothetical prote
77	3	27.3	15	2	p1r76:76	hypothetical prote
78	3	27.3	15	2	p1r76:77	hypothetical prote
79	3	27.3	15	2	p1r76:78	hypothetical prote
80	3	27.3	15	2	p1r76:79	hypothetical prote
81	3	27.3	15	2	p1r76:80	hypothetical prote
82	3	27.3	15	2	p1r76:81	hypothetical prote
83	3	27.3	15	2	p1r76:82	hypothetical prote
84	3	27.3	15	2	p1r76:83	hypothetical prote
85	3	27.3	15	2	p1r76:84	hypothetical prote
86	3	27.3	15	2	p1r76:85	hypothetical prote
87	3	27.3	15	2	p1r76:86	hypothetical prote
88	3	27.3	15	2	p1r76:87	hypothetical prote
89	3	27.3	15	2	p1r76:88	hypothetical prote
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91	3	27.3	15	2	p1r76:90	hypothetical prote
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93	3	27.3	15	2	p1r76:92	hypothetical prote
94	3	27.3	15	2	p1r76:93	hypothetical prote
95	3	27.3	15	2	p1r76:94	hypothetical prote
96	3	27.3	15	2	p1r76:95	hypothetical prote
97	3	27.3	15	2	p1r76:96	hypothetical prote
98	3	27.3	15	2	p1r76:97	hypothetical prote
99	3	27.3	15	2	p1r76:98	hypothetical prote
100	3	27.3	15	2	p1r76:99	hypothetical prote
101	3	27.3	15	2	p1r76:100	hypothetical prote
102	3	27.3	15	2	p1r76:101	hypothetical prote

104	1	18.2	9	2	100234	SRP class 1 - cytosol	176	2	18.2	1	2	S71946	matrix metallopro
105	2	18.2	9	2	147243	19 heavy chain CRD	177	2	18.2	1	2	P81643	Ig H chain V-D-J r
106	3	18.2	9	2	P12298	19 heavy chain CRD	178	2	18.2	1	2	C54823	olfactory receptor
107	4	18.2	9	2	P13129	19 heavy chain CRD	179	2	18.2	1	2	P10213	T-cell receptor al
108	5	18.2	9	2	C66079	2-phosphoglycerate dehydrogenase	180	2	18.2	1	2	P84824	T-cell receptor al
109	6	18.2	9	2	S66644	19 heavy chain CRD	181	2	18.2	1	2	S65465	cytochrome-c oxid
110	7	18.2	9	2	144613	19 heavy chain CRD	182	2	18.2	1	2	C40572	T-cell receptor be
111	8	18.2	9	2	A28024	19 heavy chain CRD	183	2	18.2	1	2	P09244	T-cell receptor be
112	9	18.2	9	2	P07379	19 heavy chain CRD	184	2	18.2	1	2	P09246	T-cell receptor be
113	10	18.2	9	2	P10634	19 heavy chain CRD	185	2	18.2	1	2	P10634	T-cell receptor be
114	11	18.2	9	2	P07379	19 heavy chain CRD	186	2	18.2	1	2	P10634	T-cell receptor be
115	12	18.2	9	2	P07379	19 heavy chain CRD	187	2	18.2	1	2	P10634	T-cell receptor be
116	13	18.2	9	2	P07379	19 heavy chain CRD	188	2	18.2	1	2	P10634	T-cell receptor be
117	14	18.2	9	2	P07379	19 heavy chain CRD	189	2	18.2	1	2	P10634	T-cell receptor be
118	15	18.2	9	2	P07379	19 heavy chain CRD	190	2	18.2	1	2	P10634	T-cell receptor be
119	16	18.2	9	2	P07379	19 heavy chain CRD	191	2	18.2	1	2	P10634	T-cell receptor be
120	17	18.2	9	2	P07379	19 heavy chain CRD	192	2	18.2	1	2	P10634	T-cell receptor be
121	18	18.2	9	2	P07379	19 heavy chain CRD	193	2	18.2	1	2	P10634	T-cell receptor be
122	19	18.2	9	2	P07379	19 heavy chain CRD	194	2	18.2	1	2	P10634	T-cell receptor be
123	20	18.2	9	2	P07379	19 heavy chain CRD	195	2	18.2	1	2	P10634	T-cell receptor be
124	21	18.2	9	2	P07379	19 heavy chain CRD	196	2	18.2	1	2	P10634	T-cell receptor be
125	22	18.2	9	2	P07379	19 heavy chain CRD	197	2	18.2	1	2	P10634	T-cell receptor be
126	23	18.2	9	2	P07379	19 heavy chain CRD	198	2	18.2	1	2	P10634	T-cell receptor be
127	24	18.2	9	2	P07379	19 heavy chain CRD	199	2	18.2	1	2	P10634	T-cell receptor be
128	25	18.2	9	2	P07379	19 heavy chain CRD	200	2	18.2	1	2	P10634	T-cell receptor be
129	26	18.2	9	2	P07379	19 heavy chain CRD	201	2	18.2	1	2	P10634	T-cell receptor be
130	27	18.2	9	2	P07379	19 heavy chain CRD	202	2	18.2	1	2	P10634	T-cell receptor be
131	28	18.2	9	2	P07379	19 heavy chain CRD	203	2	18.2	1	2	P10634	T-cell receptor be
132	29	18.2	9	2	P07379	19 heavy chain CRD	204	2	18.2	1	2	P10634	T-cell receptor be
133	30	18.2	9	2	P07379	19 heavy chain CRD	205	2	18.2	1	2	P10634	T-cell receptor be
134	31	18.2	9	2	P07379	19 heavy chain CRD	206	2	18.2	1	2	P10634	T-cell receptor be
135	32	18.2	9	2	P07379	19 heavy chain CRD	207	2	18.2	1	2	P10634	T-cell receptor be
136	33	18.2	9	2	P07379	19 heavy chain CRD	208	2	18.2	1	2	P10634	T-cell receptor be
137	34	18.2	9	2	P07379	19 heavy chain CRD	209	2	18.2	1	2	P10634	T-cell receptor be
138	35	18.2	9	2	P07379	19 heavy chain CRD	210	2	18.2	1	2	P10634	T-cell receptor be
139	36	18.2	9	2	P07379	19 heavy chain CRD	211	2	18.2	1	2	P10634	T-cell receptor be
140	37	18.2	9	2	P07379	19 heavy chain CRD	212	2	18.2	1	2	P10634	T-cell receptor be
141	38	18.2	9	2	P07379	19 heavy chain CRD	213	2	18.2	1	2	P10634	T-cell receptor be
142	39	18.2	9	2	P07379	19 heavy chain CRD	214	2	18.2	1	2	P10634	T-cell receptor be
143	40	18.2	9	2	P07379	19 heavy chain CRD	215	2	18.2	1	2	P10634	T-cell receptor be
144	41	18.2	9	2	P07379	19 heavy chain CRD	216	2	18.2	1	2	P10634	T-cell receptor be
145	42	18.2	9	2	P07379	19 heavy chain CRD	217	2	18.2	1	2	P10634	T-cell receptor be
146	43	18.2	9	2	P07379	19 heavy chain CRD	218	2	18.2	1	2	P10634	T-cell receptor be
147	44	18.2	9	2	P07379	19 heavy chain CRD	219	2	18.2	1	2	P10634	T-cell receptor be
148	45	18.2	9	2	P07379	19 heavy chain CRD	220	2	18.2	1	2	P10634	T-cell receptor be
149	46	18.2	9	2	P07379	19 heavy chain CRD	221	2	18.2	1	2	P10634	T-cell receptor be
150	47	18.2	9	2	P07379	19 heavy chain CRD	222	2	18.2	1	2	P10634	T-cell receptor be
151	48	18.2	9	2	P07379	19 heavy chain CRD	223	2	18.2	1	2	P10634	T-cell receptor be
152	49	18.2	9	2	P07379	19 heavy chain CRD	224	2	18.2	1	2	P10634	T-cell receptor be
153	50	18.2	9	2	P07379	19 heavy chain CRD	225	2	18.2	1	2	P10634	T-cell receptor be
154	51	18.2	9	2	P07379	19 heavy chain CRD	226	2	18.2	1	2	P10634	T-cell receptor be
155	52	18.2	9	2	P07379	19 heavy chain CRD	227	2	18.2	1	2	P10634	T-cell receptor be
156	53	18.2	9	2	P07379	19 heavy chain CRD	228	2	18.2	1	2	P10634	T-cell receptor be
157	54	18.2	9	2	P07379	19 heavy chain CRD	229	2	18.2	1	2	P10634	T-cell receptor be
158	55	18.2	9	2	P07379	19 heavy chain CRD	230	2	18.2	1	2	P10634	T-cell receptor be
159	56	18.2	9	2	P07379	19 heavy chain CRD	231	2	18.2	1	2	P10634	T-cell receptor be
160	57	18.2	9	2	P07379	19 heavy chain CRD	232	2	18.2	1	2	P10634	T-cell receptor be
161	58	18.2	9	2	P07379	19 heavy chain CRD	233	2	18.2	1	2	P10634	T-cell receptor be
162	59	18.2	9	2	P07379	19 heavy chain CRD	234	2	18.2	1	2	P10634	T-cell receptor be
163	60	18.2	9	2	P07379	19 heavy chain CRD	235	2	18.2	1	2	P10634	T-cell receptor be
164	61	18.2	9	2	P07379	19 heavy chain CRD	236	2	18.2	1	2	P10634	T-cell receptor be
165	62	18.2	9	2	P07379	19 heavy chain CRD	237	2	18.2	1	2	P10634	T-cell receptor be
166	63	18.2	9	2	P07379	19 heavy chain CRD	238	2	18.2	1	2	P10634	T-cell receptor be
167	64	18.2	9	2	P07379	19 heavy chain CRD	239	2	18.2	1	2	P10634	T-cell receptor be
168	65	18.2	9	2	P07379	19 heavy chain CRD	240	2	18.2	1	2	P10634	T-cell receptor be
169	66	18.2	9	2	P07379	19 heavy chain CRD	241	2	18.2	1	2	P10634	T-cell receptor be
170	67	18.2	9	2	P07379	19 heavy chain CRD	242	2	18.2	1	2	P10634	T-cell receptor be
171	68	18.2	9	2	P07379	19 heavy chain CRD	243	2	18.2	1	2	P10634	T-cell receptor be
172	69	18.2	9	2	P07379	19 heavy chain CRD	244	2	18.2	1	2	P10634	T-cell receptor be
173	70	18.2	9	2	P07379	19 heavy chain CRD	245	2	18.2	1	2	P10634	T-cell receptor be
174	71	18.2	9	2	P07379	19 heavy chain CRD	246	2	18.2	1	2	P10634	T-cell receptor be
175	72	18.2	9	2	P07379	19 heavy chain CRD	247	2	18.2	1	2	P10634	T-cell receptor be
176	73	18.2	9	2	P07379	19 heavy chain CRD	248	2	18.2	1	2	P10634	T-cell receptor be

449	16	2	11	2	S23494	muscle, basic, associ	422	2	18	2	13	1	XAV190	angiotensin conver		
450	16	2	11	2	P00929	T-cell receptor be	323	2	18	2	13	1	JN4967	neurensin - brus		
451	18	2	11	2	P00936	T-cell receptor be	324	2	18	2	13	1	A48929	glutathione peroxi		
452	18	2	11	2	P00947	T-cell receptor be	325	2	18	2	13	1	A35245	histone H1a - mous		
453	18	2	11	2	P00957	T-cell receptor be	326	2	18	2	13	1	A35245	ribosomal protein		
454	16	2	11	2	P15204	quone RSSR4 protein	327	2	18	2	13	2	S78519	myosin heavy chain		
455	18	2	11	2	A48973	transacylase A1, 1E	328	2	18	2	13	2	A23695	bradykinin like pe		
456	18	2	11	2	P00769	N6,8,12 dehydratase	329	2	18	2	13	2	A61361	hypothetical prote		
457	18	2	11	4	S52252	cytochrome c, prote	330	2	18	2	13	2	S22945	hypothetical prote		
458	18	2	11	4	S19015	cytochrome c, prote	331	2	18	2	13	2	S22945	hypothetical prote		
459	18	2	12	1	A44975	ribosomal protein	332	2	18	2	13	2	A36042	oxix protein - Esc		
460	18	2	12	1	A54709	alpha oxoacid dehydr	333	2	18	2	13	2	S12368	arqa protein - Sal		
461	18	2	12	1	A49215	uridase (EC 3.5.1.5	334	2	18	2	13	2	S70723	lipamide dehydrog		
462	18	2	12	2	S26557	T-cell receptor be	335	2	18	2	13	2	S63432	dissimilatory sulf		
463	18	2	12	2	S26557	T-cell receptor be	336	2	18	2	13	2	S63432	hypothetical prote		
464	18	2	12	2	S26557	T-cell receptor be	337	2	18	2	13	2	P02371	probable endopepti		
465	18	2	12	2	S65409	histone H2a - huma	338	2	18	2	13	2	A32454	phloroglucinol red		
466	18	2	12	2	G49439	comp. ex. polyprot	339	2	18	2	13	2	S36887	ribosomal protein		
467	18	2	12	2	S36902	em protein - wheate	340	2	18	2	13	2	P04055	hypothetical 13 pr		
468	18	2	12	2	S02222	translational elonga	341	2	18	2	13	2	P00176	acidic ribosomal p		
469	18	2	12	2	S65629	protoporphyrinogen	342	2	18	2	13	2	S09716	2S albumin large c		
470	18	2	12	2	A44674	protoporphyrinogen	343	2	18	2	13	2	S09733	photosystem 1 prot		
471	18	2	12	2	A61365	vespakinin M - hor	344	2	18	2	13	2	J02319	hypothetical 1.6K		
472	18	2	12	2	A61365	vespakinin M - hor	345	2	18	2	13	2	J02319	hypothetical 1.6K		
473	18	2	12	2	A61365	vespakinin M - hor	346	2	18	2	13	2	P02500	ribulose-bisphosph		
474	18	2	12	2	S24539	gene p.9 protein -	347	2	18	2	13	2	J01350	hypothetical prote		
475	18	2	12	2	S24539	hypothetical prote	348	2	18	2	13	2	P00389	protein QF00053 -		
476	18	2	12	2	S64123	protein-translocat	349	2	18	2	13	2	H61620	locustamytotopin 1		
477	18	2	12	2	S43443	bank protein - Sta	350	2	18	2	13	2	P00443	potassium channel		
478	18	2	12	2	A60797	cytotoxin C 1 -	351	2	18	2	13	2	B28955	polysialoglycoprot		
479	18	2	12	2	G44420	hypothetical prote	352	2	18	2	13	2	S14273	polysialoglycoprot		
480	18	2	12	2	S47547	hypothetical prote	353	2	18	2	13	2	S14273	85K glycoprotein -		
481	18	2	12	2	S47547	ribosomal protein	354	2	18	2	13	2	S14273	deoxyriboflavyltr		
482	18	2	12	2	S47547	ribosomal protein	355	2	18	2	13	2	P02556	Ig heavy chain CRO		
483	18	2	12	2	PA5947	plastocyanin 2 - A	356	2	18	2	13	2	PT0331	Ig heavy chain CRO		
484	18	2	12	2	S67528	caprin - rape (rape	357	2	18	2	13	2	P01316	Ig heavy chain DJ		
485	18	2	12	2	S17540	angiotensin III rec	358	2	18	2	13	2	P01369	Ig heavy chain DJ		
486	18	2	12	2	P02413	28K protein 44.2 -	359	2	18	2	13	2	G61458	Ig lambda chain V-		
487	18	2	12	2	PA3698	ribosomal protein	360	2	18	2	13	2	S70441	pancreatic elastas		
488	18	2	12	2	A28955	polysialoglycoprot	361	2	18	2	13	2	S70441	T-cell receptor V-		
489	18	2	12	2	A39000	hydrolase - Atrial	362	2	18	2	13	2	S47357	T-cell antigen rec		
490	18	2	12	2	S10626	lipovitellin - Afi	363	2	18	2	13	2	S47376	T-cell antigen rec		
491	18	2	12	2	A49261	regulator factor	364	2	18	2	13	2	S47400	T-cell antigen rec		
492	18	2	12	2	S24855	3-hydroxyanthranilate	365	2	18	2	13	2	P01148	urinary tract ston		
493	18	2	12	2	P01255	Ig heavy chain CRO	366	2	18	2	13	2	G56046	mannose-1-phosphat		
494	18	2	12	2	P01255	Ig heavy chain CRO	367	2	18	2	13	2	B47435	sperm motility inh		
495	18	2	12	2	S43531	8-hydroxyanthranilate	368	2	18	2	13	2	S66235	diethyl-1-peptida		
496	18	2	12	2	P01255	T-cell antigen rec	369	2	18	2	13	2	S66235	6-phosphofructokin		
497	18	2	12	2	P01255	T-cell receptor di	370	2	18	2	13	2	S33879	Ig kappa-1 chain,		
498	18	2	12	2	P01255	T-cell receptor di	371	2	18	2	13	2	S25446	Ig kappa-1 chain,		
499	18	2	12	2	A39044	T-cell receptor de	372	2	18	2	13	2	PH1636	Ig H chain V-D-J r		
500	18	2	12	2	S74395	3-hydroxyanthranilate	373	2	18	2	13	2	PH1620	Ig H chain V-D-J r		
501	18	2	12	2	146942	basic beta protein	374	2	18	2	13	2	PH1593	Ig H chain V-D-J r		
502	18	2	12	2	S68452	NAD(P)-glycohydrol	375	2	18	2	13	2	PH1596	Ig H chain V-D-J r		
503	18	2	12	2	S68452	NAD(P)-glycohydrol	376	2	18	2	13	2	G37266	Ig heavy chain C r		
504	18	2	12	2	PH1636	Ig H chain V-D-J r	377	2	18	2	13	2	D37267	Ig heavy chain C r		
505	18	2	12	2	PH1636	Ig H chain V-D-J r	378	2	18	2	13	2	PH0795	T-cell receptor al		
506	18	2	12	2	PH1636	T-cell receptor al	379	2	18	2	13	2	PH0795	T-cell receptor al		
507	18	2	12	2	PH1636	T-cell receptor be	380	2	18	2	13	2	PH0786	T-cell receptor al		
508	18	2	12	2	PH1636	hexokinase (EC 2.7	381	2	18	2	13	2	S66558	serine proteinase		
509	18	2	12	2	B32521	beta-2-microglobu	382	2	18	2	13	2	A86126	hypothetical prote		
510	18	2	12	2	B32521	beta-2-microglobu	383	2	18	2	13	2	S33063	Ig lambda chain J		
511	18	2	12	2	PH0795	T-cell receptor be	384	2	18	2	13	2	S24344	glyceroldehyde-3-p		
512	18	2	12	2	PH0795	T-cell receptor be	385	2	18	2	13	2	14	1	UMWAV	mastoparan - yello
513	18	2	12	2	PH0795	T-cell receptor be	386	2	18	2	13	2	14	1	UMVHM	mastoparan M - hor
514	18	2	12	2	S24138	2 protein - guinea	387	2	18	2	13	2	14	1	QMVHXX	mastoparan X - hor
515	18	2	12	2	S24138	beta-2-microglobu	388	2	18	2	13	2	14	1	QMVHXX	mastoparan X - hor
516	18	2	12	2	A54251	membrane cytolisin	389	2	18	2	13	2	14	1	QMVHXX	mastoparan X - hor
517	18	2	12	2	A54251	membrane cytolisin	390	2	18	2	13	2	14	1	QMVHXX	mastoparan X - hor
518	18	2	12	2	A61342	Na+/K+ exchange	391	2	18	2	13	2	14	1	NTKN1M	polistes mastopara
519	18	2	12	2	S24138	beta-2-microglobu	392	2	18	2	13	2	14	1	LEF8WC	alpha-conotoxin M1
520	18	2	12	2	P02576	NaOH2 dehydrogenas	393	2	18	2	13	2	14	1	LEF8WC	trip operon leader
521	18	2	12	2	P02576	NaOH2 dehydrogenas	394	2	18	2	13	2	14	1	LEF8WC	trip operon leader
522	18	2	12	2	A54524	20 protein, cytochr	395	2	18	2	13	2	14	2	S63414	somatostatin - S11

Annotation: Bovine pre-beta2-microglobulin tetrapeptide contains amino acid sequence from serine to
 A:Reference number: JH0328; M010:91113172; PM10:167111

A:Accession: JH0328
 A:Molecule type: protein
 A:Residues: 1-14 (KAS)
 A:Comment: Infant proboscis has the biological activity of both serine protease and trypsin
 A:Keywords: infant proboscis, infant proboscis, infant proboscis, infant proboscis, infant proboscis
 A:Reference number: JH0328; M010:91113172; PM10:167111
 A:Accession: JH0328
 A:Molecule type: protein
 A:Residues: 1-14 (KAS)
 A:Comment: Infant proboscis has the biological activity of both serine protease and trypsin
 A:Keywords: infant proboscis, infant proboscis, infant proboscis, infant proboscis, infant proboscis

Query Match 27.4% Score 31 DB 21 Length 14
 Best Local Similarity 100.0% Pred. No. 4e+03
 Matches 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 GRR 9
 II
 LB 12 GRR 14

RESULT 19

PS371

Hypothetical protein (psac region) Synchococcus sp. (fragment)

C:Species: Synchococcus sp.

C:Date: 12 Aug 1992 #sequence_revision: 12 Aug 1992 #text_change: 08 Oct 1992

C:Accession: PS0371

A:Reference number: JH0328; M010:91113172; PM10:167111

A:Accession: PS0371

A:Molecule type: protein

A:Residues: 1-14 (KAS)

A:Comment: Infant proboscis has the biological activity of both serine protease and trypsin

A:Keywords: infant proboscis, infant proboscis, infant proboscis, infant proboscis, infant proboscis

Query Match 27.4% Score 31 DB 21 Length 14
 Best Local Similarity 100.0% Pred. No. 4e+03
 Matches 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 GRR 9
 II
 LB 12 GRR 14

RESULT 20

PS0371

Hypothetical protein (psac region) Synchococcus sp. (fragment)

C:Species: Synchococcus sp.

C:Date: 12 Aug 1992 #sequence_revision: 12 Aug 1992 #text_change: 08 Oct 1992

C:Accession: PS0371

A:Reference number: JH0328; M010:91113172; PM10:167111

A:Accession: PS0371

A:Molecule type: protein

A:Residues: 1-14 (KAS)

A:Comment: Infant proboscis has the biological activity of both serine protease and trypsin

A:Keywords: infant proboscis, infant proboscis, infant proboscis, infant proboscis, infant proboscis

Query Match 27.4% Score 31 DB 21 Length 14
 Best Local Similarity 100.0% Pred. No. 4e+03
 Matches 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 GRR 9
 II
 LB 12 GRR 14

RESULT 21

PS0371

Hypothetical protein (psac region) Synchococcus sp. (fragment)

C:Species: Synchococcus sp.

C:Date: 12 Aug 1992 #sequence_revision: 12 Aug 1992 #text_change: 08 Oct 1992

C:Accession: PS0371

A:Reference number: JH0328; M010:91113172; PM10:167111

A:Accession: PS0371

A:Molecule type: protein

C:Date: 12 Sep 1993 #sequence_revision: 30 Sep 1993 #text_change: 07 May 1999

C:Accession: PH1332

A:Reference number: JH0328; M010:91113172; PM10:167111

A:Accession: PH1332

A:Molecule type: protein

A:Residues: 1-14 (KAS)

A:Comment: Infant proboscis has the biological activity of both serine protease and trypsin

A:Keywords: infant proboscis, infant proboscis, infant proboscis, infant proboscis, infant proboscis

Query Match 27.4% Score 31 DB 21 Length 14
 Best Local Similarity 100.0% Pred. No. 4e+03
 Matches 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 GRR 9
 II
 LB 12 GRR 14

RESULT 22

PH1624

In H chain V D region (clone B less 47) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02 Jun 1994 #sequence_revision: 02 Jun 1994 #text_change: 17 Mar 1999

C:Accession: PH1624

A:Reference number: JH0328; M010:91113172; PM10:167111

A:Accession: PH1624

A:Molecule type: protein

A:Residues: 1-14 (KAS)

A:Comment: Infant proboscis has the biological activity of both serine protease and trypsin

A:Keywords: infant proboscis, infant proboscis, infant proboscis, infant proboscis, infant proboscis

Query Match 27.4% Score 31 DB 21 Length 14
 Best Local Similarity 100.0% Pred. No. 4e+03
 Matches 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 GRR 9
 II
 LB 12 GRR 14

RESULT 23

PH1624

In H chain V D region (clone B less 47) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 12 Aug 2000 #sequence_revision: 18 Aug 2000 #text_change: 18 Aug 2000

C:Accession: PH1624

A:Reference number: JH0328; M010:91113172; PM10:167111

A:Accession: PH1624

A:Molecule type: protein

A:Residues: 1-14 (KAS)

A:Comment: Infant proboscis has the biological activity of both serine protease and trypsin

A:Keywords: infant proboscis, infant proboscis, infant proboscis, infant proboscis, infant proboscis

Query Match 27.4% Score 31 DB 21 Length 14
 Best Local Similarity 100.0% Pred. No. 4e+03
 Matches 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 GRR 9
 II
 LB 12 GRR 14

RESULT 24

PH1624

In H chain V D region (clone B less 47) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 12 Aug 2000 #sequence_revision: 18 Aug 2000 #text_change: 18 Aug 2000

C:Accession: PH1624

A:Reference number: JH0328; M010:91113172; PM10:167111

A:Accession: PH1624

A:Molecule type: protein

Query Match 100.0% Score 31.06 21 length 15
 Best Local Similarity 100.0% Ident. No. 4 26403
 Matches 4: Conservative 0: Mismatches 0: Gaps 0

QY 1 AIN 4

IN 1 AIN 4

RESULT 4
 P0099
 Cytochrome P-450 1A2 (human) (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 20 Feb 1999 #sequence_revision 20 Feb 1999 #text_change 20 Feb 1999
 C:Accession: P0099
 K:Kabat: Kabat, E. J., & Blythe, R. L. (1972) in: "Sequences of Proteins of Human Interest", Vol. 1, Academic Press, New York, 1-15
 A:Title: Primary structure of a human mitochondrial protein homologous to the bacte
 A:Reference number: P0099
 A:Accession: P0099
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 (15)
 A:Keywords: cytochrome P-450

Query Match 100.0% Score 31.06 21 length 15
 Best Local Similarity 100.0% Ident. No. 4 26403
 Matches 4: Conservative 0: Mismatches 0: Gaps 0

QY 5 KID 7

IN 2 KID 4

RESULT 4
 P0099
 Cytochrome P-450 1A2 (human) (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 20 Feb 1999 #sequence_revision 20 Feb 1999 #text_change 20 Feb 1999
 C:Accession: P0099
 K:Kabat: Kabat, E. J., & Blythe, R. L. (1972) in: "Sequences of Proteins of Human Interest", Vol. 1, Academic Press, New York, 1-15
 A:Title: Primary structure of a human mitochondrial protein homologous to the bacte
 A:Reference number: P0099
 A:Accession: P0099
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 (15)
 A:Keywords: cytochrome P-450

Query Match 100.0% Score 31.06 21 length 15
 Best Local Similarity 100.0% Ident. No. 4 26403
 Matches 4: Conservative 0: Mismatches 0: Gaps 0

QY 1 AIN 4

IN 1 AIN 4

RESULT 4
 P0099
 Cytochrome P-450 1A2 (human) (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 20 Feb 1999 #sequence_revision 20 Feb 1999 #text_change 20 Feb 1999
 C:Accession: P0099
 K:Kabat: Kabat, E. J., & Blythe, R. L. (1972) in: "Sequences of Proteins of Human Interest", Vol. 1, Academic Press, New York, 1-15
 A:Title: Primary structure of a human mitochondrial protein homologous to the bacte
 A:Reference number: P0099
 A:Accession: P0099
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 (15)
 A:Keywords: cytochrome P-450

Query Match 100.0% Score 31.06 21 length 15
 Best Local Similarity 100.0% Ident. No. 4 26403
 Matches 4: Conservative 0: Mismatches 0: Gaps 0

QY 1 AIN 4

IN 1 AIN 4

Query Match 100.0% Score 31.06 21 length 15
 Best Local Similarity 100.0% Ident. No. 4 26403
 Matches 4: Conservative 0: Mismatches 0: Gaps 0

Query Match 100.0% Score 31.06 21 length 15
 Best Local Similarity 100.0% Ident. No. 4 26403
 Matches 4: Conservative 0: Mismatches 0: Gaps 0

QY 8 KID 7

IN 11 KID 14

RESULT 4
 P0099
 Cytochrome P-450 1A2 (human) (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 20 Feb 1999 #sequence_revision 20 Feb 1999 #text_change 20 Feb 1999
 C:Accession: P0099
 K:Kabat: Kabat, E. J., & Blythe, R. L. (1972) in: "Sequences of Proteins of Human Interest", Vol. 1, Academic Press, New York, 1-15
 A:Title: Primary structure of a human mitochondrial protein homologous to the bacte
 A:Reference number: P0099
 A:Accession: P0099
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 (15)
 A:Keywords: cytochrome P-450

Query Match 100.0% Score 31.06 21 length 15
 Best Local Similarity 100.0% Ident. No. 4 26403
 Matches 4: Conservative 0: Mismatches 0: Gaps 0

QY 1 AIN 4

IN 1 AIN 4

RESULT 4
 P0099
 Cytochrome P-450 1A2 (human) (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 20 Feb 1999 #sequence_revision 20 Feb 1999 #text_change 20 Feb 1999
 C:Accession: P0099
 K:Kabat: Kabat, E. J., & Blythe, R. L. (1972) in: "Sequences of Proteins of Human Interest", Vol. 1, Academic Press, New York, 1-15
 A:Title: Primary structure of a human mitochondrial protein homologous to the bacte
 A:Reference number: P0099
 A:Accession: P0099
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 (15)
 A:Keywords: cytochrome P-450

Query Match 100.0% Score 31.06 21 length 15
 Best Local Similarity 100.0% Ident. No. 4 26403
 Matches 4: Conservative 0: Mismatches 0: Gaps 0

QY 1 AIN 4

IN 1 AIN 4

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;
 Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 8 RR 9
 11
 DB 8 RR 4

RESULT 47
 PI0279
 L4 heavy chain CDR3 region (clone 4 9A) - Kuman (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 13-Sep-1993 #sequence_revision: 02-Jul-1996 #text_change: 05-Nov-1999
 C:Accession: PI0279
 R:Yamada, M.; Wasserman, R.; Reichardt, P.A.; Shiner, S.; Gattuso, A.; Koyval, G.
 J. Exp. Med. 173, 345-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PI0222; M01D:910637; PMID:169102
 A:Accession: PI0279
 A:Molecule type: DNA
 A:Status: preliminary
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;
 Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 8 RR 9
 11
 DB 8 RR 4

RESULT 48
 PI0279
 L4 heavy chain CDR3 region (clone 12 10b) - Kuman (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 13-Sep-1993 #sequence_revision: 02-Jul-1996 #text_change: 05-Nov-1999
 C:Accession: PI0279
 R:Yamada, M.; Wasserman, R.; Reichardt, P.A.; Shiner, S.; Gattuso, A.; Koyval, G.
 J. Exp. Med. 173, 345-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PI0222; M01D:910637; PMID:169102
 A:Accession: PI0279
 A:Molecule type: DNA
 A:Status: preliminary
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;
 Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 8 RR 9
 11
 DB 8 RR 4

RESULT 49
 PI0279
 L4 heavy chain CDR3 region (clone 12 10b) - Kuman (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 13-Sep-1993 #sequence_revision: 02-Jul-1996 #text_change: 05-Nov-1999
 C:Accession: PI0279
 R:Yamada, M.; Wasserman, R.; Reichardt, P.A.; Shiner, S.; Gattuso, A.; Koyval, G.
 J. Exp. Med. 173, 345-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PI0222; M01D:910637; PMID:169102
 A:Accession: PI0279
 A:Molecule type: DNA
 A:Status: preliminary
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;
 Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 8 RR 9
 11
 DB 8 RR 4

RESULT 50
 PI0279
 L4 heavy chain CDR3 region (clone 12 10b) - Kuman (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 13-Sep-1993 #sequence_revision: 02-Jul-1996 #text_change: 05-Nov-1999
 C:Accession: PI0279
 R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maczaki, Y.; Nadeau
 Mamm. Genome 5, 349-355, 1994
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR
 A:Reference number: PI0279; M01D:910637; PMID:8043949
 A:Accession: PI0279
 A:Status: preliminary; translated from GH/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-8 cRES
 A:Cross-references: EMBL:U05691; NID:9497010; PILEN:AAB60462.1; PILEN:q642826

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity: 100.0%; Pred. No. 2.8e+05;
 Matches: 2; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 8 RR 9
 11
 DB 8 RR 4

Search completed: September 30, 2003, 10:09:46
 Job time: 13.4367 secs

107	2	18.2	2	176	2	18.2	11	4	154081	retinoic acid rece
108	2	18.2	2	177	2	18.2	12	1	A45975	locustamototropin -
109	2	18.2	2	178	2	18.2	12	1	A50309	alpha-conotoxin Ia
110	2	18.2	2	179	2	18.2	12	2	SL2486	exo-alpha-stiloidas
111	2	18.2	2	180	2	18.2	12	2	149215	urease (EC 3.5.1.5
112	2	18.2	2	181	2	18.2	12	2	A61509	glycoprotein hormo
113	2	18.2	2	182	2	18.2	12	2	S26056	24 heavy chain m
114	2	18.2	2	183	2	18.2	12	2	S36712	Em protein - wheat
115	2	18.2	2	184	2	18.2	12	2	S01222	translation elonga
116	2	18.2	2	185	2	18.2	12	2	S45391	probable minor cap
117	2	18.2	2	186	2	18.2	12	2	A44874	proboscipedia fr
118	2	18.2	2	187	2	18.2	12	2	S10359	tachykinin - Afric
119	2	18.2	2	188	2	18.2	12	2	A61459	vespakinin X - hor
120	2	18.2	2	189	2	18.2	12	2	S26059	gene p10 protein -
121	2	18.2	2	190	2	18.2	12	2	S49215	urease (EC 3.5.1.5
122	2	18.2	2	191	2	18.2	12	2	S24479	hypothetical prote
123	2	18.2	2	192	2	18.2	12	2	S14447	blink protein - Sta
124	2	18.2	2	193	2	18.2	12	2	A60757	enterotoxin C 1 -
125	2	18.2	2	194	2	18.2	12	2	A49763	sucrose-6-phosphat
126	2	18.2	2	195	2	18.2	12	2	S45663	bma protein - clos
127	2	18.2	2	196	2	18.2	12	2	S49547	hypothetical prote
128	2	18.2	2	197	2	18.2	12	2	A45019	acidic ribosomal p
129	2	18.2	2	198	2	18.2	12	2	PT0083	protein QA600022 -
130	2	18.2	2	199	2	18.2	12	2	PA0098	ribosomal protein
131	2	18.2	2	200	2	18.2	12	2	SL6204	6-phosphotriactokin
132	2	18.2	2	201	2	18.2	12	2	S65740	hemoglobin, extrac
133	2	18.2	2	202	2	18.2	12	2	C51306	hemocyanin chain 6
134	2	18.2	2	203	2	18.2	12	2	A35900	hydrin 1 - African
135	2	18.2	2	204	2	18.2	12	2	SL6266	lipovitellin - Afr
136	2	18.2	2	205	2	18.2	12	2	A41503	sterol carrier pro
137	2	18.2	2	206	2	18.2	12	2	PT0245	1q heavy chain CRD
138	2	18.2	2	207	2	18.2	12	2	S43170	kinesin light chdi
139	2	18.2	2	208	2	18.2	12	2	S47363	1 cell antigen rec
140	2	18.2	2	209	2	18.2	12	2	S41346	3-hydroxy-3-methyl
141	2	18.2	2	210	2	18.2	12	2	020937	1q kappa 1 chain: J
142	2	18.2	2	211	2	18.2	12	2	140533	1q gamma-2b chain
143	2	18.2	2	212	2	18.2	12	2	PH1695	1q H chain V-D-J r
144	2	18.2	2	213	2	18.2	12	2	PH1696	1q H chain V-D-J r
145	2	18.2	2	214	2	18.2	12	2	PH1551	1q H chain V-D-J r
146	2	18.2	2	215	2	18.2	12	2	S25343	1q heavy chain V r
147	2	18.2	2	216	2	18.2	12	2	S39633	neura; cell adhesi
148	2	18.2	2	217	2	18.2	12	2	S23468	2 protein; golined
149	2	18.2	2	218	2	18.2	12	2	PQ0776	1c beta 1 isotorm
150	2	18.2	2	219	2	18.2	12	2	S49073	NAH2 dehydrogenas
151	2	18.2	2	220	2	18.2	12	2	XAV138	frame shifted cyta
152	2	18.2	2	221	2	18.2	13	1	U6E181	angiostatin concer
153	2	18.2	2	222	2	18.2	13	1	U6E181	neurotensin - brus
154	2	18.2	2	223	2	18.2	13	1	U6E181	melanotropin alpha
155	2	18.2	2	224	2	18.2	13	1	U6E181	melanotropin alpha
156	2	18.2	2	225	2	18.2	13	1	U6E181	glutathione peroxi
157	2	18.2	2	226	2	18.2	13	1	A50658	neurotensin - quin
158	2	18.2	2	227	2	18.2	13	1	A26335	neurotensin [valid
159	2	18.2	2	228	2	18.2	13	1	A26335	neurotensin - comm
160	2	18.2	2	229	2	18.2	13	1	A26335	myosin heavy chain
161	2	18.2	2	230	2	18.2	13	1	A26335	lactose phosphoria
162	2	18.2	2	231	2	18.2	13	1	PH1122	oil protein - vacu
163	2	18.2	2	232	2	18.2	13	1	S21152	tryptophyllin reia
164	2	18.2	2	233	2	18.2	13	1	A05114	tryptophyllin-13 -
165	2	18.2	2	234	2	18.2	13	1	PH0460	corticostatic pept
166	2	18.2	2	235	2	18.2	13	1	A04558	protocatheuatin 3,
167	2	18.2	2	236	2	18.2	13	1	104533	hypothetical prote
168	2	18.2	2	237	2	18.2	13	1	154084	acq-46.5 protein -
169	2	18.2	2	238	2	18.2	13	1	S22095	hypothetical prote
170	2	18.2	2	239	2	18.2	13	1	S35342	oxix protein - Esc
171	2	18.2	2	240	2	18.2	13	1	S70723	lipamide dehydroq
172	2	18.2	2	241	2	18.2	13	1	S64324	hyperhelical prote
173	2	18.2	2	242	2	18.2	13	1	S64324	hyperhelical prote
174	2	18.2	2	243	2	18.2	13	1	S64324	probable endopepti
175	2	18.2	2	244	2	18.2	13	1	S64324	ribosomal protein
176	2	18.2	2	245	2	18.2	13	1	S64324	ribosomal protein
177	2	18.2	2	246	2	18.2	13	1	S64324	photosystem 2 prot
178	2	18.2	2	247	2	18.2	13	1	S64324	early nadalin 4b -
179	2	18.2	2	248	2	18.2	13	1	S64324	hypothetical 1.6k

253	18.2	13	2	184757	protein, 12 - cyto	322	18.2	14	2	PR0147	omega-gliadin 1 a
250	18.2	13	2	302419	hypothetical 1.6K	323	18.2	14	2	PR0151	omega-gliadin 2'
251	18.2	13	2	301450	hypothetical protein	324	18.2	14	2	PR0163	chaperone, trp1 re
252	18.2	13	2	PR0168	phosphorylase, hy	325	18.2	14	2	PA0104	protein OF20070 -
253	18.2	13	2	PA0189	protein, 250/1.5 x	326	18.2	14	2	S45625	cathelicidin (EC 3,
254	18.2	13	2	PA0196	collagen, 700/2 - mu	327	18.2	14	2	S21376	collagen alpha cha
255	18.2	13	2	PR0120	trans-aminocroton 1	329	18.2	14	2	PR0152	metal-binding prot
256	18.2	13	2	PR0143	beta-actin, chaperi	329	18.2	14	2	GA1308	hemocyanin chain, 3
257	18.2	13	2	PR0153	deoxyacetyl dehydr	330	18.2	14	2	S48307	DEB-A protein - fr
258	18.2	13	2	S52456	hypothetical prote	331	18.2	14	2	S12904	protein kinase (EC
259	18.2	13	2	PR0105	beta-heavy chain (60	332	18.2	14	2	PR0284	G1-inhibitor, hum
260	18.2	13	2	PR0106	beta-heavy chain (62	333	18.2	14	2	PR0223	Ig heavy chain CDR
261	18.2	13	2	PR0109	Ig heavy chain (11	334	18.2	14	2	PR0254	Ig heavy chain CDR
262	18.2	13	2	S47456	Ig heavy chain (12	335	18.2	14	2	PR0294	Ig heavy chain CDR
263	18.2	13	2	S47457	Ig heavy chain (13	336	18.2	14	2	PR0347	Ig heavy chain DJ
264	18.2	13	2	S47459	Ig heavy chain (14	337	18.2	14	2	PR0327	Ig heavy chain DJ
265	18.2	13	2	S47465	Ig heavy chain (15	338	18.2	14	2	PR0356	Ig heavy chain DJ
266	18.2	13	2	S47471	Ig heavy chain (16	339	18.2	14	2	PR0342	Ig heavy chain DJ
267	18.2	13	2	S47472	Ig heavy chain (17	340	18.2	14	2	PR0321	Ig heavy chain DJ
268	18.2	13	2	S47473	Ig heavy chain (18	341	18.2	14	2	PR0321	Ig heavy chain DJ
269	18.2	13	2	S47476	Ig heavy chain (19	342	18.2	14	2	PR0305	Ig heavy chain DJ
270	18.2	13	2	S47477	Ig heavy chain (20	343	18.2	14	2	PR0306	Ig heavy chain DJ
271	18.2	13	2	S47480	Ig heavy chain (21	344	18.2	14	2	S57574	T-cell receptor V-
272	18.2	13	2	S47481	Ig heavy chain (22	345	18.2	14	2	PR0135	T-cell receptor be
273	18.2	13	2	S47482	Ig heavy chain (23	346	18.2	14	2	PR0040	glycogen phosphory
274	18.2	13	2	S47484	Ig heavy chain (24	347	18.2	14	2	A44847	Ig mu chain V regi
275	18.2	13	2	S47485	Ig heavy chain (25	348	18.2	14	2	JS0272	hypothetical 1.5K
276	18.2	13	2	S47487	Ig heavy chain (26	349	18.2	14	2	PR01625	Ig H chain V-D-J r
277	18.2	13	2	S47488	Ig heavy chain (27	350	18.2	14	2	PR01627	Ig H chain V-D-J r
278	18.2	13	2	S47489	Ig heavy chain (28	351	18.2	14	2	PR01628	Ig H chain V-D-J r
279	18.2	13	2	S47494	Ig heavy chain (29	352	18.2	14	2	PR01649	Ig H chain V-D-J r
280	18.2	13	2	S62328	T-cell, specific TR	353	18.2	14	2	PR01617	Ig H chain V-D-J r
281	18.2	13	2	PR0166	aggrexin - lectine	354	18.2	14	2	PR01624	Ig H chain V-D-J r
282	18.2	13	2	PR0164	aggrexin - lectin	355	18.2	14	2	PR01586	Ig H chain V-D-J r
283	18.2	13	2	PR0165	Ig kappa 1 chain 1	356	18.2	14	2	PR01594	Ig H chain V-D-J r
284	18.2	13	2	PR0166	Ig kappa 1 chain 2	357	18.2	14	2	PR01597	Ig H chain V-D-J r
285	18.2	13	2	PR0167	Ig kappa 1 chain 3	358	18.2	14	2	PR01608	Ig H chain V-D-J r
286	18.2	13	2	PR0168	Ig kappa 1 chain 4	359	18.2	14	2	PR02113	Ig H chain V-D-J r
287	18.2	13	2	PR0169	Ig kappa 1 chain 5	360	18.2	14	2	PR01605	T-cell receptor al
288	18.2	13	2	PR0170	Ig kappa 1 chain 6	361	18.2	14	2	PR01606	T-cell receptor be
289	18.2	13	2	PR0171	Ig kappa 1 chain 7	362	18.2	14	2	S65392	cytochrome-c oxida
290	18.2	13	2	PR0172	Ig kappa 1 chain 8	363	18.2	14	2	PR01645	T-cell receptor be
291	18.2	13	2	PR0173	Ig kappa 1 chain 9	364	18.2	14	2	PR01615	T-cell receptor be
292	18.2	13	2	PR0174	Ig kappa 1 chain 10	365	18.2	14	2	S83754	hypothetical prote
293	18.2	13	2	PR0175	Ig kappa 1 chain 11	366	18.2	14	2	PR01778	hypothetical prote
294	18.2	13	2	PR0176	Ig kappa 1 chain 12	367	18.2	14	2	PR01786	hypothetical prote
295	18.2	13	2	PR0177	Ig kappa 1 chain 13	368	18.2	14	2	PR01791	trp operon leader
296	18.2	13	2	PR0178	Ig kappa 1 chain 14	369	18.2	14	2	PR01792	trp operon leader
297	18.2	13	2	PR0179	Ig kappa 1 chain 15	370	18.2	14	2	PR01793	trp operon leader
298	18.2	13	2	PR0180	Ig kappa 1 chain 16	371	18.2	14	2	S22217	D-arabinose 1-dehy
299	18.2	13	2	PR0181	Ig kappa 1 chain 17	372	18.2	14	2	S22218	hemoglobin beta ch
300	18.2	13	2	PR0182	Ig kappa 1 chain 18	373	18.2	14	2	S03443	hypothetical prote
301	18.2	13	2	PR0183	Ig kappa 1 chain 19	374	18.2	14	2	PR0183	trp operon leader
302	18.2	13	2	PR0184	Ig kappa 1 chain 20	375	18.2	14	2	PR0183	trp operon leader
303	18.2	13	2	PR0185	Ig kappa 1 chain 21	376	18.2	14	2	PR0183	trp operon leader
304	18.2	13	2	PR0186	Ig kappa 1 chain 22	377	18.2	14	2	S21202	alpha-glucosidase
305	18.2	13	2	PR0187	Ig kappa 1 chain 23	378	18.2	14	2	S21202	glucan 1,4-alpha-g
306	18.2	13	2	PR0188	Ig kappa 1 chain 24	379	18.2	14	2	S21202	leukocyte esterase
307	18.2	13	2	PR0189	Ig kappa 1 chain 25	380	18.2	14	2	PR02115	fibrinogenolytic p
308	18.2	13	2	PR0190	Ig kappa 1 chain 26	381	18.2	14	2	S57261	basic proteinase 1
309	18.2	13	2	PR0191	Ig kappa 1 chain 27	382	18.2	14	2	S54397	ubiquitin-carrier
310	18.2	13	2	PR0192	Ig kappa 1 chain 28	383	18.2	14	2	PR0192	hemoglobin alpha c
311	18.2	13	2	PR0193	Ig kappa 1 chain 29	384	18.2	14	2	PR0193	heterogeneous ribo
312	18.2	13	2	PR0194	Ig kappa 1 chain 30	385	18.2	14	2	PR0194	ribosomal protein
313	18.2	13	2	PR0195	Ig kappa 1 chain 31	386	18.2	14	2	PR0195	Dp116 - human
314	18.2	13	2	PR0196	Ig kappa 1 chain 32	387	18.2	14	2	PR0196	trypsin - rabbit
315	18.2	13	2	PR0197	Ig kappa 1 chain 33	388	18.2	14	2	PR0197	placental calcium-
316	18.2	13	2	PR0198	Ig kappa 1 chain 34	389	18.2	14	2	PR0198	fibrinogen alpha c
317	18.2	13	2	PR0199	Ig kappa 1 chain 35	390	18.2	14	2	PR0199	ubiquitin thioest
318	18.2	13	2	PR0200	Ig kappa 1 chain 36	391	18.2	14	2	PR0200	hypothetical leade
319	18.2	13	2	PR0201	Ig kappa 1 chain 37	392	18.2	14	2	PR0201	hypothetical prote
320	18.2	13	2	PR0202	Ig kappa 1 chain 38	393	18.2	14	2	PR0202	hypothetical prote
321	18.2	13	2	PR0203	Ig kappa 1 chain 39	394	18.2	14	2	PR0203	capsid protein VP1

glycine reductase (EC 1.4.99.7) salivary protein of alpha chain. C:Species: Gadus morhua (Atlantic cod)
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 15-Apr-1997
C:Accession: S23308
R:Gadman, J.C.; Davis, J.M.
A:Title: Glycine reductase protein: C1 properties and characterization of its gene. In: 160
A:Biochem. J. 266, 22147-22154, 1991
A:Title: Glycine reductase protein: C1 properties and characterization of its gene. In: 160
A:Reference number: S23308; M01D:9229692; PMID:1593265
A:Accession: S23308
A:Molecule type: Protein
A:Residues: 1-11 SLEN
A:Experimental source: brain
C:Function:
A:Description: may play a physiological role in the regulation of cardiovascular and
A:Note: substance P is derived by post-translational processing of preprotachykinin
C:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide; amidated carboxyl end; tachykinin
F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match: 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity: 100.0%; Prod. No. 2e-03;
Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9
II
LB 1 KPR 4

RESULT 5
S23308
Substance P. Atlantic cod
C:Species: Gadus morhua (Atlantic cod)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S23306
R:Gadman, J.C.; Conlon, J.M.
A:Title: Substance P-related and neuropeptide A-related peptides from the brain of the
A:Reference number: S23306; M01D:9229692; PMID:1376687
A:Accession: S23306
A:Molecule type: protein
A:Residues: 1-11 SLEN
A:Experimental source: brain
C:Function:
A:Description: may play a physiological role in the regulation of cardiovascular and
A:Note: substance P is derived by post-translational processing of preprotachykinin
C:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide; amidated carboxyl end (Met) #status predicted
F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match: 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity: 100.0%; Prod. No. 2e-03;
Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9
II
LB 1 KPR 4

RESULT 6
S65606
Guinoline 2-oxido-reductase alpha chain. Comamonas testosteroni (fragment)
C:Species: Comamonas testosteroni
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S65606
R:Schach, S.; Tshisaka, B.; Feilner, S.; Lingens, F.
A:Title: Guinoline 2-oxido-reductase and 2-oxo-1,2-dihydroguinoline 5,6-dioxygenase 1
A:Reference number: S65606; M01D:9229689; PMID:7536204
A:Accession: S65606
A:Molecule type: Protein
A:Residues: 1-11 SSWH
A:Experimental source: strain 63

Query Match: 27.4%; Score 3; DB 2; Length 11;
Best Local Similarity: 100.0%; Prod. No. 2e-03;
Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9
II
LB 9 KPR 11

RESULT 7
S23300
Probable substance P - smaller spotted catshark
C:Species: Scyliorhinus reticulatus (smaller spotted catshark, smaller spotted dogfish)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999
C:Accession: S23300
R:Wang, D.; Wang, Y.; Havel, N.; Baiment, R.J.; Conlon, J.M.
A:Title: Primary structures and biological activities of substance P-related peptide
A:Reference number: S23300; M01D:9229250; PMID:7685693

glycine reductase (EC 1.4.99.7) salivary protein of alpha chain. C:Species: Gadus morhua (Atlantic cod)
C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 15-Apr-1997
C:Accession: S23308
R:Gadman, J.C.; Davis, J.M.
A:Title: Glycine reductase protein: C1 properties and characterization of its gene. In: 160
A:Biochem. J. 266, 22147-22154, 1991
A:Title: Glycine reductase protein: C1 properties and characterization of its gene. In: 160
A:Reference number: S23308; M01D:9229692; PMID:1593265
A:Accession: S23308
A:Molecule type: Protein
A:Residues: 1-11 SLEN
A:Experimental source: brain
C:Function:
A:Description: may play a physiological role in the regulation of cardiovascular and
A:Note: substance P is derived by post-translational processing of preprotachykinin
C:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide; amidated carboxyl end (Met) #status predicted
F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match: 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity: 100.0%; Prod. No. 2e-03;
Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9
II
LB 1 KPR 4

RESULT 5
S23308
Substance P. Atlantic cod
C:Species: Gadus morhua (Atlantic cod)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S23306
R:Gadman, J.C.; Conlon, J.M.
A:Title: Substance P-related and neuropeptide A-related peptides from the brain of the
A:Reference number: S23306; M01D:9229692; PMID:1376687
A:Accession: S23306
A:Molecule type: protein
A:Residues: 1-11 SLEN
A:Experimental source: brain
C:Function:
A:Description: may play a physiological role in the regulation of cardiovascular and
A:Note: substance P is derived by post-translational processing of preprotachykinin
C:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide; amidated carboxyl end (Met) #status predicted
F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match: 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity: 100.0%; Prod. No. 2e-03;
Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9
II
LB 1 KPR 4

RESULT 6
S65606
Guinoline 2-oxido-reductase alpha chain. Comamonas testosteroni (fragment)
C:Species: Comamonas testosteroni
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S65606
R:Schach, S.; Tshisaka, B.; Feilner, S.; Lingens, F.
A:Title: Guinoline 2-oxido-reductase and 2-oxo-1,2-dihydroguinoline 5,6-dioxygenase 1
A:Reference number: S65606; M01D:9229689; PMID:7536204
A:Accession: S65606
A:Molecule type: Protein
A:Residues: 1-11 SSWH
A:Experimental source: strain 63

Query Match: 27.4%; Score 3; DB 2; Length 11;
Best Local Similarity: 100.0%; Prod. No. 2e-03;
Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9
II
LB 9 KPR 11

RESULT 7
S23300
Probable substance P - smaller spotted catshark
C:Species: Scyliorhinus reticulatus (smaller spotted catshark, smaller spotted dogfish)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999
C:Accession: S23300
R:Wang, D.; Wang, Y.; Havel, N.; Baiment, R.J.; Conlon, J.M.
A:Title: Primary structures and biological activities of substance P-related peptide
A:Reference number: S23300; M01D:9229250; PMID:7685693

A:Accession: S12488
 A:Molecule type: protein
 A:Residues: 113 <AAU>
 A:Experimental source: brain
 A:Keywords: may play a physiological role in the recombination and gap
 A:Title: Tandem chromosomal duplications: role of REP sequences in the recombination
 A:Reference number: S12488; PMID:9184995; PMID:278927
 A:Molecule type: DNA
 A:Residues: 113 <SHY>
 A:Keywords: immunoglobulin
 A:Title: Immunoglobulin
 A:Reference number: S12488; PMID:9184995; PMID:278927
 A:Molecule type: protein
 A:Residues: 113 <AAU>
 A:Experimental source: bone marrow pre B lymphocyte
 A:Keywords: immunoglobulin

Query Match: 27.8% Score 3; DB 2; Length 13;
 Best Local Similarity: 100.0%; Pred. No. 2.3e+03;
 Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11
 DB 4 RRS 5

RESULT 11
 S03879
 6-phosphofructokinase (EC 2.7.1.11) B - rabbit (fragment)
 A:Alternative names: phosphofructokinase B
 A:Species: Oryctolagus cuniculus (domestic rabbit)
 A:Title: The sites of phosphorylation of rabbit brain phosphofructo 1 kinase by cyclo
 A:Reference number: S03879; PMID:89194250; PMID:2539199
 A:Accession: S03879
 A:Molecule type: protein
 A:Residues: 113 <VAL>
 A:Keywords: glycolysis; phosphotransferase

Query Match: 27.8% Score 3; DB 2; Length 13;
 Best Local Similarity: 100.0%; Pred. No. 2.3e+03;
 Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11
 DB 4 RRS 6

RESULT 12
 PH1586
 14 H chain VDJ region (clone P less 224) mouse (fragment)
 A:Species: Mus musculus (house mouse)
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1586; PMID:93301609; PMID:835387
 A:Accession: PH1586
 A:Molecule type: DNA
 A:Residues: 113 <LEU>
 A:Experimental source: bone marrow pre B lymphocyte
 A:Keywords: immunoglobulin

Query Match: 27.8% Score 3; DB 2; Length 13;
 Best Local Similarity: 100.0%; Pred. No. 2.3e+03;
 Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11
 DB 4 RRS 5

RESULT 13
 S12488
 argA protein Salmonella typhimurium (fragment)
 A:Species: Salmonella typhimurium

A:Accession: S12488
 A:Molecule type: protein
 A:Residues: 113 <AAU>
 A:Experimental source: brain
 A:Keywords: may play a physiological role in the recombination and gap
 A:Title: Tandem chromosomal duplications: role of REP sequences in the recombination
 A:Reference number: S12488; PMID:9184995; PMID:278927
 A:Molecule type: DNA
 A:Residues: 113 <SHY>
 A:Keywords: immunoglobulin
 A:Title: Immunoglobulin
 A:Reference number: S12488; PMID:9184995; PMID:278927
 A:Molecule type: protein
 A:Residues: 113 <AAU>
 A:Experimental source: bone marrow pre B lymphocyte
 A:Keywords: immunoglobulin

Query Match: 27.8% Score 3; DB 2; Length 13;
 Best Local Similarity: 100.0%; Pred. No. 2.3e+03;
 Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11
 DB 4 RRS 5

RESULT 11
 S03879
 6-phosphofructokinase (EC 2.7.1.11) B - rabbit (fragment)
 A:Alternative names: phosphofructokinase B
 A:Species: Oryctolagus cuniculus (domestic rabbit)
 A:Title: The sites of phosphorylation of rabbit brain phosphofructo 1 kinase by cyclo
 A:Reference number: S03879; PMID:89194250; PMID:2539199
 A:Accession: S03879
 A:Molecule type: protein
 A:Residues: 113 <VAL>
 A:Keywords: glycolysis; phosphotransferase

Query Match: 27.8% Score 3; DB 2; Length 13;
 Best Local Similarity: 100.0%; Pred. No. 2.3e+03;
 Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11
 DB 4 RRS 6

RESULT 12
 PH1586
 14 H chain VDJ region (clone P less 224) mouse (fragment)
 A:Species: Mus musculus (house mouse)
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A:Reference number: PH1586; PMID:93301609; PMID:835387
 A:Accession: PH1586
 A:Molecule type: DNA
 A:Residues: 113 <LEU>
 A:Experimental source: bone marrow pre B lymphocyte
 A:Keywords: immunoglobulin

Query Match: 27.8% Score 3; DB 2; Length 13;
 Best Local Similarity: 100.0%; Pred. No. 2.3e+03;
 Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RRS 11
 DB 4 RRS 5

RESULT 13
 S12488
 argA protein Salmonella typhimurium (fragment)
 A:Species: Salmonella typhimurium

Cross-references: S04955
 A:Title: Isolation of heparin-binding protein from bovine pituitary and characterization of its structure
 A:Reference number: S04955; MIM:14241704; PMID:14241704
 A:Accession: S04955
 A:Molecule type: protein
 A:Residues: 115
 C:Keywords: growth factor

Query Match: 27.2%, Score 2: 18.2, Length 8;
 Best Local Similarity: 100.0%; P: 0.0; M: 2.8e+05;
 Matches: 2: Conservative 0; Mismatches 0; Gaps 0;

QY 6 MKP 8
 DB 1 MKP 5

RESULT 27
 P01407
 A:Title: Isolation of heparin-binding protein from bovine pituitary and characterization of its structure
 A:Reference number: S29175
 A:Accession: S29175
 A:Molecule type: protein
 A:Residues: 115
 C:Keywords: growth factor

Query Match: 27.2%, Score 2: 18.2, Length 8;
 Best Local Similarity: 100.0%; P: 0.0; M: 2.8e+05;
 Matches: 2: Conservative 0; Mismatches 0; Gaps 0;

QY 2 ROK 4
 DB 1 ROK 5

RESULT 28
 P01407
 A:Title: Isolation of heparin-binding protein from bovine pituitary and characterization of its structure
 A:Reference number: S29175
 A:Accession: S29175
 A:Molecule type: protein
 A:Residues: 115
 C:Keywords: growth factor

Query Match: 27.2%, Score 2: 18.2, Length 8;
 Best Local Similarity: 100.0%; P: 0.0; M: 2.8e+05;
 Matches: 2: Conservative 0; Mismatches 0; Gaps 0;

QY 1 AK 2
 DB 1 AK 4

RESULT 29
 P01407
 A:Title: Isolation of heparin-binding protein from bovine pituitary and characterization of its structure
 A:Reference number: S29175
 A:Accession: S29175
 A:Molecule type: protein
 A:Residues: 115
 C:Keywords: growth factor

Query Match: 27.2%, Score 2: 18.2, Length 8;
 Best Local Similarity: 100.0%; P: 0.0; M: 2.8e+05;
 Matches: 2: Conservative 0; Mismatches 0; Gaps 0;

Cross-references: T10077
 A:Title: Isolation of heparin-binding protein from bovine pituitary and characterization of its structure
 A:Reference number: T10077; MIM:14241704; PMID:14241704
 A:Accession: T10077
 A:Molecule type: protein
 A:Residues: 115
 C:Keywords: growth factor

Query Match: 27.2%, Score 2: 18.2, Length 8;
 Best Local Similarity: 100.0%; P: 0.0; M: 2.8e+05;
 Matches: 2: Conservative 0; Mismatches 0; Gaps 0;

QY 9 RR 10
 DB 2 RR 5

RESULT 28
 P01407
 A:Title: Isolation of heparin-binding protein from bovine pituitary and characterization of its structure
 A:Reference number: T10077; MIM:14241704; PMID:14241704
 A:Accession: T10077
 A:Molecule type: protein
 A:Residues: 115
 C:Keywords: growth factor

Query Match: 27.2%, Score 2: 18.2, Length 8;
 Best Local Similarity: 100.0%; P: 0.0; M: 2.8e+05;
 Matches: 2: Conservative 0; Mismatches 0; Gaps 0;

QY 9 RR 10
 DB 6 RR 5

RESULT 29
 P01407
 A:Title: Isolation of heparin-binding protein from bovine pituitary and characterization of its structure
 A:Reference number: T10077; MIM:14241704; PMID:14241704
 A:Accession: T10077
 A:Molecule type: protein
 A:Residues: 115
 C:Keywords: growth factor

Query Match: 27.2%, Score 2: 18.2, Length 8;
 Best Local Similarity: 100.0%; P: 0.0; M: 2.8e+05;
 Matches: 2: Conservative 0; Mismatches 0; Gaps 0;

QY 9 RR 10
 DB 6 RR 5

RESULT 29
 P01407
 A:Title: Isolation of heparin-binding protein from bovine pituitary and characterization of its structure
 A:Reference number: T10077; MIM:14241704; PMID:14241704
 A:Accession: T10077
 A:Molecule type: protein
 A:Residues: 115
 C:Keywords: growth factor

Query Match: 27.2%, Score 2: 18.2, Length 8;
 Best Local Similarity: 100.0%; P: 0.0; M: 2.8e+05;
 Matches: 2: Conservative 0; Mismatches 0; Gaps 0;

QY 9 RR 10
 DB 6 RR 5

A:Status: Preliminary
A:Residue type: DNA
A:Residues: 1-8 <EV>
C:Gene: ICS
A:Gene: Flybase: P element
A:Cross-references: Flybase: FB000055

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 11

DB 3 RS 4

RESULT 36

PT0424

C:Species: Mus musculus (man)
C:Title: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-Aug-1994

C:Accession: PT0424

R:Kamada, M.; Wasserman, R.; Reichardt, S.A.; Shaner, S.; Cohen, A.; Kovata, G.
J. Exp. Med. 173, 355-407, 1991

A:Title: Preferential utilization of specific amino acids in heavy chain diversity and
A:Reference number: PT0222; M0ID:910637; PMID:159936

A:Accession: PT0424

A:Molecule type: DNA

A:Residues: 1-8 <YAW>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RR 10

DB 6 RR 7

RESULT 37

PT0630

C:Species: Mus musculus (mouse)

C:Title: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-Aug-1994

C:Accession: PT0630

R:Gartagly, R.E.; Rechrade, D.E.; Barber, W. F. J. Exp. Med.

J. Immunol. 143, 1680-1684, 1989

A:Title: Structures of histamine receptors determined by the action of acid protease

A:Reference number: A45800; M0ID:894146; PMID:254966

A:Accession: PT0630

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <CAR>

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2

DB 2 AR 3

RESULT 38

PT0618

C:Species: Mus musculus (house mouse)

C:Title: 02-Jan-1994 #sequence_revision 02-Jan-1994 #text_change 17-Mar-1999

C:Accession: PT0618

R:Kobayashi, O.A.; Campos-Torres, G.; Leder, P.

J. Exp. Med. 178, 417-429, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less

A:Reference number: PT0580; M0ID:940160; PMID:8315387

A:Accession: PT0618

A:Molecule type: DNA

A:Residues: 1-8 <EV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less

A:Reference number: PT0580; M0ID:940160; PMID:8315387

A:Accession: PT0618

A:Molecule type: DNA

A:Residues: 1-8 <EV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2

DB 2 AR 3

RESULT 39

PT0639

C:Species: Mus musculus (house mouse)

C:Title: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999

C:Accession: A54823

R:Cross, A.; Simon, L.; Cedar, H.; Axel, R.

Cell 78, 823-834, 1994

A:Title: Allelic inactivation regulates olfactory receptor gene expression.

A:Reference number: A54823; M0ID:94373818; PMID:8087849

A:Accession: A54823

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <CHE>

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RR 10

DB 4 RR 4

RESULT 40

PT0639

C:Species: Mus musculus (house mouse)

C:Title: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0639

R:Feeney, A.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have low N region

A:Reference number: PT0509; M0ID:9127601; PMID:1711558

A:Accession: PT0639

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <EE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2

DB 7 AR 8

RESULT 41

PT0691

C:Species: Mus musculus (house mouse)

C:Title: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0691

A:Title: receptor beta chain V-D-J region (154-2K) - mouse (fragment)

[illegible]

RESULT 47
 155417
 1. Species: Homo sapiens (Homo)
 2. Species: Homo sapiens (Homo)
 3. Species: Homo sapiens (Homo)
 4. Species: Homo sapiens (Homo)
 5. Species: Homo sapiens (Homo)
 6. Species: Homo sapiens (Homo)
 7. Species: Homo sapiens (Homo)
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 64. Species: Homo sapiens (Homo)
 65. Species: Homo sapiens (Homo)
 66. Species: Homo sapiens (Homo)
 67. Species: Homo sapiens (Homo)
 68. Species: Homo sapiens (Homo)
 69. Species: Homo sapiens (Homo)
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 99. Species: Homo sapiens (Homo)
 100. Species: Homo sapiens (Homo)

Query Match: 18.2% Score 21.18.2% Length 9;
 Best Local Similarity: 10.0% P-Val: 2.8e-05;
 Matches: 21 Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 QY: 8 PK 9
 DB: 11
 2 PK 3
 Search completed: September 30, 2003, 11:09:47
 Job Time: 12.4167 secs
 Query Match: 18.2% Score 21.18.2% Length 9;
 Best Local Similarity: 10.0% P-Val: 2.8e-05;
 Matches: 21 Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 QY: 8 PK 9
 DB: 11
 2 PK 3
 Search completed: September 30, 2003, 11:09:47
 Job Time: 12.4167 secs

GeneCore version 6.1.1.6
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AM protein: Protein search, using SW model

Run on: September 30, 2003, 10:07:04 : Search time 6.25 seconds
(with 1000 alignments)
82,757 Million of local queries/sec

Title: US-09-787-443-12

Perfect score: 11

Sequence: 1 AKJTKMKPRS 11

Scoring table: all20

Gap: 60.0 : Gapext: 60.0

Searches: 127863 seqs, 47026705 residues

Word size: 3

Total number of hits satisfying chosen parameters: 707

Minimum hit seq length: 8

Maximum hit seq length: 15

Post processing: testing first 500 summaries

Database: SwissProt_41.*

Prod. No. is the number of results produced by choice to give a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	EB	ID	Description
1	3	27.3	11	1	1	0.0	QZAL_MOUSE	P04744 creatinase 1
2	3	27.3	11	1	1	0.0	IKNA_GALWE	P25408 galus protein
3	3	27.3	11	1	1	0.0	IKNA_ONCMY	P25409 creatinase 1
4	3	27.3	11	1	1	0.0	IKNA_SALCA	P14444 stylolysin
5	3	27.3	15	1	1	0.0	IKNA_PANAE	P15451 panis 1and
6	3	27.3	15	1	1	0.0	IKNA_PANAE	P15451 panis 1and
7	2	18.2	8	1	1	0.0	IKNA_PANAE	P15451 panis 1and
8	2	18.2	8	1	1	0.0	IKNA_PANAE	P15451 panis 1and
9	2	18.2	8	1	1	0.0	IKNA_PANAE	P15451 panis 1and
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33	2	18.2	8	1	1	0.0	IKNA_PANAE	P15451 panis 1and

34	2	18.2	10	1	1	0.0	HPP2_BOTJA	P01022 bothrops ja
35	2	18.2	10	1	1	0.0	CATX_SHEEP	P83205 ovis aries
36	2	18.2	10	1	1	0.0	COXK_ONCMY	P80332 oncorhynch
37	2	18.2	10	1	1	0.0	COXM_RAT	P80431 rattus norv
38	2	18.2	10	1	1	0.0	COXO_RABIT	P80336 eryctolagus
39	2	18.2	10	1	1	0.0	COXQ_SHEEP	P80337 ovis aries
40	2	18.2	10	1	1	0.0	FIBB_CERS1	P14537 coratotheri
41	2	18.2	10	1	1	0.0	GON1_CHEPR	P80677 chelyosoma
42	2	18.2	10	1	1	0.0	GON1_PETMA	P04378 petromyzon
43	2	18.2	10	1	1	0.0	GON3_PETMA	P10948 petromyzon
44	2	18.2	10	1	1	0.0	LPK2_LOCM1	P1488 locusta miq
45	2	18.2	10	1	1	0.0	MP2_MCOG	P81533 microplitis
46	2	18.2	10	1	1	0.0	PVK_LOCM1	P83382 locusta miq
47	2	18.2	10	1	1	0.0	QZOB_COMTE	P80465 comamonas t
48	2	18.2	10	1	1	0.0	SLAP_BACTG	P49325 bacillus th
49	2	18.2	10	1	1	0.0	TKNB_CHICK	P19851 gallus gall
50	2	18.2	10	1	1	0.0	TKU1_UREUN	P40751 urechis uni
51	2	18.2	10	1	1	0.0	TKU2_UREUN	P40752 urechis uni
52	2	18.2	10	1	1	0.0	UPA9_HUMAN	P30095 homo sapien
53	2	18.2	10	1	1	0.0	XYNB_DICHA	P80717 dictyoglomu
54	2	18.2	10	1	1	0.0	BPP3_BOTIN	P30423 bothrops in
55	2	18.2	10	1	1	0.0	BPP4_BOTIN	P30424 bothrops in
56	2	18.2	10	1	1	0.0	BPPB_AKHA	P01021 eukistodon
57	2	18.2	10	1	1	0.0	CS15_BACSU	P81095 bacillus su
58	2	18.2	10	1	1	0.0	ESL_RAT	P56571 rattus norv
59	2	18.2	10	1	1	0.0	MHE1_KLEIN	P80580 klebsiella
60	2	18.2	10	1	1	0.0	PKC1_CARMO	P82684 carausius m
61	2	18.2	10	1	1	0.0	RR2_CONAM	P43341 conopholis
62	2	18.2	10	1	1	0.0	RS30_ONCMY	P83328 oncorhynch
63	2	18.2	10	1	1	0.0	TIN1_HOPTI	P82651 hoplobatr
64	2	18.2	10	1	1	0.0	TKN2_UREPU	P88616 uperoleia r
65	2	18.2	10	1	1	0.0	TKNA_CHICK	P19850 gallus gall
66	2	18.2	10	1	1	0.0	TKNA_HORSE	P01290 equus cabal
67	2	18.2	10	1	1	0.0	TKNA_RANCA	P22688 rana catesb
68	2	18.2	10	1	1	0.0	TKNA_RANCA	P29207 rana ridibu
69	2	18.2	10	1	1	0.0	TKND_RANCA	P22691 rana catesb
70	2	18.2	10	1	1	0.0	UX52_YEAST	P99013 saccharomyc
71	2	18.2	10	1	1	0.0	CXAL_CONIM	P50983 conus imper
72	2	18.2	10	1	1	0.0	FAR7_PENNO	P83322 penaeus mon
73	2	18.2	10	1	1	0.0	GHAR_RANRU	P40754 rana rugosa
74	2	18.2	10	1	1	0.0	LMT1_LOCM1	P22395 locusta miq
75	2	18.2	10	1	1	0.0	NO40_LOTJA	O22426 lotus japon
76	2	18.2	10	1	1	0.0	NO40_SESQU	O24369 sesbania ro
77	2	18.2	10	1	1	0.0	PKK4_PERAM	P82619 periplaneta
78	2	18.2	10	1	1	0.0	PKK2_PERAM	P82690 periplaneta
79	2	18.2	10	1	1	0.0	PKK2_PERAM	P81555 periplaneta
80	2	18.2	10	1	1	0.0	RS19_GLYEP	O46490 clover yell
81	2	18.2	10	1	1	0.0	RS19_TORHP	O56251 tomato big
82	2	18.2	10	1	1	0.0	IKN1_KASMA	P88613 kassina mac
83	2	18.2	10	1	1	0.0	V14K_WSSV	P82006 white spot
84	2	18.2	10	1	1	0.0	ADFB_TENNO	P83109 tenebrio mo
85	2	18.2	10	1	1	0.0	AH4_PROUSE	P29262 prunus sero
86	2	18.2	10	1	1	0.0	BP37_LEUMA	P81754 leucophaea
87	2	18.2	10	1	1	0.0	HPP1_BOTJA	P01020 bothrops ja
88	2	18.2	10	1	1	0.0	CH6G_CANFA	P49818 canis fami
89	2	18.2	10	1	1	0.0	FIBB_HYLLA	P14472 hylabates l
90	2	18.2	10	1	1	0.0	FIBB_PABIT	P14478 eryctolagus
91	2	18.2	10	1	1	0.0	LMN1_LOCM1	P38496 locusta miq
92	2	18.2	10	1	1	0.0	LM14_LOCM1	P41490 locusta miq
93	2	18.2	10	1	1	0.0	MIA_ANCCA	P41589 anolis caro
94	2	18.2	10	1	1	0.0	MIA_CAMOR	P01198 camelus dro
95	2	18.2	10	1	1	0.0	NEUT_BUPMA	P81796 bufo marinu
96	2	18.2	10	1	1	0.0	NEUT_CAVPO	P12560 cavia porce
97	2	18.2	10	1	1	0.0	NEUT_CHICK	P13724 gallus gall
98	2	18.2	10	1	1	0.0	NEUT_RANTE	P41536 gallus temp
99	2	18.2	10	1	1	0.0	NEUT_TRIVU	P31745 trichosurus
100	2	18.2	10	1	1	0.0	NO40_PEA	P55959 pisum sativ
101	2	18.2	10	1	1	0.0	NO40_VICSA	P55961 vicia sativ
102	2	18.2	10	1	1	0.0	ORCK_ORCLT	P37086 orconectes
103	2	18.2	10	1	1	0.0	PSAJ_PEA	P17229 pisum sativ
104	2	18.2	10	1	1	0.0	SA2A_ONCMY	P82238 oncorhynch
105	2	18.2	10	1	1	0.0	SA2B_ONCMY	P82239 oncorhynch
106	2	18.2	10	1	1	0.0	TY11_PHYRO	P04096 phyllomedus

107	2	18.2	14	1	CAL2_FASHE	P83342 tasgetola he	1	9.1	8	1	FAR4_MACRS	P83275 macrobrachi
108	2	18.2	14	1	EPIU_PANEA	P83435 canis fam.1	1	9.1	8	1	FAR4_HORAM	P41486 homarus ame
109	2	18.2	14	1	HV14_PIG	P83355 sus scrofa	1	9.1	8	1	FAR4_MACRS	P41487 homarus ame
110	2	18.2	14	1	JAV1_KANIA	P83305 rana japoni	1	9.1	8	1	FAR4_CALVO	P83277 macrobrachi
111	2	18.2	14	1	LPW_CITFR	P83050 catibobacter	1	9.1	8	1	FUS3_FUSSO	P41863 calliphora
112	2	18.2	14	1	LPW_FOULI	P83054 escherichia	1	9.1	8	1	GLUK_HUMAN	P81010 fusarium so
113	2	18.2	14	1	LPW_RHIME	P18864 rhizoctonia m	1	9.1	8	1	HTF1_PERAM	P02729 homo sapien
114	2	18.2	14	1	MARI_ALESP	P29599 acromedusa	1	9.1	8	1	HTF2_PERAM	P04548 periplaneta
115	2	18.2	14	1	PKK6_TFRAM	P45693 periplaneta	1	9.1	8	1	HTF2_PENMO	P04549 periplaneta
116	2	18.2	14	1	RSD1_GLOBO	P34428 clostridium	1	9.1	8	1	LOCK1_LEUMA	P25419 tenebrio mo
117	2	18.2	14	1	RSD1_GLOBO	P44878 caledonia w.c	1	9.1	8	1	LOCK1_LEUMA	P21140 leucophaea
118	2	18.2	14	1	RSD1_PEPAP	P44878 caledonia w.c	1	9.1	8	1	LOCK1_LEUMA	P21141 leucophaea
119	2	18.2	14	1	SMS1_PYCSO	P20763 myxococcus	1	9.1	8	1	LOCK1_LEUMA	P21142 leucophaea
120	2	18.2	14	1	SMS1_PYCSO	P33866 alibonita m	1	9.1	8	1	LOCK1_LEUMA	P21143 leucophaea
121	2	18.2	14	1	TA3_HVIM2	P12589 macula leu.2	1	9.1	8	1	LOCK5_LEUMA	P19987 leucophaea
122	2	18.2	14	1	TA3_HVIM2	P12589 macula leu.2	1	9.1	8	1	LOCK5_LEUMA	P19988 leucophaea
123	2	18.2	14	1	ACT1_FUNPS	P81095 pectus fides	1	9.1	8	1	LOCK6_LEUMA	P19989 leucophaea
124	2	18.2	14	1	AFIL1_MALGA	P83341 malva pavi1	1	9.1	8	1	LOCK6_LEUMA	P19990 leucophaea
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171	2	18.2	14	1	AFIL1_MALGA	P83341 malva pavi1	1	9.1	8	1	LOCK6_LEUMA	P19990 leucophaea
172	2	18.2	14	1	AFIL1_MALGA	P83341 malva pavi1	1	9.1	8	1	LOCK6_LEUMA	P19990 leucophaea
173	2	18.2	14	1	AFIL1_MALGA	P83341 malva pavi1	1	9.1	8	1	LOCK6_LEUMA	P19990 leucophaea
174	2	18.2	14	1	AFIL1_MALGA	P83341 malva pavi1	1	9.1	8	1	LOCK6_LEUMA	P19990 leucophaea
175	2	18.2	14	1	AFIL1_MALGA	P83341 malva pavi1	1	9.1	8	1	LOCK6_LEUMA	P19990 leucophaea
176	2	18.2	14	1	AFIL1_MALGA	P83341 malva pavi1	1	9.1	8	1	LOCK6_LEUMA	P19990 leucophaea
177	2	18.2	14	1	AFIL1_MALGA	P83341 malva pavi1	1	9.1	8	1	LOCK6_LEUMA	P19990 leucophaea
178	2	18.2	14	1	AFIL1_MALGA	P83341 malva pavi1	1	9.1	8	1	LOCK6_LEUMA	P19990 leucophaea
179	2	18.2	14	1	AFIL1_MALGA	P83341 malva pavi1	1	9.1	8	1	LOCK6_LEUMA	P19990 leucophaea

[illegible]

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27 7 KPR 9
28 111
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RESULT 4
TKNA:CALMW STANDARD: REF: 11 AA
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E1 01-DEC-1992 (Ref. 24, Created)
E2 01-DEC-1992 (Ref. 24, Last sequence update)
E3 15-SEP-2003 (Ref. 42, Last annotation update)
E4 SUBSTANCE P
E5 GADUS MURTON (Atlantic cod)
E6 Eukaryotic Metazoa: Chordata: Vertebrata: Euteleostomi:
E7 Actinopterygii: Neopterygii: Teleostei: Euteleostei:
E8 Actinopterygii: Paracanthopterygii: Gadiformes: Gadidae: Gadus
E9 NCB: TaxID:6049;
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